

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:28:30 ; Search time 12.3488 Seconds  
(without alignments)  
140.178 Million cell updates/sec

Title: US-09-641-801-21

Perfect score: 18

Sequence: 1 LOPEIMGVFKVKTWPK 18

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

PIR 76: \*  
1: Pirl: \*  
2: pirl2: \*  
3: pirl3: \*  
4: pirl4: \*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	22.2	9	2	PC7073
2	4	22.2	15	2	PA0105
3	3	16.7	6	2	I49808
4	3	16.7	6	2	I65546
5	3	16.7	8	2	G33098
6	3	16.7	8	2	A61597
7	3	16.7	8	2	A35180
8	3	16.7	8	2	S53008
9	3	16.7	9	2	S77984
10	3	16.7	10	1	XASNPC
11	3	16.7	10	1	RHAQ1
12	3	16.7	10	2	PT0322
13	3	16.7	10	2	B61218
14	3	16.7	10	2	S74147
15	3	16.7	11	2	A33917
16	3	16.7	11	2	PC4267
17	3	16.7	11	2	S78765
18	3	16.7	11	2	H84082
19	3	16.7	12	2	S07206
20	3	16.7	12	2	C39109
21	3	16.7	12	2	A60757
22	3	16.7	12	2	S36899
23	3	16.7	12	2	A35585
24	3	16.7	12	2	PA0098
25	3	16.7	12	2	A61503
26	3	16.7	12	2	D20907
27	3	16.7	12	2	PQ0786
28	3	16.7	13	1	XAV19B
29	3	16.7	13	2	S39413

30	3	16.7	13	2	H64124
31	3	16.7	13	2	PA0023
32	3	16.7	13	2	H44957
33	3	16.7	14	2	PC2373
34	3	16.7	14	2	PS0371
35	3	16.7	14	2	B56863
36	3	16.7	14	2	PA0015
37	3	16.7	14	2	A61002
38	3	16.7	14	2	A61308
39	3	16.7	14	2	B61308
40	3	16.7	14	2	S39111
41	3	16.7	14	2	S00150
42	3	16.7	14	2	PH1625
43	3	16.7	14	2	PH1627
44	3	16.7	14	2	PH1594
45	3	16.7	14	2	S21747
46	3	16.7	14	2	PA0044
47	3	16.7	15	2	S26791
48	3	16.7	15	2	PA0034
49	3	16.7	15	2	PA0014
50	3	16.7	15	2	PN0173
51	3	16.7	15	2	PA0059
52	3	16.7	15	2	PA0106
53	3	16.7	15	2	PA0080
54	3	16.7	15	2	S10388
55	3	16.7	15	2	S10386
56	3	16.7	15	2	B41436
57	3	16.7	15	2	A32971
58	3	16.7	15	2	FN0662
59	3	16.7	15	2	PH1613
60	3	16.7	15	4	I38032
61	3	16.7	16	2	S03532
62	3	16.7	16	2	D49021
63	3	16.7	16	2	S42237
64	3	16.7	16	2	B44896
65	3	16.7	16	2	S65709
66	3	16.7	16	2	C61414
67	3	16.7	17	2	PN0587
68	3	16.7	17	2	S03531
69	3	16.7	17	2	S50901
70	3	16.7	17	2	A48179
71	3	16.7	17	2	B61414
72	3	16.7	17	2	S59512
73	3	16.7	17	2	S69164
74	3	16.7	17	2	PD0005
75	3	16.7	18	1	DRUPPD
76	3	16.7	18	2	I52651
77	3	16.7	18	2	A25941
78	3	16.7	18	2	A56871
79	3	16.7	18	2	PN0149
80	3	16.7	18	2	I40062
81	3	16.7	18	2	A45590
82	3	16.7	18	2	A32917
83	3	16.7	18	2	G84114
84	3	16.7	18	4	S40664
85	3	16.7	19	2	C21182
86	3	16.7	19	2	S19532
87	3	16.7	19	2	S19813
88	3	16.7	19	2	B46592
89	3	16.7	19	2	S69166
90	3	16.7	20	2	A60728
91	3	16.7	20	2	S13274
92	3	16.7	20	2	S46488
93	3	16.7	20	2	C20554
94	3	16.7	20	2	H49034
95	3	16.7	20	2	S33001
96	3	16.7	20	2	S59494
97	3	16.7	20	2	S18582
98	3	16.7	20	2	T50757
99	3	16.7	20	2	A85645
100	3	16.7	20	2	A05310

hypothetical prote  
protein QA300052 -  
protein P18 - comm  
probable IMP dehyd  
hypothetical prote  
photosystem I reac  
seed storage prote  
photosystem II oxy  
hemocyanin chain 2  
hemocyanin chain 4  
Ig heavy chain V r  
ovostatin - duck (  
Ig H chain V-D-J r  
Ig H chain V-D-J r  
Ig H chain V-D-J r  
glutamate dehydrog  
NADH2 dehydrogenas  
Ig heavy chain V r  
protein QA300024 -  
seed storage prote  
seed storage prote  
protein QF200021 -  
protein QF200076 -  
translation elonga  
Ig heavy chain J r  
Ig heavy chain J r  
ovostatin - green  
heparin-binding le  
dystrophin-associa  
Ig H chain V-D-J r  
hypothetical MN1/T  
Ig heavy chain J r  
Ig heavy chain J7  
hypothetical prote  
heat shock protein  
major allergen Myr  
chymotrypsin [BC 3  
tyrosine 3-monooxy  
Ig heavy chain J5  
chlorophyll a/b-bi  
methane monooxygen  
chymotrypsin [BC 3  
probable integrin  
ferredoxin a1 - Ja  
very-high-density  
pigment-dispersing  
brain-derived neur  
Ig heavy chain J-H  
retinol-binding pr  
beta-Gliadine 13 -  
shikimate 5-dehydr  
beta-pigment-dispe  
protein phosphatas  
hypothetical prote  
INS150A/INS150B mu  
4K prothoracicotro  
globin - polychaet  
globin - polychaet  
lactase-phlorizin  
ferredoxin b - Jap  
cytochrome P450 3A  
cytochrome [2Fe-2S  
peptidylprolyl iso  
hemocyanin subunit  
nuclear antigen EB  
hypothetical prote  
formate dehydrogen  
hypothetical prote  
puik protein [lmpo  
Amino terminal of  
apolipoprotein E -

## ALIGNMENTS

RESULT 1  
PC7073  
ubiquinol-cytochrome-c reductase (EC 1.10.2.2) core protein II - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 03-Jun-2002  
C;Accession: PC7073  
R;Tsugita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Matsui, T.; Watanabe, Y.;  
Electrophoresis 21, 1853-1871, 2000  
A;Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles of b

A;Reference number: PC7072  
A;Accession: PC7073  
A;Molecule type: protein  
A;Residues: 1-9 <TSU>  
C;Keywords: brain; core protein; oxidoreductase

Query Match 22.2%; Score 4; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0;

Qy 9 PKVK 12  
|||  
Db 6 PKVK 9

RESULT 2  
PA0105  
heat shock protein dnaJ type - fungus (Fusarium sporotrichioides) (fragment)  
C;Species: Fusarium sporotrichioides  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001  
C;Accession: PA0105  
R;Chow, L.P.; Fukaya, N.; Sugitara, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.  
submitted to JIPID, October 1994  
A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich

A;Reference number: PA0051  
A;Accession: PA0105  
A;Molecule type: protein  
A;Residues: 1-15 <CHO>  
C;Keywords: heat shock; stress-induced protein

Query Match 22.2%; Score 4; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0;

Qy 11 VKET 14  
|||  
Db 1 VKET 4

RESULT 3  
I49808  
D-Sp2.5 region - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 05-Nov-1999  
C;Accession: I49808  
R;Kurosawa, Y.; Toneygawa, S.  
J. Exp. Med. 155, 201-218, 1982  
A;Title: Organization, structure, and assembly of immunoglobulin heavy chain diversity D  
A;Reference number: I49808; PMID:6798155  
A;Accession: I49808  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-6 <RES>  
A;Cross-references: GB:J00432; NID:G194370; PIDN:AAA37904.1; PID:G450452  
C;Genetics:  
A;Gene: Igh

Query Match 16.7%; Score 3; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0;

Qy 14 TMV 16  
|||  
Db 2 TMV 4

RESULT 4  
I65546  
MHC H2-L antigen - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 05-Nov-1999  
C;Accession: I65546  
R;Kimura, A.; Israel, A.; Le Bail, O.; Kourilsky, P.  
Cell 44, 261-272, 1986  
A;Title: Detailed analysis of the mouse H-2Kb promoter: Enhancer-like sequences and th  
A;Reference number: I52778; PMID:86106202; PMID:3510743  
A;Accession: I65546  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-6 <RES>  
A;Cross-references: GB:M12483; NID:G199565; PIDN:AAA39663.1; PID:9554234

Query Match 16.7%; Score 3; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0;

Qy 15 MVP 17  
|||  
Db 1 MVP 3

RESULT 5  
G33098  
205K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)  
C;Species: Plasmodium falciparum  
C;Date: 24-Aug-1990 #sequence\_revision 24-Aug-1990 #text\_change 09-Jun-2000  
C;Accession: G33098  
R;Nichols, J.H.; Hager, L.P.  
submitted to the Protein Sequence Database, May 1990  
A;Reference number: A33098  
A;Accession: G33098  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-8 <NIC>

Query Match 16.7%; Score 3; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0;

Qy 7 GVP 9  
|||  
Db 1 GVP 3

RESULT 6  
A61597  
cytochrome P450 AL-1 - rat (fragment)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 06-Jan-1995  
C;Accession: A61597  
R;Shimeno, H.; Toda, A.; Ogata, S.; Nagamatsu, A.  
Drug Metab. Dispos. 19, 291-297, 1991  
A;Title: Purification and aminopyrine monooxygenase activity of liver microsomal cyto  
A;Reference number: A61597; PMID:91292910; PMID:1676625  
A;Accession: A61597  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-8 <SHI>

Query Match 16.7%; Score 3; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0;

Qy 11 VKE 13



Db 5 VKE 7

RESULT 7  
A35180  
neutral proteinase (EC 3.4.-.-), calcium-activated - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 10-Aug-1990 #sequence\_revision 10-Aug-1990 #text\_change 21-Mar-1996  
C:Accession: A35180  
R;Yoshihara, Y.; Ueda, H.; Fujii, N.; Shide, A.; Vajima, H.; Satoh, M.  
J. Biol. Chem. 265, 5809-5815, 1990  
A:Title: Purification of a novel type of calcium-activated neutral protease from rat brain  
A:Reference number: A35180; MUID:90202830; PMID:2318836  
A:Accession: A35180  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-8 <VOS>  
C:Keywords: hydrolase

Query Match 16.7%; Score 3; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GVP 9  
DB 6 GVP 8

RESULT 8  
S53008  
citrate synthase - cucurbit  
C:Species: Cucurbita sp. (cucurbit)  
C:Date: 14-Jul-1995 #sequence\_revision 03-Nov-1995 #text\_change 17-Mar-1999  
C:Accession: S53008  
R;Kato, A.; Hayashi, M.; Mori, H.; Nishimura, M.  
Plant Mol. Biol. 27, 377-390, 1995  
A:Title: Molecular characterization of a glyoxysomal citrate synthase that is synthesized in  
A:Reference number: S53007; MUID:95195164; PMID:7888626  
A:Accession: S53008  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-8 <KAT>

Query Match 16.7%; Score 3; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TMV 16  
DB 4 TMV 6

RESULT 9  
S77984  
cytochrome-c oxidase (EC 1.9.3.1) chain V1a - bigeye tuna (fragment)  
C:Species: Thunnus obesus (bigeye tuna)  
C:Date: 17-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 30-Jan-1998  
C:Accession: S77984  
R;Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lottspeich, F.; Kadenbach, B.  
submitted to the Protein Sequence Database, June 1997  
A:Reference number: S77980  
A:Accession: S77984  
A:Molecule type: protein  
A:Residues: 1-9 <ARN>  
A:Experimental source: heart  
C:Genetics:  
A:Genome: nuclear  
C:Function:  
A:Pathway: oxidative phosphorylation; respiratory chain  
C:Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane

Query Match 16.7%; Score 3; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPE 4  
DB 3 QPE 5

RESULT 10  
XASNPC  
angiotensin-converting enzyme inhibitor - aspic viper  
C:Species: Vipera aspis (aspic viper)  
C:Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 08-Dec-1995  
C:Accession: A60377  
R;Komori, Y.; Sugihara, H.  
Int. J. Biochem. 22, 767-771, 1990  
A:Title: Characterization of a new inhibitor for angiotensin converting enzyme from tilapia  
A:Reference number: A60377; MUID:90382616; PMID:2169439  
A:Accession: A60377  
A:Molecule type: protein  
A:Residues: 1-10 <KOM>  
C:Superfamily: bradykinin-potentiating peptide  
C:Keywords: angiotensin-converting enzyme inhibitor; pyroglutamic acid  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 16.7%; Score 3; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKV 11  
DB 6 PKV 8

RESULT 11  
RHAQ1  
gonadoliberin I - American alligator  
N:Alternate names: gonadotropin-releasing hormone I  
C:Species: Alligator mississippiensis (American alligator)  
C:Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 18-Mar-1997  
C:Accession: A60066  
R;Lovejoy, D.A.; Fischer, W.H.; Parker, D.B.; McRory, J.E.; Park, M.; Lance, V.; Swan: Regul. Pept. 33, 105-116, 1991  
A:Title: Primary structure of two forms of gonadotropin-releasing hormone from brains  
A:Reference number: A60066; MUID:91352338; PMID:1882082  
A:Accession: A60066  
A:Molecule type: protein  
A:Residues: 1-10 <LOV>  
C:Superfamily: gonadoliberin  
C:Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 16.7%; Score 3; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQP 3  
DB 7 LQP 9

RESULT 12  
PT0322  
Ig heavy chain CRD3 region (clone J2-106A) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C:Accession: PT0322  
R;Yanada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and  
A:Reference number: PT0222; MUID:91108337; PMID:1899102  
A:Accession: PT0322

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A;Molecule type: DNA  
A;Residues: 1-10 <YAM>  
A;Experimental source: B lymphocyte  
C;Keywords: heterotetramer; immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 MGX 8  
|||  
DB 8 MGX 10

RESULT 13  
B61218  
alpha-gliadin 6Ha - grass (Haynaldia villosa) (fragment)  
C;Species: Haynaldia villosa, Dasypyrum villosum  
C;Date: 19-Mar-1997 #sequence\_revision 19-Dec-1997 #text\_change 17-Mar-1999  
C;Accession: B61218  
R;Shewry, P.R.; Sabelli, P.A.; Parmar, S.; Lafandra, D.  
Biochem. Genet. 29, 207-211, 1991  
A;Title: alpha-type prolamins are encoded by genes on chromosomes 4Ha and 6Ha of Haynaldia villosa  
A;Reference number: A61218; MUID:91515394; PMID:1859356  
A;Accession: B61218  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-10 <SHE>  
C;Keywords: seed; storage protein

Query Match 16.7%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQP 3  
|||  
DB 8 LQP 10

RESULT 14  
S74147  
glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - pig (fragment)  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 03-Jun-2002  
C;Accession: S74147  
R;Fukuda, A.; Osawa, T.; Hitomi, K.; Uchida, K.  
Arch. Biochem. Biophys. 333, 419-426, 1996  
A;Title: 4-Hydroxy-2-nonenal cytotoxicity in renal proximal tubular cells: protein modification  
A;Reference number: S74147; MUID:96404942; PMID:8809082  
A;Accession: S74147  
A;Molecule type: protein  
A;Residues: 1-10 <FUK>  
A;Experimental source: LLC-PK1 cells (renal tubular epithelial cells)  
C;Keywords: NAD; oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KVK 12  
|||  
DB 2 KVK 4

RESULT 15  
A33917  
dihydroorotase (EC 3.5.2.3) - Chinese hamster (fragment)  
C;Species: Cricetus griseus (Chinese hamster)  
C;Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 07-Nov-1997  
C;Accession: A33917  
R;Simmer, J.P.; Kelly, R.E.; Scully, J.L.; Grayson, D.R.; Rinker Jr., A.G.; Bergh, S.T.;  
Proc. Natl. Acad. Sci. U.S.A. 86, 4382-4386, 1989  
A;Title: Mammalian aspartate transcarbamylase (ATCase): sequence of the ATCase domain an

A;Reference number: A33917; MUID:89282776; PMID:2543974  
A;Accession: A33917  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-11 <SIM>  
A;Cross-references: GB:M23652  
C;Superfamily: rudimentary enzyme; aspartate/ornithine carbamoyltransferase homology;  
arabamoyl-phosphate synthase (glutamine-hydrolyzing) large chain homology; carbamoyl-p;  
C;Keywords: hydrolase

Query Match 16.7%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KVK 12  
|||  
DB 5 KVK 7

RESULT 16  
PC4267  
ribosomal protein L12.1 - rice (fragment)  
C;Species: Oryza sativa (rice)  
C;Date: 28-May-1997 #sequence\_revision 18-Jul-1997 #text\_change 18-Jul-1997  
C;Accession: PC4267  
R;Kawakami, T.; Kamo, M.; Chen, M.C.; Tsugita, A.  
submitted to JIPID, April, 1997  
A;Reference number: PC4267  
A;Accession: PC4267  
A;Molecule type: protein  
A;Residues: 1-11 <KAM>  
A;Experimental source: strain Japonica Nihonbare

Query Match 16.7%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKV 11  
|||  
DB 7 PKV 9

RESULT 17  
S78765  
ribosomal protein MRP-S24, mitochondrial - bovine (fragment)  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
C;Accession: S78765  
R;Graack, H.R.  
submitted to the Protein Sequence Database, July 1999  
A;Reference number: S78760  
A;Accession: S78765  
A;Molecule type: protein  
A;Residues: 1-11 <GRA>  
C;Keywords: mitochondrion  
F;1-11/Product: ribosomal protein MRP-S24 (fragment) #status experimental <MAT>

Query Match 16.7%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VPK 10  
|||  
DB 5 VPK 7

RESULT 18  
H84082  
hypothetical protein BH3464 [imported] - Bacillus halodurans (strain C-125)  
C;Species: Bacillus halodurans  
C;Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001  
C;Accession: H84082  
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; F

Nucleic Acids Res. 28, 4317-4331, 2000  
 A>Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and  
 A;Reference number: A83650; MUID:20512582; PMID:11058132  
 A;Accession: H84082  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-11 <STO>  
 A;Cross-references: GB:AP001518; GB:BA000004; NID:G10175792; PIDN:BAB07183.1; GSPDB:GN00  
 A;Experimental source: strain C-125  
 C;Genetics:  
 A;Gene: BH3464

Query Match 16.7%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3e+03; Indels 0; Gaps 0;  
 Matches 3; Conservative 0; Mismatches 0;

QY 11 VKE 13  
 ||||  
 Db 3 VKE 5

RESULT 19  
 S07206  
 kassinin - Senegal running frog  
 C;Species: *Kassina senegalensis* (Senegal running frog)  
 C;Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 02-Sep-2000  
 C;Accession: S07206  
 R;Anastasi, A.; Montecucchi, P.; Erspamer, V.; Visser, J.  
 Experientia 33, 857-858, 1977  
 A>Title: Amino acid composition and sequence of kassinin, a tachykinin dodecapeptide fro  
 A;Reference number: S07206; MUID:77246385; PMID:891753  
 A;Accession: S07206  
 A;Molecule type: protein  
 A;Residues: 1-12 <ANA>  
 C;Superfamily: unassigned animal peptides  
 C;Keywords: amidated carboxyl end  
 F;12/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 16.7%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VPK 10  
 ||||  
 Db 2 VPK 4

RESULT 20  
 C39109  
 hypothetical 1.2K protein - hepatitis C virus  
 N;Alternate names: hypothetical protein 3  
 C;Species: hepatitis C virus  
 C;Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 07-May-1999  
 C;Accession: C39109; JQ1586  
 R;Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Tekamp  
 Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991  
 A>Title: Characterization of the terminal regions of hepatitis C viral RNA: identification  
 A;Reference number: A39109; MUID:91156678; PMID:1705704  
 A;Accession: C39109  
 A;Status: not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 1-12 <HAN>  
 A;Cross-references: GB:M58406  
 R;Kumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.  
 J. Gen. Virol. 73, 1521-1525, 1992

A>Title: Cloning and sequencing of the structural region and expression of putative core  
 A;Reference number: JQ1584; MUID:92300349; PMID:11318944  
 A;Accession: JQ1586  
 A;Molecule type: genomic RNA  
 A;Residues: 1-12 <KUM>  
 A;Experimental source: strain U.K.

Query Match 16.7%; Score 3; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 GVP 9  
 ||||  
 Db 6 GVP 8

RESULT 21  
 A60757  
 enterotoxin C-1 - *Staphylococcus aureus* (fragments)  
 C;Species: *Staphylococcus aureus*  
 C;Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 30-Sep-1993  
 C;Accession: A60757  
 R;Bohach, G.A.; Handley, J.P.; Schlievert, P.M.  
 Infect. Immun. 57, 23-28, 1989  
 A>Title: Biological and immunological properties of the carboxyl terminus of staphyl  
 A;Reference number: A60757; MUID:89079292; PMID:2909489  
 A;Accession: A60757  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-12 <BOH>

Query Match 16.7%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KVK 12  
 ||||  
 Db 4 KVK 6

RESULT 22  
 S36899  
 ribosomal protein S6 - *Mycobacterium bovis* (fragment)  
 C;Species: *Mycobacterium bovis*  
 C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 13-Jan-1995  
 C;Accession: S36899  
 R;Ohara, N.; Kimura, M.; Higashi, Y.; Yamada, T.  
 FEBS Lett. 331, 9-14, 1993  
 A>Title: Isolation and amino acid sequence of the 30S ribosomal protein S19 from *Mycc*  
 A;Reference number: S36887; MUID:94009653; PMID:8405418  
 A;Accession: S36899  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-12 <OHA>  
 C;Keywords: protein biosynthesis; ribosome

Query Match 16.7%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EIM 6  
 ||||  
 Db 5 EIM 7

RESULT 23  
 A35585  
 cytokinin-binding factor 1 - durum wheat  
 C;Species: *Triticum durum* (durum wheat)  
 C;Date: 21-Sep-1990 #sequence\_revision 21-Sep-1990 #text\_change 30-Sep-1993  
 C;Accession: A35585  
 R;Brinegar, A.C.; Cooper, G.; Stevens, A.; Hauer, C.R.; Shabanowitz, J.; Hunt, D.F.;  
 Proc. Natl. Acad. Sci. U.S.A. 85, 5927-5931, 1988  
 A>Title: Characterization of a benzyladenine binding-site peptide isolated from a whe  
 by mass spectrometry; MUID:88320357; PMID:3413067  
 A;Reference number: A35585  
 A;Accession: A35585  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-12 <BRI>

Query Match 16.7%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQP 3  
 |||  
 Db 3 LQP 5

## RESULT 24

PA0098  
 ribosomal protein S3 - fungus (Fusarium sporotrichoides) (fragment)  
 C:Species: Fusarium sporotrichoides  
 C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001  
 C:Accession: PA0098  
 R:Chow, L.P.; Fukaya, N.; Sugiyama, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.  
 A:Submitted to JIPID, October 1994  
 A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich  
 A:Reference number: PA0051  
 A:Accession: PA0098  
 A:Molecule type: protein  
 A:Residues: 1-12 <CHO>

Query Match 16.7%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VPK 10  
 |||  
 Db 6 VPK 8

## RESULT 25

AG1503  
 sterol carrier protein-2-like protein - chicken (fragment)  
 C:Species: Gallus gallus (chicken)  
 C>Date: 15-Oct-1994 #sequence\_revision 15-Oct-1994 #text\_change 11-May-2000  
 C:Accession: AG1503  
 R:Reinhart, M.P.; Avart, S.J.; Foglia, T.  
 Comp. Biochem. Physiol. B 100, 243-248, 1991  
 A:Title: Purification, characterization and comparison with mammalian SCP-2 of a chicken  
 A:Reference number: AG1503; PMID:92191564; PMID:1799965  
 A:Accession: AG1503  
 A>Status: Preliminary  
 A:Molecule type: protein  
 A:Residues: 1-12 <REI>

Query Match 16.7%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKV 11  
 |||  
 Db 6 PKV 8

## RESULT 26

D20907  
 Ig kappa-1 chain J4 segment (b95 allotype) - rabbit  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C>Date: 10-Aug-1990 #sequence\_revision 10-Aug-1990 #text\_change 05-Nov-1999  
 C:Accession: D20907; D53275  
 R:Emorine, L.; Max, E.E.  
 Nucleic Acids Res. 11, 8877-8890, 1983  
 A:Title: Structural analysis of a rabbit immunoglobulin kappa2 J-C locus reveals multiple  
 A:Reference number: A20907; PMID:84169523; PMID:6324107  
 A:Accession: D20907  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-12 <EMO>  
 A:Cross-references: GB:X00231; NID:q1577; PIDN:CAA25049.1; PID:e8275; PID:q1364234  
 R:Ayadi, H.; Marche, P.N.; Cazenave, P.A.  
 Immunogenetics 34, 201-207, 1991

A:Title: Evolution of the rabbit immunoglobulin kappa chain genes.

A:Reference number: A53275; PMID:91372868; PMID:1909995

A:Accession: D53275

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-12 <AYA>

A:Note: sequence extracted from NCBI backbone (NCBIN:56069, NCBIP:56166)

C:Comment: This J4 segment may not be functional because of a short space between the

C:Keywords: heterotetramer; immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TMV 16  
 |||  
 Db 7 TMV 9

## RESULT 27

PQ0786  
 NADH2 dehydrogenase (EC 1.6.99.3) 26K chain - fava bean mitochondrion (fragment)  
 N:Alternate names: complex I 26K chain; NADH-ubiquinone reductase 26K chain  
 C:Species: mitochondrion Vicia faba (fava bean)  
 C>Date: 03-May-1994 #sequence\_revision 07-Oct-1994 #text\_change 03-Jun-2002  
 C:Accession: PQ0786  
 R:Leterme, S.; Boutry, M.  
 Plant Physiol. 102, 435-443, 1993  
 A:Title: Purification and preliminary characterization of mitochondrial complex I (N

A:Reference number: PQ0775; PMID:94151437; PMID:8108509

A:Accession: PQ0786

A:Molecule type: protein

A:Residues: 1-12 <LET>

C:Comment: Complex I, mitochondrial NADH-ubiquinone reductase, is the first of the

ranging from 5K to 75K.

C:Comment: This enzyme catalyzes electron transfer from endogenous NADH to ubiquinon

C:Genetics:

A:Genome: mitochondrion

C:Keywords: electron transfer; mitochondrion; oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GVP 9  
 |||  
 Db 3 GVP 5

## RESULT 28

XAV19B  
 angiotensin-converting enzyme inhibitor V-9 - jararaca  
 C:Species: Bothrops jararaca (jararaca)  
 C>Date: 13-Jul-1981 #sequence\_revision 13-Jul-1981 #text\_change 08-Dec-1995  
 C:Accession: A01253  
 R:Ondetti, M.A.; Williams, N.J.; Sabo, E.F.; Pluscec, J.; Weaver, E.R.; Kocoy, O.  
 Biochemistry 10, 4033-4039, 1971  
 A:Title: Angiotensin-converting enzyme inhibitors from the venom of Bothrops jararac  
 A:Reference number: A90356; PMID:72118526; PMID:4334402  
 A:Accession: A01253  
 A:Molecule type: protein  
 A:Residues: 1-13 <OND>

A:Note: the structure of the peptide was confirmed by synthesis

C:Comment: This peptide also potentiates bradykinin by inhibiting the kinases that i

C:Superfamily: bradykinin-potentiating peptide

C:Keywords: angiotensin-converting enzyme inhibitor; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 16.7%; Score 3; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 3.5e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PEI 5

```

Db          |||
           9 PEI 11

RESULT 29
S39413
tubulin beta chain - turkey (fragment)
C:Species: Meleagris gallopavo (common turkey)
C>Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 07-May-1999
C:Accession: S39413
R:Ruediger, M.; Weber, K.
Eur. J. Biochem. 218, 107-116, 1993
A:Title: Characterization of the post-translational modifications in tubulin from the ma
A:Reference number: S39412; MUID:94062821; PMID:8243458
A:Accession: S39413
A:Molecule type: protein
A:Residues: 1-13 <RUE>
C:Superfamily: tubulin
C:Keywords: heterodimer; microtubule

Query Match          16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          12 KET 14
           |||
           5 KET 7
Db

RESULT 32
H44957
protein p18 - common tobacco (cv. Samsun NN) (fragment)
C:Species: Nicotiana tabacum (common tobacco)
C>Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 30-Sep-1993
C:Accession: H44957
R:Takeda, S.; Sato, F.; Ida, K.; Yamada, Y.
Plant Cell Physiol. 31, 215-221, 1990
A:Title: Characterization of polypeptides that accumulate in cultured Nicotiana tabac
A:Reference number: A44957
A:Accession: H44957
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <TAK>

Query Match          16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          7 GVP 9
           |||
           2 GVP 4
Db

RESULT 33
PC2373
probable IMP dehydrogenase (EC 1.1.1.205) [similarity] - Bacillus cereus (strain ts-4
C:Species: Bacillus cereus
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000
C:Accession: PC2373
R:Watsuno, K.; Miyamoto, T.; Yamaguchi, K.; Sayed, M.A.; Kajiwara, T.; Hatano, S.
Biosci. Biotechnol. Biochem. 59, 231-235, 1995
A:Title: Identification of DNA-binding proteins changed after induction of sporulatic
A:Reference number: PC2369; MUID:95218265; PMID:7766022
A:Accession: PC2373
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <MAS>
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homc
C:Keywords: GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis

Query Match          16.7%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          11 VKE 13
           |||
           7 VKE 9
Db

RESULT 34
PS0371
hypothetical protein (psaC region) - Synechococcus sp. (fragment)
C:Species: Synechococcus sp.
C>Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 08-Oct-1999
C:Accession: PS0371
R:Rhiel, E.; Stirewalt, V.L.; Gasparich, G.E.; Bryant, D.A.
Gene 112, 123-128, 1992
A:Title: The psaC genes of Synechococcus sp. PC7002 and Cyanophora paradoxa: cloning
A:Reference number: JS0694; MUID:92201692; PMID:1551590
A:Accession: PS0371
A:Molecule type: DNA
A:Residues: 1-14 <RHT>

```

```

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

```

A;Cross-references: GB:M86238; NID:G154574; PIDN:AAA27351.1; PID:G552030

Query Match 16.7%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQP 3  
|||  
Db 12 LQP 14

## RESULT 35

B56863 photosystem I reaction center complex small chain psaE - Synechococcus sp. (fragment)

C;Species: Synechococcus sp.  
C;Date: 05-Jan-1996 #sequence\_revision 05-Jan-1996 #text\_change 23-Feb-1996  
C;Accession: B56863  
R;Hatanaka, H.; Sonoike, K.; Hirano, M.; Katch, S.  
Biochim. Biophys. Acta 1141, 45-51, 1993  
A;Title: Small subunits of Photosystem I reaction center complexes from Synechococcus el  
A;Reference number: A56863; MUID:93168774; PMID:8382079  
A;Accession: B56863  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-14 <HAT>  
A;Experimental source: thylakoid membranes  
A;Note: sequence extracted from NCBI backbone (NCBIP:125606)  
A;Note: the species was designated as Synechococcus elongatus  
C;Keywords: photosystem I; thylakoid

Query Match 16.7%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KVK 12  
|||  
Db 6 KVK 8

## RESULT 36

PA0015

seed storage protein 12S 2 - Arabidopsis thaliana (fragment)

C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 11-Jul-1997  
C;Accession: PA0015  
R;Kano, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.  
submitted to JPIPD, July 1994

A;Description: Separation and characterization of Arabidopsis proteins by two-dimensional

A;Reference number: PA0001  
A;Accession: PA0015  
A;Molecule type: protein  
A;Residues: 1-14 <KAM>  
A;Experimental source: seed  
C;Keywords: pyrrolidone carboxylic acid; seed; storage protein  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 16.7%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GVP 9  
|||  
Db 5 GVP 7

## RESULT 37

A61002

photosystem II oxygen-evolving complex protein 1 - common tobacco (fragment)

N;Alternate names: thylakoid membrane protein  
C;Species: Nicotiana tabacum (common tobacco)  
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 17-Mar-1999  
C;Accession: A61002  
R;Bauw, G.; Rasmussen, H.H.; Van Den Bulcke, M.; Van Damme, J.; Puype, M.; Gesser, B.; d

Electrophoresis 11, 528-536, 1990  
A;Title: Two-dimensional gel electrophoresis, protein electrophoresis and microsequen  
A;Reference number: A61002; MUID:91031404; PMID:1699755

A;Accession: A61002  
A;Molecule type: protein  
A;Residues: 1-14 <BAU>  
C;Keywords: chloroplast; membrane protein; photosynthesis; photosystem II; thylakoid

Query Match 16.7%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GVP 9  
|||  
Db 2 GVP 4

## RESULT 38

A61308

hemocyanin chain 2 - Sahara scorpion (fragment)

C;Species: Androctonus australis (Sahara scorpion)  
C;Date: 17-Jul-1994 #sequence\_revision 17-Jul-1994 #text\_change 07-May-1999  
C;Accession: A61308  
R;Jolles, J.; Jolles, P.; Lamy, J.; Lamy, J.  
FEBS Lett. 106, 289-291, 1979

A;Title: Structural characterization of seven different subunits in Androctonus aust  
A;Reference number: A61308; MUID:80047238; PMID:499512  
A;Accession: A61308  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-14 <JOL>

Query Match 16.7%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VKE 13  
|||  
Db 2 VKE 4

## RESULT 39

B61308

hemocyanin chain 4 - Sahara scorpion (fragment)

C;Species: Androctonus australis (Sahara scorpion)  
C;Date: 17-Jul-1994 #sequence\_revision 17-Jul-1994 #text\_change 07-May-1999  
C;Accession: B61308  
R;Jolles, J.; Jolles, P.; Lamy, J.; Lamy, J.  
FEBS Lett. 106, 289-291, 1979

A;Title: Structural characterization of seven different subunits in Androctonus aust  
A;Reference number: A61308; MUID:80047238; PMID:499512  
A;Accession: B61308  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-14 <JOL>

Query Match 16.7%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VKE 13  
|||  
Db 2 VKE 4

## RESULT 40

B39111

Ig heavy chain V region - Pacific hagfish (fragment)

C;Species: Eptatretus stouti (Pacific hagfish)  
C;Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 16-Aug-1996  
C;Accession: B39111  
R;Varner, J.; Neame, P.; Litman, G.W.  
Proc. Natl. Acad. Sci. U.S.A. 88, 1746-1750, 1991

A;Title: A serum heterodimer from hagfish (Eptatretus stoutii) exhibits structural similarity  
A;Reference number: A39111; MUID:91156684; PMID:2000382

A;Accession: B39111

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-14 <VAR>

C;Keywords: heterotrimer; immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPE 4

DB 11 QPE 13

RESULT 41

PH1625

ovostatin - duck (fragment)

N;Alternate names: ovomacroglobulin

C;Species: Anas platyrhynchos (domestic duck)

C;Date: 02-Jun-1997 #sequence\_revision 01-Aug-1997 #text\_change 01-Aug-1997

C;Accession: S00150

R;Nagase, H.; Harris Jr., E.D.; Brew, K.

J. Biol. Chem. 261, 1421-1426, 1986

A;Title: Evidence for a thiol ester in duck ovostatin (ovomacroglobulin).

A;Reference number: S00150; MUID:86111792; PMID:3511043

A;Accession: S00150

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-14 <NAG>

A;Note: part of this sequence, including the amino end of the mature chicken and duck pr

Query Match 16.7%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 MVP 17

DB 10 MVP 12

RESULT 42

PH1625

Ig H chain V-D-J region (clone B-less 109) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999

C;Accession: PH1625

R;Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice

A;Reference number: PH1580; MUID:93301609; PMID:8315387

A;Accession: PH1625

A;Molecule type: DNA

A;Residues: 1-14 <LEV>

A;Experimental source: bone marrow pre-B lymphocyte

C;Keywords: immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 ETM 15

DB 9 ETM 11

RESULT 43

PH1627

Ig H chain V-D-J region (clone B-less 120) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999

C;Accession: PH1627

R;Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less m

A;Reference number: PH1580; MUID:93301609; PMID:8315387

A;Accession: PH1627

A;Molecule type: DNA

A;Residues: 1-14 <LEV>

A;Experimental source: bone marrow pre-B lymphocyte

C;Keywords: immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 ETM 15

DB 9 ETM 11

RESULT 44

PH1594

Ig H chain V-D-J region (wild-type clone 149) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999

C;Accession: PH1594

R;Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less m

A;Reference number: PH1580; MUID:93301609; PMID:8315387

A;Accession: PH1594

A;Molecule type: DNA

A;Residues: 1-14 <LEV>

A;Experimental source: bone marrow pre-B lymphocyte

C;Keywords: immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TMV 16

DB 6 TMV 8

RESULT 45

S21747

glutamate dehydrogenase [NAD(P)] (EC 1.4.1.3) - Pyrococcus furiosus

C;Species: Pyrococcus furiosus

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 03-Jun-2002

C;Accession: S21747

R;Robb, F.T.; Park, J.B.; Adams, M.W.W.

Biochim. Biophys. Acta 1120, 267-272, 1992

A;Title: Characterization of an extremely thermostable glutamate dehydrogenase: a key

A;Reference number: S21747; MUID:92247806; PMID:1576153

A;Accession: S21747

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-14 <ROB>

C;Keywords: oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKE 13

DB 1 VKE 3

RESULT 46

PA0044

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) 22.5K chain - Arabidopsis thaliana (fra

C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 03-Jun-2002  
C;Accession: PA00044  
R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.  
submitted to JIPID, July 1994  
A;Description: Separation and characterization of Arabidopsis proteins by two-dimensional electrophoresis  
A;Reference number: PA0001  
A;Molecule type: protein  
A;Residues: 1-14 <KAM>  
A;Experimental source: root  
C;Keywords: NAD; oxidative phosphorylation; oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KVK 12  
|||  
Db 2 KVK 4

RESULT 47  
S26791  
Ig heavy chain V region (N63P2) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1995 #sequence\_revision 02-Aug-1996 #text\_change 20-Jun-2000  
C;Accession: S26791; S19879  
R;Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.  
Eur. J. Immunol. 22, 241-245, 1992  
A;Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene family  
A;Reference number: S26786; MUID:92111632; PMID:1730251  
A;Accession: S26791  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-15 <MOR>  
A;Cross-references: EMBL:X61022; NID:G32791; PIDN:CAA43356.1; PID:gl335124; EMBL:X61234;  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 TMV 16  
|||  
Db 9 TMV 11

RESULT 48  
PA0034  
protein QA300024 - Arabidopsis thaliana (fragment)  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 06-Jun-1997  
C;Accession: PA0034  
R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.  
submitted to JIPID, July 1994  
A;Description: Separation and characterization of Arabidopsis proteins by two-dimensional electrophoresis  
A;Reference number: PA0001  
A;Accession: PA0034  
A;Molecule type: protein  
A;Residues: 1-15 <KAM>  
A;Experimental source: leaf

Query Match 16.7%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GVP 9  
|||  
Db 3 GVP 5

RESULT 49  
PA0014  
seed storage protein 12S 3 - Arabidopsis thaliana (fragment)  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 23-Mar-1995  
C;Accession: PA0014  
R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.  
submitted to JIPID, July 1994  
A;Description: Separation and characterization of Arabidopsis proteins by two-dimensional electrophoresis  
A;Reference number: PA0001  
A;Accession: PA0014  
A;Molecule type: protein  
A;Residues: 1-15 <KAM>  
A;Experimental source: seed  
C;Keywords: seed; storage protein

Query Match 16.7%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GVP 9  
|||  
Db 5 GVP 7

RESULT 50  
PN0173  
seed storage protein 12S4 - Arabidopsis thaliana (fragment)  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 22-Dec-1995 #sequence\_revision 08-Feb-1996 #text\_change 23-Mar-2001  
C;Accession: PN0173  
R;Tsugita, A.; Kamo, M.; Kawakami, M.; Ohki, Y.  
submitted to JIPID, December 1995  
A;Description: Two dimensional electrophoresis of plant proteins and standardization  
A;Reference number: PN0173  
A;Accession: PN0173  
A;Molecule type: protein  
A;Residues: 1-15 <TSU>  
A;Experimental source: seeds

Query Match 16.7%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GVP 9  
|||  
Db 5 GVP 7

RESULT 51  
PA0059  
protein QF200021 - fungus (Fusarium sporotrichioides) (fragment)  
C;Species: Fusarium sporotrichioides  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001  
C;Accession: PA0059  
R;Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.  
submitted to JIPID, October 1994  
A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides  
A;Reference number: PA0051  
A;Accession: PA0059  
A;Molecule type: protein  
A;Residues: 1-15 <CHO>

Query Match 16.7%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GVP 9  
|||  
Db 10 GVP 12

RESULT 52



PA0106  
 protein QP200076 - fungus (Fusarium sporotrichioides) (fragment)  
 C;Species: Fusarium sporotrichioides  
 C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001  
 C;Accession: PA0106  
 R;Chow, L.P.; Fukaya, N.; Sugitara, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.  
 submitted to JIPID, October 1994  
 A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichi  
 A;Reference number: PA0051  
 A;Accession: PA0106  
 A;Molecule type: protein  
 A;Residues: 1-15 <CHO>

Query Match 16.7%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KVK 12  
 |||  
 Db 11 KVK 13

RESULT 53  
 PA0080  
 translation elongation factor eEF-2 - fungus (Fusarium sporotrichioides) (fragment)  
 C;Species: Fusarium sporotrichioides  
 C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001  
 C;Accession: PA0080  
 R;Chow, L.P.; Fukaya, N.; Sugitara, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.  
 submitted to JIPID, October 1994

A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichi  
 A;Reference number: PA0051  
 A;Accession: PA0080  
 A;Molecule type: protein  
 A;Residues: 1-15 <CHO>  
 C;Keywords: protein biosynthesis

Query Match 16.7%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GVP 9  
 |||  
 Db 8 GVP 10

RESULT 54  
 S10388  
 Ig heavy chain J region (clone Re102) - little skate (fragment)  
 C;Species: Raja erinacea (little skate)  
 C;Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 21-Jul-2000  
 C;Accession: S10388  
 R;Harding, F.A.; Cohen, N.; Litman, G.W.  
 Nucleic Acids Res. 18, 1015-1020, 1990  
 A;Title: Immunoglobulin heavy chain gene organization and complexity in the skate, Raja  
 A;Reference number: S08462; MUID:90192082; PMID:2107524  
 A;Accession: S10388  
 A;Molecule type: DNA  
 A;Residues: 1-15 <HAR>  
 A;Cross-references: EMBL:X16146; NID:g64284; PIDN:CAA34271.1; PID:gl334773  
 C;Keywords: heterotetramer; immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 TMV 16  
 |||  
 Db 9 TMV 11

RESULT 55  
 S10386

Ig heavy chain J region (clone Re107) - little skate (fragment)  
 C;Species: Raja erinacea (little skate)  
 C;Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 16-Aug-1996  
 C;Accession: S10386  
 R;Harding, F.A.; Cohen, N.; Litman, G.W.  
 Nucleic Acids Res. 18, 1015-1020, 1990  
 A;Title: Immunoglobulin heavy chain gene organization and complexity in the skate, R  
 A;Reference number: S08462; MUID:90192082; PMID:2107524  
 A;Accession: S10386  
 A;Molecule type: DNA  
 A;Residues: 1-15 <HAR>  
 A;Cross-references: EMBL:X15124  
 C;Keywords: heterotetramer; immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 TMV 16  
 |||  
 Db 9 TMV 11

RESULT 56  
 B41436  
 ovostatin - green seaturtle (fragment)  
 C;Species: Chelonia mydas (green seaturtle)  
 C;Date: 21-Apr-1992 #sequence\_revision 21-Apr-1992 #text\_change 18-Jun-1993  
 C;Accession: B41436  
 R;Osada, T.; Sasaki, T.; Ikai, A.  
 J. Biochem. 103, 212-217, 1988  
 A;Title: Purification and characterization of alpha-macroglobulin and ovomacroglobul  
 A;Reference number: A41436; MUID:88227890; PMID:2453503  
 A;Accession: B41436  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-15 <OSA>

Query Match 16.7%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 MVP 17  
 |||  
 Db 10 MVP 12

RESULT 57  
 A32971  
 heparin-binding lectin - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 12-Oct-1989 #sequence\_revision 12-Oct-1989 #text\_change 16-Feb-1997  
 C;Accession: A32971  
 R;Kohnke-Godt, B.; Gabius, H.J.  
 Biochemistry 28, 6531-6538, 1989  
 A;Title: Heparin-binding lectin from human placenta: purification and partial molecu  
 A;Reference number: A32971; MUID:90001207; PMID:2790011  
 A;Accession: A32971  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-15 <KOH>  
 C;Keywords: heparin binding

Query Match 16.7%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KVK 12  
 |||  
 Db 8 KVK 10

RESULT 58

```
PN0662
dystrophin-associated glycoprotein A3a-I - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 07-May-1999
C;Accession: PN0662
R;Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.
J. Biochem. 114, 634-639, 1993
A;Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained
A;Reference number: PN0662; MUID:94156881; PMID:8113213
A;Accession: PN0662
A;Molecule type: protein
A;Residues: 1-15 <YOS>
C;Comment: This protein is retained in Duchenne type muscular dystrophy muscle.
C;Keywords: Glycoprotein; skeletal muscle

Query Match      16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GVP 9
      |||
Db      9 GVP 11

RESULT 59
PH1613
Ig H chain V-D-J region (clone B-less 17) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1613
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A;Reference number: PH1580; MUID:93301609; PMID:8315387
A;Accession: PH1613
A;Molecule type: DNA
A;Residues: 1-15 <LEV>
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin

Query Match      16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 TMV 16
      |||
Db      5 TMV 7

RESULT 60
I38032
hypothetical MN1/TEL mutant fusion protein type I - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 20-Apr-2000
C;Accession: I38032
R;Buijs, A.; Sherr, S.; van Baal, S.; van Bezouw, S.; van der Plas, D.; Van Kessel, A.G.
Oncogene 10, 1511-1519, 1995
A;Title: Translocation (12;22) (p13;q11) in myeloproliferative disorders results in fusion
A;Reference number: I38031; MUID:95249265; PMID:7731705
A;Accession: I38032
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-15 <BUI>
A;Cross-references: EMBL:X85025; NID:g971467; PIDN:CAA59398.1; PID:g971468
C;Comment: This sequence is the chimeric product of a translocation mutation.
C;Genetics:
A;Gene: MN1/ETV6; MN1/TEL
A;Map position: 22q11/12p13
C;Keywords: fusion protein

Query Match      16.7%; Score 3; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PN0662
dystrophin-associated glycoprotein A3a-I - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 07-May-1999
C;Accession: PN0662
R;Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.
J. Biochem. 114, 634-639, 1993
A;Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained
A;Reference number: PN0662; MUID:94156881; PMID:8113213
A;Accession: PN0662
A;Molecule type: protein
A;Residues: 1-15 <YOS>
C;Comment: This protein is retained in Duchenne type muscular dystrophy muscle.
C;Keywords: Glycoprotein; skeletal muscle

Query Match      16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GVP 9
      |||
Db      9 GVP 11

RESULT 61
S03532
Ig heavy chain J region (JH-7) - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 21-Nov-1993 #sequence_revision 08-Nov-1996 #text_change 20-Jun-2000
C;Accession: S03532
R;Schwager, J.; Grossberger, D.; du Pasquier, L.
EMBO J. 7, 2409-2415, 1988
A;Title: Organization and rearrangement of immunoglobulin M genes in the amphibian X.
A;Reference number: S01158; MUID:89052653; PMID:2903824
A;Accession: S03532
A;Molecule type: DNA
A;Residues: 1-16 <SCH>
A;Cross-references: EMBL:X14918; NID:g64805; PIDN:CAA33046.1; PID:gl334660
A;Note: the authors translated the codon AAC for residue 1 as Asp
C;Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match      16.7%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 TMV 16
      |||
Db      10 TMV 12

RESULT 62
D49021
Ig heavy chain J7 region - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C;Accession: D49021
R;Haire, R.N.; Amemiya, C.T.; Suzuki, D.; Litman, G.W.
J. Exp. Med. 171, 1721-1737, 1990
A;Title: Eleven distinct V-H gene families and additional patterns of sequence varia
A;Reference number: A47624; MUID:90237760; PMID:2110243
A;Accession: D49021
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-16 <HAI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin

Query Match      16.7%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 TMV 16
      |||
Db      10 TMV 12

RESULT 63
S42237
hypothetical protein 2 - Staphylococcus aureus plasmid pNS1
C;Species: Staphylococcus aureus
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 15-Oct-1999
C;Accession: S42237
R;Noguchi, N.; Aoki, T.; Sasatsu, M.; Kono, M.; Shishido, K.; Ando, T.
FEMS Microbiol. Lett. 37, 283-288, 1986
A;Title: Determination of the complete nucleotide sequence of pNS1, a staphylococcal
A;Reference number: S42236
A;Accession: S42237
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-16 <NOG>
A;Cross-references: EMBL:M16217; NID:gl50832; PIDN:AAA19178.1; PID:g501833
```

C:Genetics: plasmid pNS1

Query Match 16.7%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKE 13  
|||  
Db 14 VKE 16

#### RESULT 64

B44896 heat shock protein 18 - Streptomyces albus (fragment)

C:Species: Streptomyces albus  
C:Date: 31-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 04-Dec-1994  
C:Accession: B44896  
C:Guglielmi, G.; Mazodier, P.; Thompson, C.J.; Davies, J.

J. Bacteriol. 173, 7374-7381, 1991  
A:Title: A survey of the heat shock response in four Streptomyces species reveals two groups of heat shock proteins  
A:Reference number: A44896; MUID:92041638; PMID:1682303

A:Accession: B44896

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-16 <GUG>

A>Note: sequence extracted from NCBI backbone (NCBI:P65107)

Query Match 16.7%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKE 13  
|||  
Db 14 VKE 16

#### RESULT 65

S65709

major allergen Myr p I - bulldog ant (Myrmecia pilosula) (fragment)

C:Species: Myrmecia pilosula

C:Date: 06-Dec-1996 #sequence\_revision 13-Mar-1997 #text\_change 07-May-1999  
C:Accession: S65709  
C:Street, M.D.; Donovan, G.R.; Baldo, B.A.

Biochim. Biophys. Acta 1305, 87-97, 1996

A:Title: Molecular cloning and characterization of the major allergen Myr p II from the bulldog ant (Myrmecia pilosula)

A:Reference number: S65709; MUID:96180991; PMID:8605256

A:Accession: S65709

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-16 <STR>

Query Match 16.7%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKV 11  
|||  
Db 7 PKV 9

#### RESULT 66

C61414

chymotrypsin (EC 3.4.21.1) - slider turtle (fragment)

C:Species: Pseudemys scripta (slider)

C:Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 07-May-1999

C:Accession: C61414

R; Bhargava, A.K.; Barnard, E.A.

J. Mol. Evol. 2, 187-198, 1973

A:Title: Evolution in the pancreatic chymotrypsinogen series: N-terminal sequence determination of the slider turtle (Pseudemys scripta) chymotrypsin

A:Reference number: A61414; MUID:76146602; PMID:4807189

A:Accession: C61414

A>Status: preliminary

A:Molecule type: protein  
A:Residues: 1-16 <BHA>  
C:Keywords: hydrolase; protein digestion; serine proteinase

Query Match 16.7%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GVP 9  
|||  
Db 2 GVP 4

#### RESULT 67

PN0587

NiAlternate names: oxygen oxidoreductase; tetrahydropteridine; tyrosine hydroxylase  
C:Species: Macaca fuscata (Japanese macaque)

C:Date: 03-May-1994 #sequence\_revision 07-Oct-1994 #text\_change 31-Mar-2000

C:Accession: PN0587

Richinose, H.; Ohye, T.; Fujita, K.; Yoshida, M.; Ueda, S.; Nagatsu, T.

Biochem. Biophys. Res. Commun. 195, 158-165, 1993

A:Title: Increased heterogeneity of tyrosine hydroxylase in humans.

A:Reference number: PN0575; MUID:93371398; PMID:7689834

A:Accession: PN0587

A:Molecule type: genomic RNA

A:Residues: 1-17 <ICH>

A:Cross-references: GB:L14801

A:Experimental source: kidney

C:Comment: This enzyme catalyzes the first and rate-limiting step of catecholamine biogenesis: the hydroxylation of phenylalanine to tyrosine

C:Superfamily: phenylalanine 4-monooxygenase

C:Keywords: bipterin; monooxygenase; oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQP 3  
|||  
Db 15 LQP 17

#### RESULT 68

S03531

Ig heavy chain J5 region - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C:Date: 21-Nov-1993 #sequence\_revision 08-Nov-1996 #text\_change 20-Jun-2000

C:Accession: S03531; C49021

R; Schwager, J.; Grossberger, D.; du Pasquier, L.

EMBO J. 7, 2409-2415, 1988

A:Title: Organization and rearrangement of immunoglobulin M genes in the amphibian Xenopus laevis

A:Reference number: S01158; MUID:89052653; PMID:2903824

A:Accession: S03531

A:Molecule type: DNA

A:Residues: 1-17 <SCH>

A:Cross-references: EMBL:X14918; NID:g64805; PIDN:CAA33044.1; PID:g1334658

R; Haire, R.N.; Amemiya, C.T.; Suzuki, D.; Litman, G.W.

J. Exp. Med. 171, 1721-1737, 1990

A:Title: Eleven distinct V-H gene families and additional patterns of sequence variation in the immunoglobulin V region: immunoglobulin homology

A:Reference number: A47624; MUID:90237760; PMID:2110243

A:Accession: C49021

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 3-17 <HAI>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TMV 16  
|||

```
Db      11 TWV 13

RESULT 69
S50901
chlorophyll a/b-binding protein lhcb4 - spinach (fragment)
N;Alternate names: light-harvesting complex LHCIIa protein
C;Species: Spinacia oleracea (spinach)
C;Date: 19-Mar-1997 #sequence_revision 23-Apr-1999 #text_change 23-Apr-1999
C;Accession: S50901
R;Walters, R.G.; Ruban, A.V.; Horton, P.
Eur. J. Biochem. 226, 1063-1069, 1994
A;Title: Higher plant light-harvesting complexes LHCIIa and LHCIIc are bound by dicyclohexylphosphoribosyl pyrophosphate
A;Reference number: S50900; MUID:95112835; PMID:7813461
A;Accession: S50901
A;Molecule type: protein
A;Residues: 1-17 <WAL>
C;Superfamily: chlorophyll a/b-binding protein
C;Keywords: chlorophyll; chloroplast; light-harvesting complex; photosynthesis; photosynthesis; photosynthesis

Query Match      16.7%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LQP 3
      |||
Db      4 LQP 6

RESULT 70
A48179
methane monooxygenase (EC 1.14.13.25) regulatory protein B - Methylococcus capsulatus (strain ATCC 35061)
C;Species: Methylococcus capsulatus
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 31-Dec-1993
C;Accession: A48179
R;Pilkington, S.J.; Salmond, G.P.C.; Murrell, J.C.; Dalton, H.
FEMS Microbiol. Lett. 72, 345-348, 1990
A;Title: Identification of the gene encoding the regulatory protein B of soluble methane monooxygenase
A;Reference number: A48179
A;Accession: A48179
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-17 <PIL>
C;Keywords: oxidoreductase

Query Match      16.7%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 IMG 7
      |||
Db      10 IMG 12

RESULT 71
B61414
chymotrypsin (EC 3.4.21.1) - painted turtle (fragment)
C;Species: Chrysemys picta (painted turtle)
C;Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 07-May-1999
C;Accession: B61414
R;Bhargava, A.K.; Barnard, E.A.
J. Mol. Evol. 2, 187-198, 1973
A;Title: Evolution in the pancreatic chymotrypsinogen series: N-terminal sequence determination of chymotrypsin
A;Reference number: A61414; MUID:76146602; PMID:4807189
A;Accession: B61414
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-17 <BHA>
C;Keywords: hydrolase; serine proteinase

Query Match      16.7%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 IMG 7
      |||
Db      10 IMG 12

RESULT 72
S59512
probable integrin alpha3 betal - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 07-May-1999
C;Accession: S59512
R;McCormick, J.I.; Johnstone, R.M.
Biochem. J. 311, 743-751, 1995
A;Title: Identification of the integrin alpha(3)beta(1) as a component of a partially purified integrin
A;Reference number: S59512; MUID:96067588; PMID:7487928
A;Accession: S59512
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-17 <MCC>

Query Match      16.7%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 VKE 13
      |||
Db      10 VKE 12

RESULT 73
S69164
ferredoxin al - Japanese radish (fragments)
C;Species: Kaiware daikon (Japanese radish)
C;Date: 10-Mar-1998 #sequence_revision 10-Mar-1998 #text_change 17-Apr-1998
C;Accession: S69164
R;Obata, S.; Nishimura, M.; Nagai, K.; Sakihama, N.; Shin, M.
Arch. Biochem. Biophys. 316, 797-802, 1995
A;Title: Four ferredoxins from Japanese radish leaves.
A;Reference number: S69164; MUID:95168867; PMID:7864635
A;Accession: S69164
A;Molecule type: protein
A;Residues: 1-17 <OBA>
C;Keywords: 2Fe-2S; electron transfer; iron-sulfur protein

Query Match      16.7%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 KVK 12
      |||
Db      4 KVK 6

RESULT 74
PD0005
very-high-density lipoprotein - sand crayfish (fragment)
N;Alternate names: VLDL
C;Species: Ibacus ciliatus (sand crayfish)
C;Date: 13-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 07-May-1999
C;Accession: PD0005
R;Komatsu, M.; Ando, S.
Biosci. Biotechnol. Biochem. 62, 459-463, 1998
A;Title: A very-high-density lipoprotein with clotting ability from hemolymph of sand crayfish
A;Reference number: PD0005; MUID:98233268; PMID:9571775
A;Accession: PD0005
A;Molecule type: protein
A;Residues: 1-17 <KOM>
C;Comment: This protein plays an important role in the defense process of crustacea,

Query Match      16.7%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 LQP 3  
|||  
Db 1 LQP 3

RESULT 75  
DRUFPD  
pigment-dispersing hormone - Atlantic sand fiddler crab  
N/Alternate names: PDH  
C/Species: Uca pugilator (Atlantic sand fiddler crab)  
C/Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 08-Dec-1995  
C/Accession: A25144  
R/Rao, K.R.; Riehm, J.P.; Zahnow, C.A.; Kleinholz, L.H.; Tarr, G.E.; Johnson, L.; Norton  
Proc. Natl. Acad. Sci. U.S.A. 82, 5319-5322, 1985  
A/Title: Characterization of a pigment-dispersing hormone in eyestalks of the fiddler crab  
A/Reference number: A25144  
A/Accession: A25144  
A/Molecule type: protein  
A/Residues: 1-18 <RAO>  
C/Superfamily: pigment-dispersing hormone  
C/Keywords: amidated carboxyl end; neuropeptide  
P/18/Modified site: amidated carboxyl end (Ala) #status experimental

Query Match 16.7%; Score 3; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PKV 11  
|||  
Db 12 PKV 14

Search completed: November 25, 2003, 19:36:08  
Job time : 13.3488 secs

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:17:40 ; Search time 6.38372 Seconds  
(without alignments)  
132.600 Million cell updates/sec

Title: US-09-641-801-21

Perfect score: 18

Sequence: 1 LQPEIMGVPKVKETWPK 18

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	22.2	19	1	LPGE_ECOLI
2	3	16.7	7	1	E105_LITRU
3	3	16.7	8	1	VGLG_HSV2B
4	3	16.7	9	1	COXE_THUOB
5	3	16.7	10	1	BPP_VIPAS
6	3	16.7	10	1	GONI_ALIMI
7	3	16.7	10	1	UPA5_HUMAN
8	3	16.7	11	1	CS15_BACSU
9	3	16.7	12	1	PORD_METTM
10	3	16.7	12	1	TKN_KASSE
11	3	16.7	13	1	BPPI_BOTJA
12	3	16.7	13	1	E121_LITRU
13	3	16.7	13	1	E122_LITRU
14	3	16.7	15	1	RS6_BACST
15	3	16.7	16	1	FIBA_MELE
16	3	16.7	16	1	FIBA_MUSVI
17	3	16.7	16	1	MMPX_SOLTU
18	3	16.7	16	1	ODPB_SOLTU
19	3	16.7	18	1	AL13_CARMA
20	3	16.7	18	1	DRPH_UCAPU
21	3	16.7	18	1	RL24_PROVU
22	3	16.7	19	1	FIBB_PIG
23	3	16.7	20	1	CS21_STRTR
24	3	16.7	20	1	LECB_RIHO
25	3	16.7	20	1	PUEK_RHOSH
26	2	11.1	4	1	DCML_PSECH
27	2	11.1	6	1	ASP2_LACSN
28	2	11.1	6	1	E101_LITRU
29	2	11.1	6	1	OVN_LEPDE
30	2	11.1	6	1	UN06_CLOPA
31	2	11.1	7	1	LANC_CARUI
32	2	11.1	7	1	TFPV_PACDA
33	2	11.1	7	1	UF04_MOUSE

34	2	11.1	7	1	WMA3_ACHFU
35	2	11.1	8	1	CKKN_MACEU
36	2	11.1	8	1	FUSS_FUSSO
37	2	11.1	8	1	NPE_BOVIN
38	2	11.1	8	1	PKK3_PERAM
39	2	11.1	8	1	RS7_MYCIT
40	2	11.1	8	1	UH05_RAT
41	2	11.1	8	1	UPA1_HUMAN
42	2	11.1	9	1	AL10_CARMA
43	2	11.1	9	1	BS43_SERPL
44	2	11.1	9	1	CONO_CONGE
45	2	11.1	9	1	FAR3_PENMO
46	2	11.1	9	1	FLA2_TREHY
47	2	11.1	9	1	FRF1_SARBU
48	2	11.1	9	1	LMT3_LOCMI
49	2	11.1	9	1	NEF_HV12B
50	2	11.1	9	1	RT33_BOVIN
51	2	11.1	9	1	SAP_STOVA
52	2	11.1	9	1	TKC1_CALVO
53	2	11.1	9	1	TKL1_LOCM1
54	2	11.1	9	1	TRF4_LEUMA
55	2	11.1	9	1	UF02_MOUSE
56	2	11.1	9	1	ULAD_HUMAN
57	2	11.1	9	1	ULAK_MOUSE
58	2	11.1	9	1	UPA7_HUMAN
59	2	11.1	10	1	COXA_ONCMY
60	2	11.1	10	1	COXH_ONCMY
61	2	11.1	10	1	COXK_ONCMY
62	2	11.1	10	1	FAR6_PANRE
63	2	11.1	10	1	GAJU_HUMAN
64	2	11.1	10	1	LABA_JATMU
65	2	11.1	10	1	LPK2_LOCM1
66	2	11.1	10	1	ODE2_BOVIN
67	2	11.1	10	1	PNEU_HUMAN
68	2	11.1	10	1	PNEU_RAT
69	2	11.1	10	1	PORB_METTM
70	2	11.1	10	1	RL16_ACHLA
71	2	11.1	10	1	SP34_DICMU
72	2	11.1	10	1	SPI_HALRO
73	2	11.1	10	1	SYK_CAMUP
74	2	11.1	10	1	TKL2_LOCM1
75	2	11.1	10	1	TKL3_LOCM1
76	2	11.1	10	1	TKL4_LOCM1
77	2	11.1	10	1	TRP5_LEUMA
78	2	11.1	10	1	TRP7_LEUMA
79	2	11.1	10	1	TRP8_LEUMA
80	2	11.1	10	1	TRP9_LEUMA
81	2	11.1	10	1	UPA4_HUMAN
82	2	11.1	10	1	UPA8_HUMAN
83	2	11.1	10	1	UPA9_HUMAN
84	2	11.1	10	1	URE3_MORMO
85	2	11.1	10	1	VEG6_BACSU
86	2	11.1	10	1	BPPE_AKHA
87	2	11.1	11	1	COXA_CANFA
88	2	11.1	11	1	HS70_PINPS
89	2	11.1	11	1	MLG_THETS
90	2	11.1	11	1	MORN_HUMAN
91	2	11.1	11	1	RS30_ONCMY
92	2	11.1	11	1	TINI_HOPTI
93	2	11.1	11	1	TKC2_CALVO
94	2	11.1	11	1	TKN1_PSEGU
95	2	11.1	11	1	TKN2_PSEGU
96	2	11.1	11	1	TKN2_PSEGU
97	2	11.1	11	1	TKN2_PSEGU
98	2	11.1	11	1	TKN2_PSEGU
99	2	11.1	11	1	TKN3_PSEGU
100	2	11.1	11	1	TKN3_PSEGU

ALIGNMENTS

RESULT 1

```
LPGE ECOLI
ID _LPGE_ECOLI STANDARD; PRT; 19 AA.
AC P33236;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Gef leader peptide.
GN GEFL OR B0018.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92048481; PubMed=1943701;
RA Poulsen L.K., Refn A., Molin S., Andersson P.;
RT "The gef gene from Escherichia coli is regulated at the level of
translation."
RL Mol. Microbiol. 5:1639-1648(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.P.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474(1997).
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE000112; AAC73129.1; ALT_TERM.
DR EcoGene; EG12074; g9FL.
SQ Leader peptide; Complete proteome.
KW SEQUENCE 19 AA; 2259 MW; 19B3EDF371EB0BEB CRC64;

Query Match 22.2%; Score 4; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KVKE 13
DB 13 KVKE 16

RESULT 2
EI05 LITRU
ID EI05 LITRU STANDARD; PRT; 7 AA.
AC P82101;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Electrin 5.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=skin secretion;
RA Wahlitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella."
RL Aust. J. Chem. 52:639-645(1999).
CC -----
```

```
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 834 MW; 6DD05B076B0B5030 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PEI 5
DB 4 PEI 6

RESULT 3
VGLG HSV2B STANDARD; PRT; 8 AA.
ID VGLG HSV2B
AC P81780;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Glycoprotein G (Fragment).
OS Herpes simplex virus (type 2 / strain B4327UR).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=103921;
RN [1]
RP SEQUENCE.
RA Liljeqvist J.-A., Svennerholm B., Bergstrom T.;
RL Submitted (APR-1999) to the SWISS-PROT data bank.
CC -|- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1 AND
CC 2: GH, GB, GC, GG, GD, GI, AND GE.
CC -|- MISCELLANEOUS: GLYCOPROTEIN G IS MUCH LARGER IN HSV-2 THAN IN
CC HSV-1.
KW Glycoprotein.
FT NON_TER 8
SQ SEQUENCE 8 AA; 683 MW; 7B47686772C86588 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GVP 9
DB 3 GVP 5

RESULT 4
COXE THUOB STANDARD; PRT; 9 AA.
ID COXE THUOB
AC P80975;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Cytochrome c oxidase polypeptide VIa (EC 1.9.3.1) (Fragment).
OS Thunus obesus (Bigeye tuna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8241;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=97454291; PubMed=9310366;
RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
RA Kadenbach B.;
RT "The subunit structure of cytochrome-c oxidase from tuna heart and
RT liver."
RL Eur. J. Biochem. 248:99-103(1997).
CC -|- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
```

CC - MITOCHONDRIAL ELECTRON TRANSPORT.  
 CC - CATALYTIC ACTIVITY: 4 ferriocytochrome c + O(2) = 4 ferriocytochrome  
 CC c + 2 H(2)O.  
 CC - SUBCELLULAR LOCATION: Mitochondrial inner membrane.  
 CC - SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIA FAMILY.  
 DR PIR; S77984; S77984.  
 DR InterPro; IPR001349; COX6A.  
 DR PROSITE; PS01329; COX6A; PARTIAL.  
 KW Oxidoreductase; Inner membrane; Mitochondrion.  
 FT NON\_TER 1 1  
 FT NON\_TER 9 9  
 SQ SEQUENCE 9 AA; 1136 MW; 62E072C9CB0776DB CRC64;  
 Query Match 16.7%; Score 3; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;  
 Matches 3; Conservative 0; Mismatches 0;  
 QY 2 QPE 4  
 Db 3 QPE 5  
 RESULT 5  
 BPP VIPAS  
 ID - BPP VIPAS STANDARD; PRT; 10 AA.  
 AC P31351;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bradykinin-potentiating peptide (Angiotensin-converting  
 DE enzyme inhibitor)  
 OS Vipera aspis (Aspic viper).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidodactylia; Squamata; Scleroglossa; Serpentes; Colubroidae;  
 OC Viperidae; Viperinae; Vipera.  
 OX NCBI\_TaxID=8706;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=90382616; PubMed=2169439;  
 RA Komori Y., Sugihara H.;  
 RT "Characterization of a new inhibitor for angiotensin converting  
 RT enzyme from the venom of Vipera aspis aspis.";  
 RL Int. J. Biochem. 22:767-771(1990).  
 CC - FUNCTION: This peptide both inhibits the activity of the  
 CC angiotensin-converting enzyme and enhances the action of  
 CC bradykinin by inhibiting the kinases that inactivate it.  
 CC It acts as an indirect hypotensive agent.  
 DR PIR; A60377; XASNPC.  
 KW Hypotensive agent; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1  
 FT MOD\_RES 1 1  
 SQ SEQUENCE 10 AA; 1062 MW; 3BA827C327686773 CRC64;  
 Query Match 16.7%; Score 3; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03; Indels 0; Gaps 0;  
 Matches 3; Conservative 0; Mismatches 0;  
 QY 9 PKV 11  
 Db 6 PKV 8  
 RESULT 6  
 GONI ALLMI  
 ID - GONI ALLMI STANDARD; PRT; 10 AA.  
 AC P37041; P20407;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Gonadoliberin I (Gonadotropin-releasing hormone I) (GnRH-I) (LH-RH I)  
 DE (Luliberin I).  
 OS Alligator mississippiensis (American alligator).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Crocodylidae; Alligatorinae; Alligator.  
 OX NCBI\_TaxID=8496;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=91352338; PubMed=1882082;  
 RA Lovejoy D.A., Fischer W.H., Parker D.B., McRory J.E., Park M.,  
 RA Lance V., Swanson P., Rivier J.E., Sherwood N.M.;  
 RT "Primary structure of two forms of gonadotropin-releasing hormone  
 RT from brains of the American alligator (Alligator mississippiensis).";  
 RL Regul. Pept. 33:105-116(1991).  
 CC - FUNCTION: Stimulates the secretion of gonadotropins.  
 CC - SUBCELLULAR LOCATION: Secreted.  
 CC - SIMILARITY: Belongs to the GnRH family.  
 DR PIR; A60066; RHA01.  
 DR InterPro; IPR002012; GnRH.  
 DR Pfam; PF00446; GnRH; 1.  
 DR PROSITE; PS00473; GnRH; 1.  
 KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1  
 FT MOD\_RES 10 10  
 SQ SEQUENCE 10 AA; 1172 MW; 284B23D7286B45A3 CRC64;  
 Query Match 16.7%; Score 3; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LQP 3  
 Db 7 LQP 9  
 RESULT 7  
 UPAS HUMAN  
 ID - UPAS HUMAN STANDARD; PRT; 10 AA.  
 AC P30091;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Unknown protein from 2D-page of plasma (Spot 13) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Plasma;  
 RX MEDLINE=93092937; PubMed=1459097;  
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,  
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,  
 RA Hochstrasser D.F.;  
 RT "Plasma protein map: an update by microsequencing.";  
 RT Electrophoresis 13:707-714(1992).  
 RL - MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 4.85, ITS MW IS: 40 kDa.  
 CC - MISCELLANEOUS: THIS SPOT IS ON A POSITION THOUGHT TO BE THAT OF  
 CC ZN-ALPHA-2 GLYCOPROTEIN, BUT IT DOES NOT CORRESPOND TO THAT  
 CC PROTEIN.  
 DR SWISS-2DPAGE; P30091; HUMAN.  
 FT NON\_TER 1 1  
 FT VARIANT 9 9  
 FT VARIANT 9 9  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1109 MW; C3DA94C732C32776 CRC64;  
 Query Match 16.7%; Score 3; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 9 PKV 11  
 Db 4 PKV 6



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Query Match      16.7%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      11 VKE 13
Db      8 VKE 10

RESULT 10
TKN_KASSE
ID_TKN_KASSE STANDARD; PRT; 12 AA.
AC P08511;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Kassinin.
OS Kassina senegalensis (Senegal running frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Hyperoliidae;
OC Kassina.
OX NCBI_TaxID=8415;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=77246385; PubMed=891753;
RA Anastasi A., Montecucchi P.C., Erspamer V., Visser J.;
RT "Amino acid composition and sequence of kassinin, a tachykinin
dodecapeptide from the skin of the African frog Kassina
senegalensis.";
RL Experientia 33:857-858(1977).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
MUSCLES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; S07206; S07206.
DR PDB; 1MYU; 16-OCT-02.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW 3D-structure.
FT MOD_RES 12 12
SQ SEQUENCE 12 AA; 1336 MW; 91757AB89DD6DAB5 CRC64;

Query Match      16.7%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 VPK 10
Db      2 VPK 4

RESULT 11
BPPI_BOTJA
ID_BPPI_BOTJA STANDARD; PRT; 13 AA.
AC P01020; P30421;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S3,1 (13A) (Angiotensin-converting
enzyme inhibitor V-9).
DE Bothrops jararaca (Jararaca), and
OS Bothrops insularis (Island jararaca) (Queimada jararaca),
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724, 8723;
RN [1]

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RP SEQUENCE.
RC SPECIES=B.jararaca; TISSUE=Venom;
RX MEDLINE=72118526; PubMed=4334402;
RA Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R.,
RA Kocy O.;
RT "Angiotensin-converting enzyme inhibitors from the venom of Bothrops
RT jararaca. Isolation, elucidation of structure, and synthesis.";
RL Biochemistry 10:4033-4039(1971).
RN [2]
RP SEQUENCE.
RC SPECIES=B.insularis; TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; A01253; XAVI9B.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 13 AA; 1388 MW; 6924FC97D83D6774 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PEI 5
Db |||
9 PEI 11

RESULT 12
EI21_LITRU STANDARD; PRT; 13 AA.
ID EI21_LITRU STANDARD; PRT; 13 AA.
AC P82097;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Electrin 2.1.
OS Litoria rubella (Desert tree frog);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litori electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD_RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1599 MW; C1808EF326F57322 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KVK 12
Db |||
5 KVK 7

RESULT 13
EI22_LITRU STANDARD; PRT; 13 AA.
ID EI22_LITRU STANDARD; PRT; 13 AA.

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AC P82098;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Electrin 2.2.
OS Litoria rubella (Desert tree frog);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litori electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD_RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1598 MW; C1808EF33B357322 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KVK 12
Db |||
5 KVK 7

RESULT 14
RS6_BACST STANDARD; PRT; 15 AA.
ID RS6_BACST STANDARD; PRT; 15 AA.
AC P59582;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE 30S ribosomal protein S6 (BS9) (Fragment).
GN RPSF.
OS Bacillus stearothermophilus
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RP SEQUENCE.
RC STRAIN=10;
RX PubMed=4607606;
RA Yaguchi M., Matheson A.T., Visentin L.P.;
RT "Prokaryotic ribosomal proteins: N-terminal sequence homologies and
RT structural correspondence of 30 S ribosomal proteins from Escherichia
RT coli and Bacillus stearothermophilus.";
RL FEBS Lett. 46:296-300(1974).
CC -!- FUNCTION: Binds together with S18 to 16S ribosomal RNA (By
CC similarity).
CC -!- SIMILARITY: BELONGS TO THE S6P FAMILY OF RIBOSOMAL PROTEINS.
DR HAMAP; MF_00360; -; 1.
DR PROSITE; PS01048; RIBOSOMAL S6; PARTIAL.
KW Ribosomal protein; rRNA-binding.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1974 MW; 18C5E2E851E09572 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EIM 6
Db |||
5 EIM 7

RESULT 15

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FIBA_MELME          STANDARD;          PRT;          16 AA.
ID FIBA_MELME
AC P14456;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Meles meles (Eurasian badger).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Melinae;
OC Meles.
OC NCBI_TaxID=9662;
OX [1]
RP SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 39:1789-1791(1965).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 16 FIBRINOPEPTIDE A.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1708 MW; 09433547919E7C74 CRC64;

Query Match          16.7%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKE 13
DB 3 VKE 5

RESULT 16
FIBA MUSVI          STANDARD;          PRT;          16 AA.
ID FIBA MUSVI
AC P14458;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Mustela vison (American mink).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
OC Mustela.
OC NCBI_TaxID=9667;
OX [1]
RP SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 16 FIBRINOPEPTIDE A.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1679 MW; 09432A57919E7C66 CRC64;

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Query Match          16.7%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKE 13
DB 3 VKE 5

RESULT 17
MMPX SOLTU          STANDARD;          PRT;          16 AA.
ID MMPX SOLTU
AC P80501;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Unidentified mitochondrial matrix protein (Fragment).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Lamids; Solanales; Solanaceae; Solanum.
OC NCBI_TaxID=4113;
OX [1]
RP SEQUENCE.
RA TISSUE=Tuber;
RX MEDLINE=97077345; PubMed=8919912;
RT Jansch L., Kruft V., Schmitz U.K., Braun H.P.;
RT "New insights into the composition, molecular mass and stoichiometry
RT of the protein complexes of plant mitochondria.";
RL Plant J. 9:357-368(1996).
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC Mitochondrion.
KW NON_TER 16 16
SQ SEQUENCE 16 AA; 1768 MW; C58D4DB48AA18B8D CRC64;

Query Match          16.7%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VPK 10
DB 4 VPK 6

RESULT 18
ODPB SOLTU          STANDARD;          PRT;          16 AA.
ID ODPB SOLTU
AC P81419;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pyruvate dehydrogenase E1 component beta subunit, mitochondrial
DE (EC 1.2.4.1) (PDBE1-B) (Fragment).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Lamids; Solanales; Solanaceae; Solanum.
OC NCBI_TaxID=4113;
OX [1]
RP SEQUENCE.
RA STRAIN=cv. Romano; TISSUE=Tuber;
RX MEDLINE=98399821; PubMed=9729464;
RT Millar A.H., Knorr C., Leaver C.J., Hill S.A.;
RT "Plant mitochondrial pyruvate dehydrogenase complex: purification and
RT identification of catalytic components in potato.";
RL Biochem. J. 334:571-576(1998).
CC -!- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall
CC conversion of pyruvate to acetyl-CoA and CO(2). It contains
CC multiple copies of three enzymatic components: pyruvate
CC dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and
CC lipoamide dehydrogenase (E3).
CC -!- CATALYTIC ACTIVITY: Pyruvate + lipoamide = S-

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CC      acetylhydroliposamide + CO(2).
CC      -!- COFACTOR: THIAMINE PYROPHOSPHATE.
CC      -!- SUBUNIT: Tetramer of two alpha and two beta subunits (by
CC      similarity).
CC      -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
KW      Glycolysis; Oxidoreductase; Flavoprotein; Thiamine pyrophosphate;
KW      phosphorylation; Mitochondrion.
FT      NON_TER 16 16
SQ      SEQUENCE 16 AA; 1705 MW; FF6ED80EC804F797 CRC64;

Query Match      16.7%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 VKE 13
DB      4 VKE 6

RESULT 19
AL13_CARMA
ID      AL13_CARMA STANDARD; PRT; 18 AA.
AC      P81816;
DT      30-MAY-2000 (Rel. 39, Created)
DT      30-MAY-2000 (Rel. 39, Last sequence update)
DT      30-MAY-2000 (Rel. 39, Last annotation update)
DE      Carcinustatin 13.
OS      Carcinus maenas (Common shore crab) (Green crab).
OC      Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC      Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC      Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX      NCBI_TaxID=6759;
RN      [1]
RP      TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX      MEDLINE=98121193; PubMed=9461295;
RA      Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA      Thorpe A.;
RT      Isolation and identification of multiple neuropeptides of the
RT      allatostatin superfamily in the shore crab Carcinus maenas.;
RT      Eur. J. Biochem. 250:727-734(1997).
CC      -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC      -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW      Neuropeptide; Amidation; Multigene family.
FT      MOD_RES 18 18 AMIDATION (POTENTIAL).
SQ      SEQUENCE 18 AA; 2225 MW; 3531112C8160AE27 CRC64;

Query Match      16.7%; Score 3; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PKV 11
DB      11 PKV 13

RESULT 20
DRPH_UCAPU
ID      DRPH_UCAPU STANDARD; PRT; 18 AA.
AC      P08871;
DT      01-NOV-1988 (Rel. 09, Created)
DT      01-NOV-1988 (Rel. 09, Last sequence update)
DT      15-DEC-1998 (Rel. 37, Last annotation update)
DE      Pigment-dispersing hormone (PDH) (Light adapting distal retinal
DE      pigment hormone) (ORPH).
OS      Uca pugnator (Atlantic sand fiddler crab) (Caluca pugnator).
OC      Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC      Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC      Eubrachyura; Ocypodoidea; Ocypodidae; Ocypodinae; Uca complex;
OC      Celuca.
OX      NCBI_TaxID=6772;
RN      [1]
RP      SEQUENCE.

Rao K.R., Riehm J.P., Zahnaw C.A., Kleinholz L.H., Tarr G.E.,
Johnson L., Norton S., Landau M., Semmes O.J., Sattelsberg R.M.,
Jorenby W.H., Hintz M.F.;
"Characterization of a pigment-dispersing hormone in eyestalks of the
fiddler crab Uca pugnator.";
Proc. Natl. Acad. Sci. U.S.A. 82:5319-5322(1985).
[2]
SEQUENCE.
RX      MEDLINE=93230895; PubMed=8472537;
RA      Loehr J., Klein J., Webster S.G., Dirksen H.;
RT      "Quantification, immunofluorescence purification and sequence analysis of
RT      a pigment-dispersing hormone of the shore crab, Carcinus maenas
RT      (L.).";
Comp. Biochem. Physiol. 104B:699-706(1993).
CC      -!- FUNCTION: CAUSES THE MIGRATION OF THE DISTAL RETINAL PIGMENT
CC      INTO THE PROXIMAL END OF THE PIGMENT CHROMATOPHORE CELLS AND
CC      THUS DECREASES THE AMOUNT OF LIGHT ENTERING THE RETINULAS.
CC      -!- SIMILARITY: TO THE PDH OF OTHER ARTHROPODS.
DR      PIR; A25144; DRUFPD.
KW      Hormone; Amidation.
FT      DOMAIN 6 9 IMPORTANT FOR DRPH ACTIVITY.
FT      MOD_RES 18 18 AMIDATION.
SQ      SEQUENCE 18 AA; 1928 MW; 25D5CE8D016F544E CRC64;

Query Match      16.7%; Score 3; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PKV 11
DB      12 PKV 14

RESULT 21
RL24_PROVU
ID      RL24_PROVU STANDARD; PRT; 18 AA.
AC      P20032;
DT      01-FEB-1991 (Rel. 17, Created)
DT      01-FEB-1991 (Rel. 17, Last sequence update)
DT      15-DEC-1998 (Rel. 37, Last annotation update)
DE      50S ribosomal protein L24 (Fragment).
GN      RPLX.
OS      Proteus vulgaris.
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC      Enterobacteriaceae; Proteus.
OX      NCBI_TaxID=585;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=89125589; PubMed=2464692;
RA      Carretti D.P., Matheakis L.C., Kearney K.R., Vu L., Nomura M.;
RT      "Translational regulation of the spc operon in Escherichia coli.
RT      Identification and structural analysis of the target site for S8
RT      repressor protein.";
J. Mol. Biol. 204:309-329(1988).
CC      -!- FUNCTION: THIS PROTEIN IS FOUND IN THE RIBONUCLEOPROTEIN CORE AND
CC      IS INVOLVED IN THE EARLY ASSEMBLY OF THE 50S SUBUNIT. IT IS NOT
CC      INVOLVED IN THE FUNCTIONS OF THE MATURE 50S SUBUNIT.
CC      -!- SIMILARITY: BELONGS TO THE L24P FAMILY OF RIBOSOMAL PROTEINS.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; M36264; AAA5661.1; -
DR      InterPro; IPR005825; Ribosomal L24_26.
DR      PROSITE; PS01108; RIBOSOMAL_L24; PARTIAL.
KW      Ribosomal protein.
FT      NON_TER 1 1
SQ      SEQUENCE 18 AA; 2202 MW; 43606F53C5CBA57C CRC64;

```

Query Match 16.7%; Score 3; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 KET 14  
 ||||  
 Db 14 KET 16

RESULT 22  
 FIBB\_PIG STANDARD; PRT; 19 AA.  
 AC P14477;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).  
 GN FGB.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE.  
 RA Blomback B., Blomback M., Grondahl N.J.;  
 RT "Studies on fibrinopeptides from mammals."  
 RL Acta Chem. Scand. 19:1789-1791(1965).  
 CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT  
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET  
 CC AGGREGATION.  
 CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS  
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.  
 CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY  
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA  
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES  
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.  
 CC InterPro; IPR002181; Fibrinogen C.  
 DR PROSITE; PS00514; FIBRIN AG C DOMAIN; PARTIAL.  
 KW Blood coagulation; Plasma; Sulfation.  
 FT PEPTIDE 1 19 FIBRINOPEPTIDE B.  
 FT MOD\_RES 4 4 SULFATION.  
 FT NON\_TER 19 13  
 SQ SEQUENCE 19 AA; 2200 MW; 09F87E44F4F3863D CRC64;

Query Match 16.7%; Score 3; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKV 11  
 ||||  
 Db 12 PKV 14

RESULT 23  
 CS21\_STRTR STANDARD; PRT; 20 AA.  
 AC P81621;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE 21 kDa cold-shock induced protein (fragment).  
 OS Streptococcus thermophilus.  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 OC Streptococcus.  
 OX NCBI\_TaxID=1308;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=PB18;  
 RX MEDLINE=99456673; PubMed=10525839;  
 RA Ferrin C., Guimont C., Bracquart P., Gaillard J.L.;  
 RT "Expression of a new cold shock protein of 21.5 kDa and of the major  
 RT cold shock protein by Streptococcus thermophilus after cold shock."

RL Curr. Microbiol. 39:342-347(1999).  
 CC -!- INDUCTION: By cold shock.  
 FT NON\_TER 20 20  
 SQ SEQUENCE 20 AA; 2290 MW; 9C2CA57F266B80AD CRC64;

Query Match 16.7%; Score 3; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 KET 14  
 ||||  
 Db 5 KET 7

RESULT 24  
 LECB\_IRHO STANDARD; PRT; 20 AA.  
 ID LECB\_IRHO  
 AC P36231;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-JUN-1994 (Rel. 29, Last annotation update)  
 DE N-acetyl-D-galactosamine-binding lectin subunit B (A-disaccharide-  
 DE binding lectin subunit B) (Fragment).  
 DE Ixus hollandica (Dutch iris).  
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Iridaceae;  
 OC Iris.  
 OX NCBI\_TaxID=35876;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=cv. Golden Harvest, and cv. Prof. Blaauw; TISSUE=Bulb;  
 RX MEDLINE=94171801; PubMed=8125993;  
 RA Mo H., van Damme E.J.M., Peumans W.J., Goldstein I.J.;  
 RT "Isolation and characterization of an  
 RT N-acetyl-D-galactosamine-binding lectin from Dutch iris bulbs which  
 RT recognizes the blood group A disaccharide (GalNAc alpha 1-3Gal)."  
 RL J. Biol. Chem. 269:7665-7673(1994).  
 CC -!- FUNCTION: GAL / GALNAc-SPECIFIC LECTIN. AGGLUTINATES BOTH NATIVE  
 CC AND TRYPSIN-TREATED RABBIT ERYTHROCYTES BUT NOT HUMAN ERYTHROCYTES  
 CC IRRESPECTIVE OF BLOOD GROUP TYPE.  
 CC -!- SUBUNIT: DISULFIDE-LINKED HETERODIMER OF A AND B CHAINS.  
 KW Lectin.  
 FT NON\_TER 20 20  
 SQ SEQUENCE 20 AA; 2246 MW; DE08DA025FD17D56 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 ETM 15  
 ||||  
 Db 10 ETM 12

RESULT 25  
 PUFK\_RHOSH STANDARD; PRT; 20 AA.  
 ID PUFK\_RHOSH  
 AC Q53121; O08033;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Transcriptional regulatory protein pufK.  
 GN PUFK.  
 OS Rhodobacter sphaeroides (Rhodospseudomonas sphaeroides).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;  
 OC Rhodobacteraceae; Rhodobacter.  
 OX NCBI\_TaxID=1063;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;  
 RX MEDLINE=96349111; PubMed=8760918;  
 RA Gong L., Kaplan S.;  
 RT "translational control of puf operon expression in Rhodobacter

```
RT spheraoides 2.4.1.1;
RL Microbiology 142:2057-2069 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
RA McGlynn P.;
RT "R.sphaeroides genes bchC, bchX, bchY, bchZ and pufO.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
RX MEDLINE=20115911; PubMed=10648776;
RA Choudhary M., Kaplan S.;
RT "DNA sequence analysis of the photosynthesis region of Rhodobacter
sphaeroides 2.4.1.1.";
RL Nucleic Acids Res. 28:862-867 (2000).
CC -!- FUNCTION: INVOLVED IN THE TRANSCRIPTIONAL REGULATION OF PUFB.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; S82643; AAB46798.1; -.
DR EMBL; AJ010302; CAB38751.1; -.
DR EMBL; AF195122; AAF24301.1; -.
DR PIR; T50757; T50757.
KW Transcription regulation.
SQ SEQUENCE 20 AA; 2262 MW; 764DBD64B9DD990C CRC64;

Query Match 16.7%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 MVP 17
DB 1 MVP 3

RESULT 26
DCML_PSECH STANDARD; PRT; 4 AA.
AC P19916;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO
DE dehydrogenase subunit L) (CO-DH L) (Fragment).
GN CUTL.
OS Pseudomonas carboxydohydrogena.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae.
OX NCBI_TaxID=290;
RN [1]
RP SEQUENCE.
RX MEDLINE=90055678; PubMed=2818128;
RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
RT "Homology and distribution of CO dehydrogenase structural genes in
RT carboxydrotrophic bacteria.";
RL Arch. Microbiol. 152:335-341 (1989).
CC -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
CC dioxide.
CC -!- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
CC acceptor.
CC -!- COFACTOR: Molybdenum (molybdopterin).
CC -!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
CC SMALL.
DR PIR; P01140; P01140.
KW Oxidoreductase; Molybdenum.
FT NON_TER 4
```

```
SQ SEQUENCE 4 AA; 441 MW; 7761E876F0000000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 MG 7
DB 1 MG 2

RESULT 27
ASP2_LACSN STANDARD; PRT; 6 AA.
ID ASP2_LACSN STANDARD; PRT; 6 AA.
AC P82655;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Acid shock protein 2 (Fragment).
OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1625;
RN [1]
RP SEQUENCE.
RC STRAIN=CB1.
RX MEDLINE=21322712; PubMed=11429463;
RA De Angelis M., Bini L., Pallini V., Coconcelli P.S., Gobetti M.;
RT "The acid-stress response in Lactobacillus sanfranciscensis CB1.";
RL Microbiology 147:1863-1873 (2001).
CC -!- INDUCTION: Overexpressed in acid environments.
FT NON_TER 6
SQ SEQUENCE 6 AA; 778 MW; 6AA45B5B132A8000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 KE 13
DB 2 KE 3

RESULT 28
EI01_LITRU STANDARD; PRT; 6 AA.
ID EI01_LITRU STANDARD; PRT; 6 AA.
AC P82036;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Electrin 1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645 (1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD_RES 6
SQ SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 8 VP 9  
||  
Db 2 VP 3

## RESULT 29

OVN LEPDE STANDARD; PRT; 6 AA.  
AC P42585;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Oviductal motility stimulating peptide (Lep-OVM)  
OS Leptinotarsa decemlineata (Colorado potato beetle).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cuculiformia;  
OC Phytophaga; Chrysomeloidea; Chrysomelidae; Chrysomelinae;  
OC Chrysomelini; Leptinotarsa.  
OX NCBI\_TaxID=7539;  
RN [1]  
RP SEQUENCE AND SYNTHESIS.  
RC TISSUE=Head;  
RX MEDLINE=91271080; PubMed=2052497;  
RA Spittaels K., Schoofs L., Grauwels L., Smet H., van Damme J.,  
RA Proost P., Torrekens S., de Loof A.;  
RT "Isolation, identification and synthesis of novel oviductal motility  
stimulating head peptide in the Colorado potato beetle, Leptinotarsa  
decemlineata.";  
RL Peptides 12:31-36(1991).  
CC -!- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE  
OVIDUCT.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 6  
SQ SEQUENCE 6 AA; 720 MW; 6B07632BDD03000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 PE 4  
||  
Db 5 PE 6

## RESULT 30

UN06\_CLOPA STANDARD; PRT; 6 AA.  
AC P81351;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE Unknown protein CP 6 from 2D-page (Fragment).  
OS Clostridium pasteurianum.  
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
OC Clostridium.  
OX NCBI\_TaxID=1501;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=W5;  
RX MEDLINE=98291870; PubMed=9629918;  
RA Flengsrud R., Skjeldal L.;  
RT "Two-dimensional gel electrophoresis separation and N-terminal  
sequence analysis of proteins from Clostridium pasteurianum W5.";  
RL Electrophoresis 19:802-806(1998).  
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
PROTEIN IS: 5.0, ITS MW IS: 75.9 kDa.  
FT NON\_TER 6  
SQ SEQUENCE 6 AA; 657 MW; 605B1DC1A45A8000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EI 5  
||  
Db 5 EI 6

## RESULT 31

LANC\_CARUI STANDARD; PRT; 7 AA.  
AC P36360;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Lantibiotic carnocin UI49 (Fragment).  
OS Carnobacterium sp. (strain UI49).  
OC Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;  
OC Carnobacterium.  
OX NCBI\_TaxID=35782;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92321768; PubMed=1622206;  
RA Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,  
RA Nes I.F.;  
RT "Purification and characterization of a new bacteriocin isolated from  
a Carnobacterium sp.";  
RL Appl. Environ. Microbiol. 58:1417-1422(1992).  
CC -!- FUNCTION: LANTHIONINE-CONTAINING PEPTIDE ANTIBIOTIC (LANTIBIOTIC).  
CC ACTIVE ON GRAM-POSITIVE BACTERIA.  
KW Antibiotic; Bacteriocin; Lantibiotic.  
FT NON\_TER 7  
SQ SEQUENCE 7 AA; 786 MW; 741776D05B05B810 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3  
||  
Db 5 QP 6

## RESULT 32

TPFY\_PACDA STANDARD; PRT; 7 AA.  
AC P83455;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Tryptophyllin-1 (Pdt-1).  
OS Pachymedusa dactinolor (Giant mexican leaf frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
OC Phyllomedusinae; Pachymedusa.  
OX NCBI\_TaxID=75988;  
RN [1]  
RP SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF  
PRO-7.  
RC TISSUE=Skin secretion;  
RA Chen T.B., Orr D.F., Shaw C.;  
RT "Pachymedusa dactinolor tryptophyllin-1 (Pdt-1): structural  
characterization, pharmacological activity and cloning of precursor  
cDNA.";  
RL Submitted (SEP-2002) to the SWISS-PROT data bank.  
CC -!- FUNCTION: Myoactive. Has selective relaxing activity on vascular  
smooth muscle.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
CC -!- MASS SPECTROMETRY: MW=809.2; METHOD=MALDI.  
DR GO; GO:000576; C:extracellular; NAS.  
DR GO; GO:0045986; P:negative regulation of smooth muscle contra. .; NAS.  
KW Amphibian defense peptide; Amidation; Hydroxylation.  
FT MOD\_RES 3 3 3  
MOD\_RES 7 7 7  
AMIDATION.

```
SQ SEQUENCE 7 AA; 794 MW; 7772D37DC7776350 CRC64;
Query Match 11.1%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VP 9
DB 6 VP 7

RESULT 33
UF04 MOUSE STANDARD; PRT; 7 AA.
AC P3842;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P46) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast;
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC -!- PROTEIN IS: 5.0, ITS MW IS: 46 kDa.
FT NON TER 7
SQ SEQUENCE 7 AA; 766 MW; 68640AB77632700 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PK 10
DB 1 PK 2

RESULT 34
WMA3 ACHFU STANDARD; PRT; 7 AA.
AC P35921;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Wamide-3.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RX MEDLINE=93265912; PubMed=8495720;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RT "Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from
ganglia of the African giant snail, Achatina fulica.";
RL FEBS Lett. 323:104-108(1993).
DR PIR: S33244; S33244.
KW Neuropeptide; Amidation.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 965 MW; 7362D5B69B132310 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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QY 12 KE 13
DB 2 KE 3

RESULT 35
CCKN MACEU STANDARD; PRT; 8 AA.
AC P30369;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Cholecystokinin (CCK).
GN CCK.
OS Macropus eugenii (Tamar wallaby), and
OS Dasyurus viverrinus (Southeastern quoll).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
NCBI_TaxID=9315, 9279;
RN [1]
RP SEQUENCE.
RC SPECIES=M. eugenii, and D. viverrinus;
RC TISSUE=Brain;
RX MEDLINE=88234141; PubMed=3375140;
RA Fan Z.W., Eng J., Shaw G., Yallow R.S.;
RT "Cholecystokinin octapeptide purified from brains of Australian
marsupials.";
RL Peptides 9:429-431(1988).
CC -!- FUNCTION: THIS PEPTIDE HORMONE INDUCES GALL BLADDER CONTRACTION
CC -!- AND THE RELEASE OF PANCREATIC ENZYMES IN THE GUT. ITS FUNCTION
CC IN THE BRAIN IS NOT CLEAR.
CC -!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
DR PIR: A43001; A43001.
DR PIR: PQ0012; PQ0012.
DR InterPro: IPR001651; Gastrin.
DR PROSITE: PS00259; GASTRIN; 1.
KW Amidation; Sulfation; Hormone.
FT MOD_RES 2 2 SULFATION.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1064 MW; DDCAA68378768B5A CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 MG 7
DB 3 MG 4

RESULT 36
FUSS FUSSO STANDARD; PRT; 8 AA.
AC P81010;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Allergen Fus s I3596* (Fragment).
OS Fusarium solani (subsp. pisi) (Nectria haematococca).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
NCBI_TaxID=70791;
RN [1]
RP SEQUENCE.
RC STRAIN=IARI 3596; TISSUE=Mycelium;
RA Verma J., Gangal S.V.;
RL Submitted (JUL-1997) to the SWISS-PROT data bank.
KW Allergen.
FT NON TER 8
SQ SEQUENCE 8 AA; 898 MW; C372C441F5B69041 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
```



Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;  
Matches 2; Conservative 0; Mismatches 0;

QY 5 IM 6  
||  
Db 2 IM 3

## RESULT 37

NPB\_BOVIN  
ID\_NPB\_BOVIN STANDARD; PRT; 8 AA.  
AC P15507;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Neuropeptide B.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Brain;  
RX MEDLINE=86067985; PubMed=3865193;  
RA Yang H.-Y.T., Fratta W., Majane E.A., Costa E.;  
RT "Isolation, sequencing, synthesis, and pharmacological  
RT characterization of two brain neuropeptides that modulate the action  
RT of morphine";  
RL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).  
CC -!- FUNCTION: MODULATES THE ACTION OF MORPHINE.  
CC PIR; B24749; B24749.  
KW Neuropeptide; Amidation.  
FT MOD RES 8  
SQ SEQUENCE 8 AA; 1082 MW; 87D416C776D9C729 CRC64;  
AMIDATION.

Query Match 11.1%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3  
||  
Db 4 QP 5

## RESULT 38

PK3\_PERAM  
ID\_PPK3\_PERAM STANDARD; PRT; 8 AA.  
AC P82618;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Pyrokinin-3 (Pea-PK-3) (FXPRL-amide).  
OS Periplaneta americana (American cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
OC Blattidae; Periplaneta.  
OX NCBI\_TaxID=6978;  
RN [1]  
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
RC TISSUE=retrocerebral complex;  
RX MEDLINE=99212469; PubMed=10196736;  
RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;  
RT "Differential distribution of pyrokinin-isoforms in cerebral and  
RT abdominal neurohemal organs of the American cockroach.";  
RL Insect Biochem. Mol. Biol. 29:139-144(1999).  
RN [2]  
RP TISSUE SPECIFICITY.  
RX MEDLINE=20189894; PubMed=10723010;  
RA Predel R., Eckert M.;  
RT "Tagma-specific distribution of FXPRLamides in the nervous system of  
RT the American cockroach.";  
RL J. Comp. Neurol. 419:352-363(2000).

CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
(MYOTROPIC ACTIVITY).  
CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.  
CC -!- MASS SPECTROMETRY: MW=996.5; METHOD=MALDI.  
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
KW Neuropeptide; Amidation; Pyrokinin.  
FT MOD RES 8  
SQ SEQUENCE 8 AA; 997 MW; 0B34177409D772C7 CRC64;  
AMIDATION.

Query Match 11.1%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VP 9  
||  
Db 2 VP 3

## RESULT 39

RS7\_MYCIT  
ID\_RS7\_MYCIT STANDARD; PRT; 8 AA.  
AC P33564;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE 30S ribosomal protein S7 (Fragment).  
DE RPSG.  
GN RPSG.  
OS Mycobacterium intracellulare.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
OX NCBI\_TaxID=1767;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93197130; PubMed=8451173;  
RA Nair J., Rouse D.A., Morris S.L.;  
RT "Nucleotide sequence analysis of the ribosomal S12 gene of  
RT Mycobacterium intracellulare.";  
RL Nucleic Acids Res. 21:1039-1039(1993).  
CC -!- FUNCTION: One of the primary rRNA binding proteins, it binds  
CC directly to 16S rRNA where it nucleates assembly of the head  
CC domain of the 30S subunit. Is located at the subunit interface  
CC close to the decoding center, probably blocks exit of the E-site  
CC tRNA (By similarity).  
CC -!- SUBUNIT: Part of the 30S ribosomal subunit. Contacts proteins S9  
CC and S11 (By similarity).  
CC -!- SIMILARITY: BELONGS TO THE S7P FAMILY OF RIBOSOMAL PROTEINS.

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EMBL; L08171; AAA25376.1; -;  
PIR; S35538; S35538.  
DR HAWAP; MF 00480; -; 1.  
DR InterPro; IPR000235; Ribosomal\_S7.  
DR PROSITE; PS00052; RIBOSOMAL\_S7; PARTIAL.  
KW Ribosomal protein; RNA-binding; tRNA-binding.  
FT INIT MET 0 0 BY SIMILARITY.  
FT NON\_TER 8 8  
SQ SEQUENCE 8 AA; 850 MW; 63276DC768732417 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PK 10  
||  
Db 7 PK 8

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RESULT 40
UH09 RAT
ID UH09 RAT STANDARD; PRT; 8 AA.
AC P56575;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Unknown protein from 2D-page of heart tissue (Spot P9) (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Wistar; TISSUE=Heart;
RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
RA Junblut P.R.;
RL Submitted (SEP-1998) to the SWISS-PROT data bank.
CC -!- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 8.9, ITS MW IS: 42 kDa.
FT NON TER 8
SQ SEQUENCE 8 AA; 1029 MW; 9E0775A6C4140B06 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PE 4
||
Db 7 PE 8

RESULT 41
UPA1 HUMAN
ID UPA1 HUMAN STANDARD; PRT; 8 AA.
AC P30087;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 2) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.9, ITS MW IS: 65 kDa.
DR SWISS-2DPAGE; P30087; HUMAN.
FT NON TER 1
FT UNSURE 8
FT NON TER 8
SQ SEQUENCE 8 AA; 944 MW; C01772C455BB06DA CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VP 9
||
Db 6 VP 7

RESULT 42
AL10_CARMA

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ID AL10_CARMA STANDARD; PRT; 9 AA.
AC P81813;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinus maenas.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD RES 9
SQ SEQUENCE 9 AA; 963 MW; 372D79DCB4776C7 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3
||
Db 3 QP 4

RESULT 43
BS43 SERPL
ID BS43 SERPL STANDARD; PRT; 9 AA.
AC P83375;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bacteriocin serracin P 43 kDa subunit (Fragment).
OS Serratia plymuthica.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Serratia.
OX NCBI_TaxID=82996;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC STRAIN=J7;
RX MEDLINE=22293561; PubMed=12406768;
RA Jabrane A., Sabri A., Compere P., Jacques P., Vandenberghe I.,
RA Van Beeumen J., Thonart P.;
RT "Characterization of serracin P, a phage-tail-like bacteriocin, and
RT its activity against Erwinia amylovora, the fire blight pathogen.";
RL Appl. Environ. Microbiol. 68:5704-5710(2002).
CC -!- FUNCTION: Major component of a prophage tail sheath (Probable).
CC -!- FUNCTION: Antibacterial activity against Gram-negative bacterium
CC E. amylovora.
DR InterPro; IPR006498; Tail tube.
DR Pfam; PF04985; Phage tube_1.
KW Antibiotic; Bacteriocin.
FT NON TER 9
SQ SEQUENCE 9 AA; 1095 MW; 1B66D412C871B1FB CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GV 8
||
Db 5 GV 6

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RESULT 44
CONO CONGE STANDARD; PRT; 9 AA.
ID _CONO CONGE STANDARD; PRT; 9 AA.
AC P05486;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lys-conopressin G.
OS Conus geographus (Geography cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6491;
RN [1]
RP SEQUENCE.
RX MEDLINE=88058932; PubMed=3680228;
RA Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,
RA Gray W.R., Olivera B.M.;
RT "Invertebrate vasopressin/oxytocin homologs. Characterization of
RT peptides from Conus geographus and Conus striatus venoms.";
RL J. Biol. Chem. 262:15821-15824(1987).
RN [2]
RP REVIEW.
RX MEDLINE=89024586; PubMed=3052286;
RA Gray W.R., Olivera B.M., Cruz L.J.;
RT "Peptide toxins from venomous Conus snails.";
RL Annu. Rev. Biochem. 57:665-700(1988).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR; A28495; A28495.
DR InterPro; IPR000981; Neurhyp_horn.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
FT SEQUENCE 9 AA; 1037 MW; DAFC276EB4540059 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PK 10
Db 7 PK 8

RESULT 45
FAR3_PENNO STANDARD; PRT; 9 AA.
ID _FAR3_PENNO STANDARD; PRT; 9 AA.
AC P83318;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLP3 (AQFSMRLPF-amide).
OS Penaeus monodon (Pencoid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RX TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupum J., Krungkarn C., Longyant S.,
RA Chaivuthangkura P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Penaeus monodon.";
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=1121.2; METHOD=MALDI.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
CC Neuropeptide; Amidation.
FT MOD_RES 9 9
FT SEQUENCE 9 AA; 1121 MW; DA0B07340685A776 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QP 3
Db 2 QP 3

RESULT 46
FAR4_PENNO STANDARD; PRT; 9 AA.
ID _FAR4_PENNO STANDARD; PRT; 9 AA.
AC P83319;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLP4 (SQPSMRLPF-amide).
OS Penaeus monodon (Pencoid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RX TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupum J., Krungkarn C., Longyant S.,
RA Chaivuthangkura P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Penaeus monodon.";
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=1119.8; METHOD=MALDI.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
CC Neuropeptide; Amidation.
FT MOD_RES 9 9
FT SEQUENCE 9 AA; 1121 MW; DA0B07340685A776 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QP 3
Db 2 QP 3

RESULT 47
FLA2_TREHY STANDARD; PRT; 9 AA.
ID _FLA2_TREHY STANDARD; PRT; 9 AA.
AC P80159;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Flagellar filament outer layer protein flaa2 (35 kDa sheath protein)
DE (Fragment).
GN FLA2.
OS Treponema hyodysenteriae (Serpulina hyodysenteriae).
OC Bacteria; Spirochaetes; Spirochaetales; Brachyspiraceae; Brachyspira.
OX NCBI_TaxID=159;
RN [1]
RP SEQUENCE.
RC STRAIN=C5;
RX MEDLINE=93139764; PubMed=1487733;
RA Koopman M.B.H., Baats E., van Vorstenbosch C.J.A.H.V.,
RA van der Zeijst B.A.M., Kusters J.G.;
RT "The periplasmic flagella of Serpulina (Treponema) hyodysenteriae are

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RT composed of two sheath proteins and three core proteins." ;
RL J. Gen. Microbiol. 138:2697-2706(1992).
CC -!- FUNCTION: COMPONENT OF THE OUTER LAYER OF THE FLAGELLA.
CC -!- SUBUNIT: THE FLAGELLUM CONSISTS OF AN OUTER LAYER COMPOSED OF TWO
CC SHEATH PROTEINS, FLA1 (44 kDa) AND FLA2 (35 kDa) AROUND A CORE
CC THAT CONTAINS THREE PROTEINS FLA1 (37 kDa), FLA2 (34 kDa) AND
CC FLA3 (32 kDa).
CC -!- SUBCELLULAR LOCATION: Periplasmic flagellum.
KW Flagella; Periplasmic.
FT UNSURE 2 2
FT UNSURE 8 9
FT NON TER 9 9
SQ SEQUENCE 9 AA; 1129 MW; 855A19C68B4772D1 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 ET 14
DB 1 ET 2

RESULT 48
FRF1_SARBU STANDARD; PRT; 9 AA.
AC P83350;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neb-FMRFamide 1.
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7385;
RN [1]_TaxID=7385;
RP SEQUENCE, AMIDATION, AND FUNCTION.
RC TISSUE-CNS;
RX MEDLINE=22342733; PubMed=12438685;
RA Meusen T., Mertens I., Clynen E., Baggerman G., Nichols R.,
RA Nachman R.J., Huybrechts R., De Loof A., Schoofs L.;
RT "Identification in Drosophila melanogaster of the invertebrate G
RT protein-coupled FMRamide receptor."
RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).
CC -!- FUNCTION: Has modulatory actions at skeletal neuromuscular
CC junctions.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1155 MW; 2D810699CAB6C5A7 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3
DB 1 QP 2

RESULT 49
LMT3_LOCMI STANDARD; PRT; 9 AA.
AC P41489;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Locustamyotropin 3 (LOM-MT-3).
OS Locusta migratoria (Migratory locust).

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OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]_TaxID=7004;
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,
RA de Loof A.;
RT "Isolation, identification and synthesis of locustamyotropin III and
RT IV, two additional neuropeptides of Locusta migratoria: members of the
RT locustamyotropin peptide family." ;
RL Insect Biochem. Mol. Biol. 22:447-452(1992).
CC -!- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR PIR; A61620; A61620.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1140 MW; D5AE1772C9D776C6 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3
DB 3 QP 4

RESULT 50
NEF_HV128 STANDARD; PRT; 9 AA.
ID NEF_HV128
AC P12481;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Negative factor (F-protein) (27 kDa protein) (3'ORF) (Fragment).
GN NEF.
OS Human immunodeficiency virus type 1 (Z-84 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11681;
RN [1]_TaxID=11681;
RP SEQUENCE FROM N.A.
RX MEDLINE=8281278; PubMed=3395517;
RA Yourno J., Josephs S.F., Reitz M.S. Jr., Zagury D., Wong-Staal F.,
RA Gallo R.C.;
RT "Nucleotide sequence analysis of the env gene of a new Zairian
RT isolate of HIV-1." ;
RL AIDS Res. Hum. Retroviruses 4:165-173(1988).
CC -!- FUNCTION: NEF has GTPase, GTP-binding and autophosphorylating
CC activities. It seems to down-regulate the CD4(T4) antigen.
CC -!- MISCELLANEOUS: THE Z-84 ISOLATE WAS TAKEN FROM A 54 YEAR-OLD
CC ZAIREAN MALE.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; J03653; AAA44687.1; -.
DR HIV; J03653; NEFSY1.
KW AIDS; Myristate; GTP-binding.
FT LIPID 2 2 MYRISTATE (BY SIMILARITY).
FT NON TER 9 9
SQ SEQUENCE 9 AA; 967 MW; 319CB325A3733878 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;

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Best Local Similarity 100.0%; Pred. No. 1.3e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 2; Conservative 0;

QY 6 MG 7  
||  
Db 1 MG 2

RESULT 51  
RT33 BOVIN  
ID RT33 BOVIN STANDARD; PRT; 9 AA.  
AC P82926;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Mitochondrial 28S ribosomal protein S33 (S33mt) (MRP-S33) (Fragment).  
GN MRP633.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Liver;  
RX MEDLINE=21276436; PubMed=11279123;  
RA Koc E.C.; Burkhardt W.; Blackburn K.; Moseley A.; Spremulli L.L.;  
RT "The small subunit of the mammalian mitochondrial ribosome:  
RT identification of the full complement of ribosomal proteins present."  
RL J. Biol. Chem. 276:19363-19374(2001).  
CC -!- SUBUNIT: Component of the mitochondrial ribosome small subunit  
CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.  
CC -!- SUBCELLULAR LOCATION: Mitochondrial.  
KW Ribosomal protein; Mitochondrion.  
FT NON\_TER 1 1  
FT NON\_TER 9 9  
SQ SEQUENCE 9 AA; 1032 MW; D341D73776DB05B9 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3  
||  
Db 5 QP 6

RESULT 52  
SAP\_STOVA  
ID SAP\_STOVA STANDARD; PRT; 9 AA.  
AC P24047;  
DT 01-MAR-1992 (Rel. 21, Created)  
DT 01-MAR-1992 (Rel. 21, Last sequence update)  
DT 01-MAR-1992 (Rel. 21, Last annotation update)  
DE Sperm-activating peptide (SAP).  
OS Stomopneustes variolaris (Sea urchin).  
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
OC Echinoidea; Euechinoidea; Diademataceae; Phymosomatoida; Stomechinidae;  
OC Stomopneustes.  
OX NCBI\_TaxID=7663;  
RN [1]  
RP SEQUENCE, AND DISULFIDE BOND.  
RC TISSUE=Egg jelly;  
RX MEDLINE=92097763; PubMed=1756858;  
RA Yoshino K.-I., Takao T., Shimonishi Y., Suzuki N.;  
RT "Determination of the amino acid sequence of an intramolecular  
RT disulfide linkage-containing sperm-activating peptide by tandem mass  
RT spectrometry."  
RL FEBS Lett. 294:179-182(1991).  
CC -!- FUNCTION: CAUSE STIMULATION OF SPERM RESPIRATION AND MOTILITY  
CC THROUGH INTRACELLULAR ALKALINIZATION, TRANSIENT ELEVATIONS OF  
CC CAMP, CGMP AND CALCIUM LEVELS IN SPERM CELLS, AND TRANSIENT  
CC ACTIVATION AND SUBSEQUENT INACTIVATION OF THE MEMBRANE FORM OF

CC GUANYLATE CYCLASE.  
FT DISULFID 3 8  
SQ SEQUENCE 9 AA; 1010 MW; C469B3387B076EB9 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PE 4  
||  
Db 4 PE 5

RESULT 53  
TKL1 CALVO  
ID TKL1 CALVO STANDARD; PRT; 9 AA.  
AC P41517;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Callitachykinin I.  
OS Calliphora vomitoria (Blue blowfly).  
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Calliphoridae; Calliphora.  
OX NCBI\_TaxID=27454;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RX MEDLINE=95075727; PubMed=7984492;  
RA Lundquist C.T.; Clottens F.L.; Holman G.M.; Nichols R.J.;  
RA Naessel D.R.;  
RT "Callitachykinin I and II, two novel myotropic peptides isolated from  
RT the blowfly, Calliphora vomitoria, that have resemblances to  
RT tachykinins.";  
RL Peptides 15:761-768(1994).  
CC -!- FUNCTION: MYOACTIVE PEPTIDE.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.  
KW Tachykinin; Neuropeptide; Amidation.  
FT MOD\_RES 9 9  
FT AMIDATION.  
SQ SEQUENCE 9 AA; 981 MW; 2417C86B59DC1B7 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GV 8  
||  
Db 7 GV 8

RESULT 54  
TKL1 LOOMI  
ID TKL1 LOOMI STANDARD; PRT; 9 AA.  
AC P16223;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Locustatachykinin I (TK-I).  
OS Locusta migratoria (Migratory locust).  
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
OX NCBI\_TaxID=7004;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Brain;  
RX MEDLINE=90184489; PubMed=2311766;  
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;  
RT "Locustatachykinin I and II, two novel insect neuropeptides with  
RT homology to peptides of the vertebrate tachykinin family."  
RL FEBS Lett. 261:397-401(1990).  
CC -!- FUNCTION: MYOACTIVE PEPTIDE. STIMULATES THE CONTRACTION OF THE

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CC      OVIDUCT AND FOREGUT.
CC      -!- SUBCELLULAR LOCATION: Secreted.
CC      -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW      Tachykinin; Neuropeptide; Amidation.
FT      MOD RES          9          9
SQ      SEQUENCE 9 AA; 939 MW; 2389C86B59C865A7 CRC64;

Query Match          11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GV 8
      |||
Db      7 GV 8

RESULT 55
ID      TRP4 LEUMA          STANDARD;          PRT;          9 AA.
AC      P81736;
DT      30-MAY-2000 (Rel. 39, Created)
DT      30-MAY-2000 (Rel. 39, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DE      Tachykinin-related peptide 4 (LemRP 4).
OS      Leucophaea maderae (Madeira cockroach).
OC      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC      Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC      Blaberidae; Leucophaea.
OX      NCBI_TaxID=6988;
RN      [1] _SEQUENCE
RP      SEQUENCE
RC      TISSUE=Midgut;
RX      MEDLINE=97053012; PubMed=8897641;
RA      Muren J.E., Naessel D.R.;
RT      "Isolation of five tachykinin-related peptides from the midgut of
RT      the cockroach Leucophaea maderae: existence of N-terminally extended
RT      isoforms.";
RL      Regul. Pept. 65:185-196(1996).
CC      -!- FUNCTION: MYOACTIVE PEPTIDE. INCREASES THE AMPLITUDE AND FREQUENCY
CC      OF SPONTANEOUS CONTRACTIONS AND TONUS OF HINDGUT MUSCLE.
CC      -!- SUBCELLULAR LOCATION: Secreted.
CC      -!- TISSUE SPECIFICITY: MIDGUT.
CC      -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW      Tachykinin; Neuropeptide; Amidation.
FT      MOD RES          9          9
SQ      SEQUENCE 9 AA; 953 MW; 2403987699C865A7 CRC64;

Query Match          11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 MG 7
      |||
Db      6 MG 7

RESULT 56
ID      UF02 MOUSE          STANDARD;          PRT;          9 AA.
AC      P38640;
DT      01-OCT-1994 (Rel. 30, Created)
DT      01-OCT-1994 (Rel. 30, Last sequence update)
DT      01-FEB-1995 (Rel. 31, Last annotation update)
DE      Unknown protein from 2D-page of fibroblasts (P32) (Fragment).
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1] _SEQUENCE
RP      SEQUENCE
RC      TISSUE=Fibroblast;
RX      MEDLINE=95009907; PubMed=7523108;
RA      Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;

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RT      "Separation and sequencing of familiar and novel murine proteins
RT      using preparative two-dimensional gel electrophoresis.";
RL      Electrophoresis 15:735-745(1994).
CC      -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC      PROTEIN IS: 6.0, ITS MW IS: 32 kDa.
FT      NON TER          9          9
SQ      SEQUENCE 9 AA; 1102 MW; 7E73EAB6D05B1AAB CRC64;

Query Match          11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 EI 5
      |||
Db      4 EI 5

RESULT 57
ID      ULAD HUMAN          STANDARD;          PRT;          9 AA.
AC      P31929;
DT      01-JUL-1993 (Rel. 26, Created)
DT      01-JUL-1993 (Rel. 26, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Unknown protein from 2D-page of liver tissue (Spot 106) (Fragment).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1] _SEQUENCE
RP      SEQUENCE
RC      TISSUE=Liver;
RX      MEDLINE=94147969; PubMed=8313870;
RA      Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,
RA      Tissot J.-D., Balroch A., Appel R.D., Hochstrasser D.F.;
RT      "Human liver protein map: update 1993.";
RL      Electrophoresis 14:1216-1222(1993).
CC      -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC      PROTEIN IS: 6, ITS MW IS: 15 kDa.
FT      SWISS-2DPAGE; P31929; HUMAN.
FT      NON TER          9          9
SQ      SEQUENCE 9 AA; 1129 MW; D02DFB41B6D33322 CRC64;

Query Match          11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 VK 12
      |||
Db      2 VK 3

RESULT 58
ID      ULAK MOUSE          STANDARD;          PRT;          9 AA.
AC      P99031;
DT      15-DEC-1998 (Rel. 37, Created)
DT      15-DEC-1998 (Rel. 37, Last sequence update)
DT      15-DEC-1998 (Rel. 37, Last annotation update)
DE      Unknown protein from 2D-page of liver tissue (Spot 2D-0014LD)
DE      (Fragment).
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1] _SEQUENCE
RP      SEQUENCE
RC      TISSUE=Liver;
RA      Sanchez J.-C., Rouge V., Frutiger S., Hughes G.J., Yan J.X.,
RA      Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F.,
RA      Cowthorne M.;
RL      Submitted (AUG-1998) to the SWISS-PROT data bank.
CC      -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN

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CC PROTEIN IS: 6.0, ITS MW IS: 12.5 kDa.  
 DR SWISS-2DPAGE; P99031; MOUSE.  
 FT NON TER 9  
 SQ SEQUENCE 9 AA; 1106 MW; E1E842C3240B145A CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KV 11  
 ||  
 Db 6 KV 7

RESULT 59  
 ID UPA7 HUMAN STANDARD; PRT; 9 AA.  
 AC P30093;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Unknown protein from 2D-page of plasma (Spot 18) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Plasma;  
 RX MEDLINE=93092937; PubMed=1459097;  
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,  
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,  
 RA Hochstrasser D.F.;  
 RT "Plasma protein map: an update by microsequencing."  
 RL Electrophoresis 13:707-714(1992).  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 5.05, ITS MW IS: 37 kDa.  
 DR SWISS-2DPAGE; P30093; HUMAN.  
 FT NON TER 1 1  
 FT UNSURE 5 5  
 FT NON TER 9 9  
 SQ SEQUENCE 9 AA; 1042 MW; 5C14477AEB0772C7 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PE 4  
 ||  
 Db 4 PE 5

RESULT 60  
 ID COXA ONCMY STANDARD; PRT; 10 AA.  
 AC P80328;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Cytochrome c oxidase polypeptide Va (EC 1.9.3.1) (Fragment).  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 OX NCBI\_TaxID=8022;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Liver;  
 RX MEDLINE=94237150; PubMed=8181469;  
 RA Freund R., Kadenbach B.;  
 RT "Identification of tissue-specific isoforms for subunits Vb and VIIa  
 of cytochrome c oxidase isolated from rainbow trout.";  
 RL Eur. J. Biochem. 221:1111-1116(1994).

CC -!- FUNCTION: THIS IS THE HEME A-CONTAINING CHAIN OF CYTOCHROME C  
 OXIDASE. THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.  
 CC -!- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome  
 CC c + 2 H(2)O.  
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.  
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VA FAMILY.  
 DR PIR; S43625; S43625.  
 KR Oxidoreductase; Heme; Mitochondrion; Inner membrane.  
 KW NON\_TER 10 10  
 FT SEQUENCE 10 AA; 1144 MW; C535CSB1AB02C33D CRC64;  
 SQ

Query Match 11.1%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KV 11  
 ||  
 Db 4 KV 5

RESULT 61  
 ID COXH ONCMY STANDARD; PRT; 10 AA.  
 AC P80331;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 01-OCT-1994 (Rel. 30, Last annotation update)  
 DE Cytochrome c oxidase polypeptide Vic (EC 1.9.3.1) (Fragment).  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 OX NCBI\_TaxID=8022;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Liver;  
 RX MEDLINE=94237150; PubMed=8181469;  
 RA Freund R., Kadenbach B.;  
 RT "Identification of tissue-specific isoforms for subunits Vb and VIIa  
 of cytochrome c oxidase isolated from rainbow trout.";  
 RL Eur. J. Biochem. 221:1111-1116(1994).  
 CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE  
 CC CHAINS OF CYTOCHROME C OXIDASE. THE TERMINAL OXIDASE IN  
 CC MITOCHONDRIAL ELECTRON TRANSPORT.  
 CC -!- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome  
 CC c + 2 H(2)O.  
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.  
 DR PIR; S43630; S43630.  
 KW Oxidoreductase; Inner membrane; Mitochondrion.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 977 MW; E11B40769DC772DA CRC64;

Query Match 11.1%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VP 9  
 ||  
 Db 4 VP 5

RESULT 62  
 ID COXK ONCMY STANDARD; PRT; 10 AA.  
 AC P80332;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Cytochrome c oxidase polypeptide Vira-heart (EC 1.9.3.1) (Fragment).  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

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OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=94237150; PubMed=8181469;
RA Freund R., Kadenbach B.;
RT "Identification of tissue-specific isoforms for subunits Vb and VIIa
of cytochrome c oxidase isolated from rainbow trout.";
RL Eur. J. Biochem. 221:1111-1116(1994).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferrocytochrome
c + 2 H2O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIA FAMILY.
DR PIR; S43631; S43631.
KW Oxidoreductase; Inner membrane; Mitochondrion.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1174 MW; 4C8D81CAFAF772C3 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KV 11
DB 3 KV 4

RESULT 63
FAR6_PANRE
ID FAR6_PANRE STANDARD; PRT; 10 AA.
AC P82660;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE FMRFamide-like neuropeptide PF6 (NGAFQPFVRF-amide).
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
OX NCBI_TaxID=6233;
RN [1]
RP SEQUENCE, FUNCTION, AND AMIDATION.
RA Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,
RA Maule A.G.;
RT "Isolation, characterization and pharmacology of RMRFamide-related
peptides (Farps) from free-living nematode, Panagrellus redivivus.";
RL Submitted (JUL-2000) to the SWISS-PROT data bank.
CC -!- FUNCTION: MYOACTIVE.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 10 10
SQ SEQUENCE 10 AA; 1132 MW; CB13E4C9D776C76D CRC64;

Query Match 11.1%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QP 3
DB 5 QP 6

RESULT 64
GAJU_HUMAN
ID GAJU_HUMAN STANDARD; PRT; 10 AA.
AC P01358;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last annotation update)
DE Gastric juice peptide.

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75150968; PubMed=5538385;
RA Heathcote J.G., Washington R.J.;
RT "Peptides of normal human gastric juice.";
RL Int. J. Protein Res. 2:117-126(1970).
DR PIR; A01628; GXHU1.
DR MIM; 137220; -.
DR GO; GO:0007586; P:digestion; NAS.
FT PEPTIDE 1 10
FT PEPTIDE 2 10
SQ SEQUENCE 10 AA; 1004 MW; CFEC6AB02C387D CRC64;

Query Match 11.1%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KV 11
DB 5 KV 6

RESULT 65
LABA_JATMU
ID LABA_JATMU STANDARD; PRT; 10 AA.
AC P13270;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Labaditin.
OS Jatropha multifida (Physic nut).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Malpighiales; Euphorbiaceae; Jatropha.
OX NCBI_TaxID=3996;
RN [1]
RP SEQUENCE.
RC TISSUE=LateX;
RA Kosasi S., van der Sluis W.G., Boelens R., T'Hart L.A., Labadie R.P.;
RT "Labaditin, a novel cyclic decapeptide from the latex of Jatropha
multifida L. (Euphorbiaceae). Isolation and sequence determination
by means of two-dimensional NMR.";
RL FEBS Lett. 256:91-96(1989).
CC -!- FUNCTION: LABADITIN IS AN ACTIVE PEPTIDE WHICH INHIBITS THE
CLASSICAL PATHWAY OF COMPLEMENT ACTIVATION IN VITRO. ACTIVITY
SEEMS TO BE BASED ON AN INTERACTION WITH C1.
CC -!- PTM: This is a cyclic peptide.
CC -!- DISEASE: LATEX OF THIS PLANT IS USED IN FOLKLORIC MEDICINE FOR
TREATMENT OF INFECTED WOUNDS, SKINS INFECTIONS AND SCABIES.
SQ SEQUENCE 10 AA; 1089 MW; D98AAD6362D1B362 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GV 8
DB 2 GV 3

RESULT 66
LPK2_LOCMI
ID LPK2_LOCMI STANDARD; PRT; 10 AA.
AC P41488;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Locustapyrrolin 2 (LOM-PK-2) (FXPRL-amide).
OS Locusta migratoria (Migratory locust).

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OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
 ON NCBI\_TaxID=7004;  
 RP SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=94094539; PubMed=7903606;  
 RA Schoofs L., Holman G.M., Nachman R., Proost P., van Damme J.,  
 RA de Loof A.;  
 RT "Isolation, identification and synthesis of locustapyrokinin II from  
 RT Locusta migratoria, another member of the FXPRL-amide peptide  
 RT family.";  
 RL Comp. Biochem. Physiol. 106C:103-109(1993).  
 CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY (MYOTROPIC  
 CC ACTIVITY).  
 CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
 DR InterPro; IPR001484; Pyrokinin.  
 DR PROSITE; PS00539; PYROKININ; 1.  
 KW Neuropeptide; Amidation; Pyrokinin; Pyroglutamate carboxylic acid.  
 FT MOD\_RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.  
 FT MOD\_RES 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1145 MW; CFAF4271A9D1B772 CRC64;  
 Query Match 11.1%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 VP 9  
 DB 3 VP 4  
 RESULT 67  
 ODP2\_BOVIN  
 ID ODP2\_BOVIN STANDARD; PRT; 10 AA.  
 AC P11180;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DT 01-JUL-1989 (Rel. 11, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Dihydropolipoamide acetyltransferase component of pyruvate dehydrogenase  
 DE complex [EC 2.3.1.12] (E2) (Fragment).  
 GN DLAT.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=88024154; PubMed=3117054;  
 RA Bradford A.P., Howell S., Aitken A., James L.A., Yeaman S.J.;  
 RT "Primary structure around the lipocate-attachment site on the E2  
 RT component of bovine heart pyruvate dehydrogenase complex.";  
 RL Biochem. J. 245:919-922(1987).  
 CC -!- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall  
 CC conversion of pyruvate to acetyl-CoA and CO(2). It contains  
 CC multiple copies of three enzymatic components: pyruvate  
 CC dehydrogenase (E1), dihydropolipoamide acetyltransferase (E2) and  
 CC lipopamide dehydrogenase (E3).  
 CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + dihydropolipoamide = CoA + S-  
 CC acetyldihydropolipoamide.  
 CC -!- COFACTOR: THE E2 COMPONENT CONTAINS TWO COVALENTLY-BOUND LIPOYL  
 CC COFACTOR.  
 CC -!- SUBUNIT: FORMS A 24-POLYPEPTIDE STRUCTURAL CORE WITH OCTAHEDRAL  
 CC SYMMETRY.  
 CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.  
 CC -!- SIMILARITY: BELONGS TO THE 2-OXOACID DEHYDROGENASE FAMILY.  
 CC -!- SIMILARITY: Contains 2 lipoyl-binding domains.  
 DR InterPro; IPR003016; Lipoyl.  
 DR PROSITE; PS00189; LIPOYL; PARTIAL.  
 KW Glycolysis; Transferase; Acyltransferase; Repeat; Mitochondrion;  
 KW Lipoyl.

FT NON\_TER 1 1 LIPOYL.  
 FT BINDING 5 5  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1066 MW; 889BECDAAD33AB1 CRC64;  
 Query Match 11.1%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 13 ET 14  
 DB 2 ET 3  
 RESULT 68  
 PNEU\_HUMAN  
 ID PNEU\_HUMAN STANDARD; PRT; 10 AA.  
 AC P22103;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Pneumadin (PNM).  
 DE Pneumadin (PNM).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Lung;  
 RX MEDLINE=91110910; PubMed=2274681;  
 RA Batra V.K., Mathur M., Mir S.A., Kapoor R., Kumar M.A.;  
 RT "Pneumadin: a new lung peptide which triggers antidiuresis.";  
 RL Regul. Pept. 30:77-87(1990).  
 CC -!- FUNCTION: ANTIURETIC PEPTIDE THAT TRIGGERS THE RELEASE OF ADH.  
 DR PIR; B33143; B33143.  
 DR GO; GO:0030103; P:vasopressin secretion; NAS.  
 KW Amidation.  
 FT MOD\_RES 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 956 MW; 640378DAA723276B CRC64;  
 Query Match 11.1%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 GV 8  
 DB 9 GV 10  
 RESULT 69  
 PNEU\_RAT  
 ID PNEU\_RAT STANDARD; PRT; 10 AA.  
 AC P21996;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Pneumadin (PNM).  
 DE Rattus norvegicus (Rat).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Lung;  
 RX MEDLINE=91110910; PubMed=2274681;  
 RA Batra V.K., Mathur M., Mir S.A., Kapoor R., Kumar M.A.;  
 RT "Pneumadin: a new lung peptide which triggers antidiuresis.";  
 RL Regul. Pept. 30:77-87(1990).  
 CC -!- FUNCTION: THIS ANTIURETIC PEPTIDE TRIGGERS THE RELEASE OF ADH.  
 DR PIR; A33143; A33143.  
 KW Amidation.  
 FT MOD\_RES 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1048 MW; 641D00DAA723276B CRC64;

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Query Match      11.1%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GV 8
      |||
DB      9 GV 10

RESULT 70
PORB METTM      STANDARD;      PRT;      10 AA.
AC P80901;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Pyruvate synthase subunit porB (EC 1.2.7.1) (Pyruvate oxidoreductase
DE beta chain) (POR) (Pyruvic-ferredoxin oxidoreductase beta subunit)
DE (Fragment).
GN PORB.
OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=79929;
RN [1]
RP SEQUENCE.
RX MEDLINE=97261844; PubMed=9108258;
RA Tersteegen A., Linder D., Thauer R.K., Hedderich R.;
RT "Structures and functions of four anabolic 2-oxoacid oxidoreductases
RT in Methanobacterium thermoautotrophicum.";
RL Eur. J. Biochem. 244:862-868(1997).
CC -!- CATALYTIC ACTIVITY: Pyruvate + CoA + oxidized ferredoxin = acetyl-
CC CoA + CO(2) + reduced ferredoxin.
CC -!- SUBUNIT: HETEROTETRAMER OF ONE ALPHA, ONE BETA, ONE DELTA AND ONE
CC GAMMA CHAIN.
CC -!- MISCELLANEOUS: As a pH optimum of 10.0 and an optimal temperature
CC of 80 degrees Celsius.
KW Oxidoreductase.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1232 MW; 167011DAF6DB0760 CRC64;

Query Match      11.1%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PE 4
      |||
DB      4 PE 5

RESULT 71
RL16 ACHLA
ID PL16 ACHLA      STANDARD;      PRT;      10 AA.
AC P29221;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE 50S ribosomal protein L16 (Fragment).
GN RPLP.
OS Acholeplasma laidlawii.
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
OC Acholeplasmataceae; Acholeplasma.
OX NCBI_TaxID=2148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92210505; PubMed=1556079;
RA Lim P.O., Sears B.B.;
RT "Evolutionary relationships of a plant-pathogenic mycoplasma-like
RT organism and Acholeplasma laidlawii deduced from two ribosomal protein
RT gene sequences.";
RL J. Bacteriol. 174:2606-2611(1992).
CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA AND IS

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CC LOCATED AT THE A SITE OF THE PEPTIDYLTRANSFERASE CENTER
CC (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE L16P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
CC EMBL; M74771; AAA21914.1; -.
CC PIR; F41839; F41839.
CC InterPro; IPR00114; Ribosomal_L16.
CC PROSITE; PS00586; RIBOSOMAL_L16_1; PARTIAL.
CC PROSITE; PS00701; RIBOSOMAL_L16_2; PARTIAL.
KW Ribosomal protein; rRNA-binding.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1324 MW; B3386A21B4032766 CRC64;

Query Match      11.1%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PK 10
      |||
DB      4 PK 5

RESULT 72
SP34 DICMU
ID SP34 DICMU      STANDARD;      PRT;      10 AA.
AC P81545;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Surface protein P34 (Fragment).
GN P34.
OS Dictyostelium mucoroides (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=31287;
RN [1]
RP SEQUENCE.
RA Schreiner S.J.;
RT "Characterization of a surface protein in macrocysts of Dictyostelium
RT mucoroides.";
RL Submitted (NOV-1998) to the SWISS-PROT data bank.
CC -!- FUNCTION: THIS PROTEIN IS PRESENT IN THE MACROCYST PRIMARY WALL
CC WHICH IS PRODUCED BY AMOEBAE DURING THE ONSET OF SEXUAL
CC REPRODUCTION.
CC -!- SUBCELLULAR LOCATION: MACROCYST PRIMARY WALL.
KW Cell wall.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1190 MW; 1B6A707AA3345B50 CRC64;

Query Match      11.1%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 EI 5
      |||
DB      2 EI 3

RESULT 73
SPI HALRO
ID SPI HALRO      STANDARD;      PRT;      10 AA.
AC Q10997;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)

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DE Serine proteinase inhibitor (Fragment).  
OS Halocynthia roretzi (Sea squirt).  
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;  
OC Stolidobranchia; Pyuridae; Halocynthia.  
OX NCBI\_TaxID=7729;  
RN [1]  
RN SEQUENCE.  
RP TISSUE=Hemolymph;  
RC MEDLINE=96321313; PubMed=8759295;  
RX Shishikura F., Abe T., Ohtake S.-I., Tanaka K.;  
RA "Purification and characterization of a 58,000-Da proteinase  
RT inhibitor from the hemolymph of a solitary ascidian, Halocynthia  
RT roretzi.";  
RL Comp. Biochem. Physiol. 114B:1-9(1996).  
CC -!- FUNCTION: STRONGLY INHIBITS TRYPSIN AND PLASMA ENZYME(S) ACTIVITY.  
CC -!- SUBUNIT: Monomer.  
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
DR InterPro: IPR000215; Serpin.  
DR PROSITE; PS00284; SERPIN; PARTIAL.  
KW Serpin; Serine protease inhibitor; Glycoprotein; Plasma.  
FT NON\_TER 10 10  
SQ SEQUENCE 10 AA; 1104 MW; 4225C73B1B187AA3 CRC64;  
Query Match 11.1%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 10 KV 11  
Db 8 KV 9  
RESULT 74  
SYK CAMUP STANDARD; PRT; 10 AA.  
AC Q4564;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Lysyl-tRNA synthetase (EC 6.1.1.6) (Lysine--tRNA ligase) (LysRS)  
DE (Fragment).  
GN LYSS.  
OS Campylobacter upsaliensis.  
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;  
OC Campylobacteraceae; Campylobacter.  
OX NCBI\_TaxID=28080;  
RN [1]  
RN SEQUENCE FROM N.A.  
RC STRAIN=ATCC 43954;  
RX MEDLINE=97149302; PubMed=8996110;  
RA Bourke B., Rashid S.T., Bingham H.L., Chan V.L.;  
RT "Characterization of Campylobacter upsaliensis fur and its  
RT localization in a highly conserved region of the Campylobacter  
RT genome";  
RL Gene 183:219-224(1996).  
CC -!- CATALYTIC ACTIVITY: ATP + L-lysine + tRNA(Lys) = AMP + diphosphate  
CC + L-lysyl-tRNA(Lys).  
CC -!- COFACTOR: Binds 3 magnesium ions per subunit (By similarity).  
CC -!- SUBUNIT: Homodimer (By similarity).  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.  
-----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
DR EMBL: L77076; AAB41342.1; --  
DR HAMAP; MF\_00252; -; 1.  
DR InterPro; IPR006195; tRNA\_ligase\_II.

DR PROSITE; PS50862; AA tRNA LIGASE II; PARTIAL.  
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;  
KW Metal-binding; Magnesium.  
FT NON\_TER 1 1  
SQ SEQUENCE 10 AA; 1218 MW; 9CEA46AB13372B05 CRC64;  
Query Match 11.1%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 12 KE 13  
Db 6 KE 7  
RESULT 75  
TKL2 LOCM1 STANDARD; PRT; 10 AA.  
ID PK1224;  
AC P16224;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Locustatachykinin II (TK-II).  
OS Locusta migratoria (Migratory locust).  
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
OX NCBI\_TaxID=7004;  
RN [1]  
RN SEQUENCE.  
RP TISSUE=Brain;  
RC MEDLINE=90184489; PubMed=2311766;  
RX Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;  
RT "Locustatachykinin I and II, two novel insect neuropeptides with  
RT homology to peptides of the vertebrate tachykinin family.";  
RL FEBS Lett. 261:397-401(1990).  
CC -!- FUNCTION: MYOACTIVE PEPTIDE. STIMULATES THE CONTRACTION OF THE  
CC OVIDUCT AND FOREGUT.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.  
KW Tachykinin; Neuropeptide; Amidation.  
FT MOD\_RES 10 10  
FT AMIDATION.  
SQ SEQUENCE 10 AA; 1066 MW; 5D52CD6B59C865B7 CRC64;  
Query Match 11.1%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 7 GV 8  
Db 8 GV 9  
Search completed: November 25, 2003, 19:28:21  
Job time : 6.45515 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:25:50 ; Search time 33.8023 Seconds  
(without alignments)  
137.415 Million cell updates/sec

Title: US-09-641-801-21

Perfect score: 18

Sequence: 1 LQPEIMGVPKXETMVPK 18

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

SPTREMBL23:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	22.2	12	2	Q50019 mycobacteri
2	4	22.2	12	8	Q31851 arabisdopsis
3	4	22.2	16	2	O54357 bacillus am
4	4	22.2	18	12	Q919D5 human papil
5	4	22.2	18	12	Q919B3 human papil
6	4	22.2	18	12	Q919B5 human papil
7	4	22.2	18	12	Q919B7 human papil
8	4	22.2	18	12	Q919C5 human papil
9	4	22.2	18	12	Q919D1 human papil
10	4	22.2	18	12	Q919D3 human papil
11	4	22.2	18	12	Q919B9 human papil
12	4	22.2	18	12	Q919A8 human papil
13	4	22.2	18	12	Q919C7 human papil
14	4	22.2	18	12	Q919C9 human papil
15	4	22.2	19	2	Q9R4Q2 pseudomonas
16	4	22.2	19	6	Q9N195 bos taurus

17	3	16.7	8	6	Q95M23	Q95m23 sus scrofa
18	3	16.7	8	13	Q8JJ35	Q8jj35 ficedula hy
19	3	16.7	9	2	Q93E20	Q93e20 streptococc
20	3	16.7	9	4	Q9E997	Q9e997 homo sapien
21	3	16.7	9	10	P82440	P82440 nicotiana t
22	3	16.7	9	13	Q8AYL5	Q8ayl5 carassius a
23	3	16.7	9	13	Q8AUM7	Q8aum7 carassius a
24	3	16.7	10	1	Q50843	Q50843 methanococc
25	3	16.7	10	15	Q86324	Q86324 rous sarcom
26	3	16.7	10	15	Q86325	Q86325 rous sarcom
27	3	16.7	10	15	Q86326	Q86326 rous sarcom
28	3	16.7	11	4	O60614	O60614 homo sapien
29	3	16.7	11	4	Q9NV38	Q9nv38 homo sapien
30	3	16.7	11	7	O19718	O19718 homo sapien
31	3	16.7	11	13	Q8UUP1	Q8uup1 xenopus lae
32	3	16.7	11	16	Q9K7A4	Q9k7a4 bacillus ha
33	3	16.7	12	15	Q9ICES	Q9ice5 human immun
34	3	16.7	13	2	Q31295	Q31295 buchnera ap
35	3	16.7	13	4	Q9UE87	Q9ue87 homo sapien
36	3	16.7	13	8	Q8WEJ9	Q8wej9 ginkgo bilo
37	3	16.7	13	10	Q39380	Q39380 brassica ol
38	3	16.7	13	11	Q88176	Q88176 mus musculu
39	3	16.7	14	1	Q9UWM2	Q9uwm2 pyrocococc
40	3	16.7	14	2	Q55326	Q55326 synchococc
41	3	16.7	14	3	Q8J1G2	Q8j1g2 ashbya goss
42	3	16.7	14	4	Q9P2A2	Q9p2a2 homo sapien
43	3	16.7	14	4	Q16045	Q16045 homo sapien
44	3	16.7	14	6	Q8HYM2	Q8hyt2 felis silve
45	3	16.7	14	10	P82341	P82341 pisum sativ
46	3	16.7	14	12	Q98818	Q98818 murine minu
47	3	16.7	14	13	Q8AXQ7	Q8axq7 xenopus lae
48	3	16.7	15	3	Q9UR63	Q9ur63 emericella
49	3	16.7	15	4	Q9UE41	Q9ue41 homo sapien
50	3	16.7	15	4	Q9UCC7	Q9ucc7 homo sapien
51	3	16.7	15	4	Q9UCY1	Q9ucy1 homo sapien
52	3	16.7	15	6	O46661	O46661 macropus ro
53	3	16.7	15	6	Q9TR64	Q9tr64 oryctolagus
54	3	16.7	15	6	Q9MZ85	Q9mz85 oryctolagus
55	3	16.7	15	8	Q9TH04	Q9th04 gryus americ
56	3	16.7	15	10	Q9AT15	Q9at15 lycopersico
57	3	16.7	15	10	P93515	P93515 arabidopsis
58	3	16.7	15	10	Q9S8N8	Q9s8n8 hordeum vul
59	3	16.7	15	13	Q9PR20	Q9pr20 bothrops ja
60	3	16.7	16	2	Q51950	Q51950 staphylococ
61	3	16.7	16	2	Q9F1S7	Q9f1s7 streptococc
62	3	16.7	16	2	Q9F1S4	Q9f1s4 streptococc
63	3	16.7	16	6	Q9TQZ7	Q9tqz7 bos taurus
64	3	16.7	16	11	Q9QV11	Q9qv11 rattus sp.
65	3	16.7	16	11	Q9QUW8	Q9quw8 cavia (guin
66	3	16.7	16	12	Q88250	Q88250 sendai viru
67	3	16.7	16	12	Q84246	Q84246 sendai viru
68	3	16.7	16	12	Q88249	Q88249 sendai viru
69	3	16.7	16	12	Q99154	Q99154 sendai viru
70	3	16.7	17	1	Q50842	Q50842 methanococc
71	3	16.7	17	2	Q8VME2	Q8vme2 pseudomonas
72	3	16.7	17	2	Q9EUB3	Q9eub3 corynebacte
73	3	16.7	17	4	Q14001	Q14001 homo sapien
74	3	16.7	17	4	Q9UCC6	Q9ucc6 homo sapien
75	3	16.7	17	6	Q9XSG1	Q9xsg1 bos taurus
76	3	16.7	17	6	Q9TQZ5	Q9tqz5 macaca fasc
77	3	16.7	17	6	Q9TR21	Q9tr21 sus scrofa
78	3	16.7	17	7	Q9TNQ0	Q9tnq0 mus sp. bet
79	3	16.7	17	8	Q9T2S2	Q9t2s2 solanum tub
80	3	16.7	17	8	Q9T2H4	Q9t2h4 spinacia ol
81	3	16.7	17	11	Q9JK08	Q9jk08 mus musculu
82	3	16.7	17	12	Q919B0	Q919b0 human papil
83	3	16.7	18	2	Q52411	Q52411 thermophili
84	3	16.7	18	3	Q9F897	Q9f897 emericella
85	3	16.7	18	4	Q9UCF4	Q9ucf4 homo sapien
86	3	16.7	18	5	Q9TWW7	Q9tww7 procambarus
87	3	16.7	18	6	Q95MB1	Q95mb1 equus cabal
88	3	16.7	18	6	Q9TOR0	Q9tor0 sus scrofa
89	3	16.7	18	6	Q9TS26	Q9ts26 sus scrofa

90 Q9S8G8 psophocarpu  
 91 P70649 mus sp. syn  
 92 P70650 mus sp. syn  
 93 Q9JIE9 mus musculus  
 94 Q90791 gallus gall  
 95 Q8QFT3 gallus gall  
 96 O57600 gallus gall  
 97 O12692 simian-huma  
 98 Q9K610 bacillus ha  
 99 Q9RQ37 salmonella  
 100 Q9K4X0 planktothri

## ALIGNMENTS

## RESULT 1

Q50019 PRELIMINARY; PRT; 12 AA.  
 AC Q50019  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last annotation update)  
 DE U2266a.  
 OS Mycobacterium leprae.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1769;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Smith D.R.;  
 RA Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.  
 RL [2]  
 RN SEQUENCE FROM N.A.  
 RA Robison K.;  
 RA Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.  
 RL EMBL: U15182; AAA62981.1; --.  
 DR EMBL: U15182; AAA62981.1; --.  
 SQ SEQUENCE 12 AA; 1402 MW; DF569D9F7FD1F5A2 CRC64;

Query Match 22.2%; Score 4; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 8e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 MGVP 9  
 Db 1 MGVP 4

## RESULT 2

Q31851 PRELIMINARY; PRT; 12 AA.  
 AC Q31851  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Glyceraldehyde-3-phosphate dehydrogenase (Fragment).  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Columbia; TIGS=Leaf;  
 RX MEDLINE=94187724; PubMed=8139555;  
 RA Conley T.R.; Park S.-C.; Kwon H.-B.; Peng H.-S.; Shih M.-C.;  
 RT "Characterization of cis-acting elements in light regulation of the  
 RT nuclear gene encoding the A subunit of chloroplast isozymes  
 RT glyceraldehyde-3-phosphate dehydrogenase from Arabidopsis thaliana.";  
 RL Mol. Cell. Biol. 14:2525-2533(1994).  
 DR EMBL: L14743; AAA31640.1; --.  
 KW Chloroplast.

FT NON TER 12 12  
 SQ SEQUENCE 12 AA; 1263 MW; 81BA4C7D4BD5B9D1 CRC64;  
 Query Match 22.2%; Score 4; DB 8; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 8e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VPKV 11  
 Db 8 VPKV 11

## RESULT 3

O54357 PRELIMINARY; PRT; 16 AA.  
 AC O54357  
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE PTSI system enzyme I (Fragment).  
 GN PTSI  
 OS Bacillus amyloliquefaciens.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1390;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H;  
 RA Nicholson W.L.; Fajardo-Cavazos P.;  
 RT "DNA repair and the ultraviolet radiation resistance of bacterial  
 RT spores: from the laboratory to the environment.";  
 RL (In) Pandalai S. (eds.);  
 RL RECENT RESEARCH ADVANCES IN MICROBIOLOGY, pp.1-1, Research Signpost,  
 RL Tivandrum, India (1998).  
 DR EMBL: U60821; AAB97621.1; --.  
 FT NON TER 1 1  
 SQ SEQUENCE 16 AA; 1873 MW; D38C83850AEF4266 CRC64;

Query Match 22.2%; Score 4; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VKET 14  
 Db 9 VKET 12

## RESULT 4

Q919D5 PRELIMINARY; PRT; 18 AA.  
 AC Q919D5  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE E7 protein (Fragment).  
 GN E7.  
 OS Human papillomavirus type 16.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Papillomavirus.  
 OX NCBI\_TaxID=10581;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=HPV16E6CCL;  
 RA Watts K.J.; Thompson C.H.; Cossart Y.E.; Rose B.R.;  
 RT "Sequence variation and physical state of human papillomavirus type 16  
 RT cervical cancer isolates from Australia and New Caledonia.";  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF404692; AAL01341.1; --.  
 FT NON TER 18 18  
 SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 LOPE 4
Db      15 LOPE 18

RESULT 5
Q919B3
ID      Q919B3      PRELIMINARY;      PRT;      18 AA.
AC      Q919B3;
DT      01-DEC-2001 (TrEMBLrel. 19, Created)
DT      01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT      01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE      E7 protein (Fragment).
GN      E7.
OS      Human papillomavirus type 16.
OC      Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC      Papillomavirus.
OX      NCBI_TaxID=10581;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=HPV16E6CC12;
RA      Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT      "Sequence variation and physical state of human papillomavirus type 16
RT      cervical cancer isolates from Australia and New Caledonia.";
RL      Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF404703; AAL01364.1; -.
FT      NON_TER      18
SQ      SEQUENCE      18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match      22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 LOPE 4
Db      15 LOPE 18

RESULT 6
Q919B5
ID      Q919B5      PRELIMINARY;      PRT;      18 AA.
AC      Q919B5;
DT      01-DEC-2001 (TrEMBLrel. 19, Created)
DT      01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT      01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE      E7 protein (Fragment).
GN      E7.
OS      Human papillomavirus type 16.
OC      Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC      Papillomavirus.
OX      NCBI_TaxID=10581;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=HPV16E6CC11;
RA      Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT      "Sequence variation and physical state of human papillomavirus type 16
RT      cervical cancer isolates from Australia and New Caledonia.";
RL      Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF404702; AAL01362.1; -.
FT      NON_TER      18
SQ      SEQUENCE      18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match      22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 LOPE 4
Db      15 LOPE 18

RESULT 7

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Q919B7
ID      Q919B7      PRELIMINARY;      PRT;      18 AA.
AC      Q919B7;
DT      01-DEC-2001 (TrEMBLrel. 19, Created)
DT      01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT      01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE      E7 protein (Fragment).
GN      E7.
OS      Human papillomavirus type 16.
OC      Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC      Papillomavirus.
OX      NCBI_TaxID=10581;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=HPV16E6CC10;
RA      Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT      "Sequence variation and physical state of human papillomavirus type 16
RT      cervical cancer isolates from Australia and New Caledonia.";
RL      Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF404701; AAL01360.1; -.
FT      NON_TER      18
SQ      SEQUENCE      18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match      22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 LOPE 4
Db      15 LOPE 18

RESULT 8
Q919C5
ID      Q919C5      PRELIMINARY;      PRT;      18 AA.
AC      Q919C5;
DT      01-DEC-2001 (TrEMBLrel. 19, Created)
DT      01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT      01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE      E7 protein (Fragment).
GN      E7.
OS      Human papillomavirus type 16.
OC      Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC      Papillomavirus.
OX      NCBI_TaxID=10581;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=HPV16E6CC6;
RA      Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT      "Sequence variation and physical state of human papillomavirus type 16
RT      cervical cancer isolates from Australia and New Caledonia.";
RL      Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF404697; AAL01352.1; -.
FT      NON_TER      18
SQ      SEQUENCE      18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match      22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 LOPE 4
Db      15 LOPE 18

RESULT 9
Q919D1
ID      Q919D1      PRELIMINARY;      PRT;      18 AA.
AC      Q919D1;
DT      01-DEC-2001 (TrEMBLrel. 19, Created)
DT      01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT      01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE      E7 protein (Fragment).

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GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E6CC3;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF404694; AAL01346.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOPE 4
Db 15 LOPE 18

RESULT 10
Q919D3 ID Q919D3 PRELIMINARY; PRT; 18 AA.
AC Q919D3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E6CC2;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF404693; AAL01344.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOPE 4
Db 15 LOPE 18

RESULT 11
Q919B9 ID Q919B9 PRELIMINARY; PRT; 18 AA.
AC Q919B9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=HPV16E6CC9;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF404700; AAL01358.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOPE 4
Db 15 LOPE 18

RESULT 12
Q919A8 ID Q919A8 PRELIMINARY; PRT; 18 AA.
AC Q919A8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E6CC15;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF404706; AAL01369.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOPE 4
Db 15 LOPE 18

RESULT 13
Q919C7 ID Q919C7 PRELIMINARY; PRT; 18 AA.
AC Q919C7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein (Fragment).
GN E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E6CC5;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF404696; AAL01350.1; -.
FT NON_TER 18

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SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4  
15 LQPE 18

Db

RESULT 14

Q919C9 PRELIMINARY; PRT; 18 AA.

AC Q919C9; 19, Created

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DE E7 protein (Fragment).

GN E7.

OS Human papillomavirus type 16.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

OC Papillomavirus.

OC NCBI\_TaxID=10381;

RN [1]\_

RP SEQUENCE FROM N.A.

RC STRAIN=HPV16E6CC4;

RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;

RT "Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";

RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF04695; AAL01348.1; -.

FT NON\_TER 18

SQ SEQUENCE 18 AA; 2127 MW; A76471DB6BF77688 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4  
15 LQPE 18

Db

RESULT 15

Q9R4Q2 PRELIMINARY; PRT; 19 AA.

AC Q9R4Q2; 13, Created

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DE Ribosomal protein S21 (Fragment).

OS Pseudomonas aeruginosa.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

OC Pseudomonadaceae; Pseudomonas.

OX NCBI\_TaxID=287;

RN [1]\_

RP SEQUENCE.

RX MEDLINE=95244309; PubMed=7727274;

RA Ochi K.;

RT "Comparative ribosomal protein sequence analyses of a phylogenetically defined genus, Pseudomonas, and its relatives.";

RL Int. J. Syst. Bacteriol. 45:268-273 (1995).

DR InterPro; IPR001911; Ribosomal\_S21.

DR Pfam; PF01165; Ribosomal\_S21; I.

DR PRINTS; PR00976; RIBOSOMLS21.

SQ SEQUENCE 19 AA; 2244 MW; 0475DD42A464271C CRC64;

Query Match 22.2%; Score 4; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KVKE 13

Db

RESULT 16

Q9N195 PRELIMINARY; PRT; 19 AA.

AC Q9N195; 15, Created

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DE Parvalbumin (Fragment).

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI\_TaxID=9913;

RN [1]\_

RP SEQUENCE FROM N.A.

RA Ariza F., Harrison B., Drinkwater R.;

RT "The Assignment by Linkage Mapping of Five Genes from Human Chromosome 22 to Bovine Chromosome 5, 14 and 17.";

RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF217654; AAF26420.1; -.

FT NON\_TER 19

SQ SEQUENCE 19 AA; 2151 MW; D5EA9D89BC3EE951 CRC64;

Query Match 22.2%; Score 4; DB 6; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKET 14  
16 VKET 19

Db

RESULT 17

Q9SM23 PRELIMINARY; PRT; 8 AA.

AC Q9SM23; 19, Created

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DE Na+/K+ ATPase alpha subunit (EC 3.6.1.37) (Fragment).

GN ATP1A1.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI\_TaxID=9823;

RN [1]\_

RP SEQUENCE FROM N.A.

RC STRAIN=Pietrain;

RA Blazkova P., Stratil A., Peelman L.J., Van Poucke M., Reiner G., Geldermann H., Kopecny M.;

RT "RH mapping of the porcine ATP1A1, ATP1B1, V-ATPase, IVL genes and linkage assignments of ATP1A1 and IVL to chromosome 4.";

RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ344138; CAC51422.1; -.

FW Hydrolase.

FT NON\_TER 1

SQ SEQUENCE 8 AA; 1117 MW; 604B41AB133B02D3 CRC64;

Query Match 16.7%; Score 3; DB 6; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 KET 14  
4 KET 6

Db

RESULT 18



Q8JJ35 Q8JJ35 PRELIMINARY; PRT; 8 AA.  
 ID Q8JJ35  
 AC Q8JJ35  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Arp-citrate lyase (Fragment).  
 GN ACL.  
 OS Ficedula hypoleuca.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Passeriformes; Muscicapidae; Ficedula.  
 OX NCBI\_TaxID=46689;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Os4;  
 RA MEDLINE=21918460; PubMed=11918793;  
 RX Primer C.R., Borge T., Lindell J., Saetre G.-P.;  
 RT "Single-nucleotide polymorphism characterization in species with  
 RT limited available sequence information: high nucleotide diversity  
 RT revealed in the avian genome.";  
 RL Mol. Ecol. 11:603-612(2002).  
 DR EMBL: AF454211; AM22897.1; -.  
 KW Lyase.  
 FT NON\_TER 1 1  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 981 MW; 98C77B544681AB02 CRC64;  
 Query Match 16.7%; Score 3; DB 13; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 13 ETM 15  
 DB 2 ETM 4  
 RESULT 19  
 Q93EZ0 Q93EZ0 PRELIMINARY; PRT; 9 AA.  
 ID Q93EZ0  
 AC Q93EZ0  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE ScpB (Fragment).  
 GN SCpB.  
 OS Streptococcus agalactiae.  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 OC Streptococcus.  
 OX NCBI\_TaxID=1311;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=O90R;  
 RX MEDLINE=21424698; PubMed=11532154;  
 RA Franken C., Haase G., Brandt C., Weber-Heymann J., Martin S.,  
 RA Lammler C., Podbielski A., Luticken R., Spellerberg B.;  
 RT "Horizontal gene transfer and host specificity of beta-haemolytic  
 RT streptococci: the role of a putative composite transposon containing  
 RT scpB and lmb";  
 RL Mol. Microbiol. 41:925-935(2001).  
 DR EMBL: AF327852; AAL10713.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 9 AA; 1146 MW; 543721AB1326C403 CRC64;  
 Query Match 16.7%; Score 3; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 12 KET 14  
 DB 5 KET 7  
 RESULT 20

Q96P97 Q96P97 PRELIMINARY; PRT; 9 AA.  
 ID Q96P97  
 AC Q96P97  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Reptin52 protein (Fragment).  
 DE Homo sapiens (Human)  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kang H.S., Park Y.-J., Jung H.M., Jun D.Y., Huh T.L., Kim Y.H.;  
 RT "Characterization of TPA-responsive genes in U937 cells using ordered  
 RT differential display PCR.";  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF401216; AAL02172.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 9 AA; 981 MW; 5CDDAAA681AB1873 CRC64;  
 Query Match 16.7%; Score 3; DB 4; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 13 ETM 15  
 DB 4 ETM 6  
 RESULT 21  
 P82440 P82440 PRELIMINARY; PRT; 9 AA.  
 ID P82440  
 AC P82440  
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE 42 kDa cell wall protein (Fragment).  
 OS Nicotiana tabacum (Common tobacco).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; Lamiales; Solanales; Solanaceae; Nicotiana.  
 OX NCBI\_TaxID=4097;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=cv. PETIT HAVANA;  
 RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,  
 RA Woitaszek P., Bolwell G.P.;  
 RT "Proteomic study of secondary cell wall proteins from transformed  
 RT tobacco culture.";  
 RL Planta 0:0-0(2000).  
 CC -1- SUBCELLULAR LOCATION: CELL WALL.  
 CC -1- TISSUE SPECIFICITY: XYLEM.  
 KW Cell wall.  
 FT NON\_TER 9 9  
 SQ SEQUENCE 9 AA; 1053 MW; 298CC9D2D5BB1B07 CRC64;  
 Query Match 16.7%; Score 3; DB 10; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 QPE 4  
 DB 1 QPE 3  
 RESULT 22  
 Q8AYL5 Q8AYL5 PRELIMINARY; PRT; 9 AA.  
 ID Q8AYL5  
 AC Q8AYL5  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Cytochrome P450 aromatase (Fragment).  
GN CYP19A.  
OS Carassius auratus (Goldfish).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Carassius.  
OX NCBI\_TaxID=7957;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Tchoudakova A.V., Kishida M., Wood E., Callard G.V.;  
RT "Promoter characteristics of two Cyp19 genes differentially expressed  
in the brain and ovary of teleost fish";  
RL J. Steroid Biochem. Mol. Biol. 0:0-0(2001).  
DR EMBL; AF324897; AAN32618.1; -.  
FT NON\_TER 9  
SQ SEQUENCE 9 AA; 1060 MW; C49E76D7272B040D CRC64;  
Query Match 16.7%; Score 3; DB 13; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LQP 3  
Db 6 LQP 8  
RESULT 23  
Q8AUM7 PRELIMINARY; PRT; 9 AA.  
AC Q8AUM7;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Cytochrome P450 aromatase (Fragment).  
GN CYP19A.  
OS Carassius auratus (Goldfish).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Carassius.  
OX NCBI\_TaxID=7957;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Tchoudakova A.V., Kishida M., Wood E., Callard G.V.;  
RT "Promoter characteristics of two Cyp19 genes differentially expressed  
in the brain and ovary of teleost fish";  
RL J. Steroid Biochem. Mol. Biol. 0:0-0(2001).  
DR EMBL; AF324895; AAN32616.1; -.  
DR EMBL; AF324896; AAN32617.1; -.  
FT NON\_TER 9  
SQ SEQUENCE 9 AA; 961 MW; C49E76D7272B187D CRC64;  
Query Match 16.7%; Score 3; DB 13; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LQP 3  
Db 6 LQP 8  
RESULT 24  
Q50843 PRELIMINARY; PRT; 10 AA.  
AC Q50843;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last annotation update)  
DE RNA polymerase gene 3', flanking region with AT-rich DNA sequence  
(fragment).  
OS Methanococcus voltae.  
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;  
OC Methanococcaceae; Methanococcus.  
OX NCBI\_TaxID=2188;

RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85230552; PubMed=4006907;  
RA Bollschweiler C., Kuehn R., Klein A.;  
RT "Non-repetitive AT-rich sequences are found in intergenic regions of  
RT Methanococcus voltae DNA";  
RL EMBO J. 4:805-809(1985).  
DR EMBL; X02517; CAA26353.1; -.  
FT NON\_TER 10  
SQ SEQUENCE 10 AA; 1149 MW; 27F22A2772CAA9C8 CRC64;  
Query Match 16.7%; Score 3; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 8.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 VPK 10  
Db 6 VPK 8  
RESULT 25  
Q86324 PRELIMINARY; PRT; 10 AA.  
AC Q86324;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Gp37 (Fragment).  
GN ENV.  
OS Rous sarcoma virus.  
OC Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.  
OX NCBI\_TaxID=11886;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Schmidt-Ruppin subgroup A;  
RX MEDLINE=98083689; PubMed=9421881;  
RA Hara H., Kaji A.;  
RT "The U3 region of the long terminal repeat of a subgroup A  
RT transformation-defective rous sarcoma virus (tdPH2010) converts a  
RT noncytopathic virus to a cytopathic virus";  
RL Virus Genes 15:171-180(1997).  
DR EMBL; U41726; AAB60580.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 10 AA; 1119 MW; 27ED415BB0776D8 CRC64;  
Query Match 16.7%; Score 3; DB 15; Length 10;  
Best Local Similarity 100.0%; Pred. No. 8.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 QPE 4  
Db 4 QPE 6  
RESULT 26  
Q86325 PRELIMINARY; PRT; 10 AA.  
AC Q86325;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Gp37 (Fragment).  
GN ENV.  
OS Rous sarcoma virus.  
OC Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.  
OX NCBI\_TaxID=11886;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Schmidt-Ruppin subgroup A;  
RX MEDLINE=98083689; PubMed=9421881;  
RA Hara H., Kaji A.;  
RT "The U3 region of the long terminal repeat of a subgroup A  
RT transformation-defective rous sarcoma virus (tdPH2010) converts a  
RT noncytopathic virus to a cytopathic virus";  
RL Virus Genes 15:171-180(1997).  
DR EMBL; U41726; AAB60580.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 10 AA; 1119 MW; 27ED415BB0776D8 CRC64;  
Query Match 16.7%; Score 3; DB 15; Length 10;  
Best Local Similarity 100.0%; Pred. No. 8.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 QPE 4  
Db 4 QPE 6

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RT noncytopathic virus to a cytopathic virus.";
RL Virus Genes 15:171-180(1997).
DR EMBL: U41727; AAB60581.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1119 MW; 27ED4115BB0776D8 CRC64;

Query Match 16.7%; Score 3; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPE 4
Db 4 QPE 6

RESULT 27
Q86326 PRELIMINARY; PRT; 10 AA.
AC Q86326;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Gp37 (Fragment).
GN ENV.
OS Rous sarcoma virus.
OC Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
OC NCBI_TaxID=11886;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Schmidt-Ruppin subgroup A;
RX MEDLINE=98083689; PubMed=9421881;
RA Hara H., Kaji A.;
RT "The U3 region of the long terminal repeat of a subgroup A
RT transformation-defective rous sarcoma virus (tdpH2010) converts a
RT noncytopathic virus to a cytopathic virus.";
RL Virus Genes 15:171-180(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Schmidt-Ruppin subgroup A;
RX MEDLINE=82271824; PubMed=6287213;
RA Takeya T., Hanafusa H., Jungmans R.P., Ju G., Skalka A.M.;
RT "Comparison between the viral transforming gene (src) of recovered
RT avian sarcoma virus and its cellular homolog.";
RL Mol. Cell. Biol. 1:1024-1037(1981).
DR EMBL: U41729; AAB84421.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1119 MW; 27ED4115BB0776D8 CRC64;

Query Match 16.7%; Score 3; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QPE 4
Db 4 QPE 6

RESULT 28
O60614 PRELIMINARY; PRT; 11 AA.
AC O60614;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MTG8 related protein (Fragment).
GN MTG8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;

RT MEDLINE=99009318; PubMed=9790752;
RA Calabi F., Cilli V.;
RT "CBA2T1, a gene rearranged in human leukemia, is a member of a
RT multigene family.";
RL Genomics 52:332-341(1998).
DR EMBL: AF052211; ARC64700.1; -.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1047 MW; CF001CE4DD86772 CRC64;

Query Match 16.7%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GVP 9
Db 3 GVP 5

RESULT 29
Q9NY38 PRELIMINARY; PRT; 11 AA.
AC Q9NY38;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Heavy metal-responsive transcription factor (Fragment).
GN MTF-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Auf der Maur A., Belser T., Wang Y., Gunes C., Lichtlen P.,
RA Georgiev O., Schaffner W.;
RT "Characterization of the mouse gene for the heavy metal-responsive
RT transcription factor MTF-1.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ251881; CAB71327.1; -.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1099 MW; A8653693773772C6 CRC64;

Query Match 16.7%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 MVP 17
Db 4 MVP 6

RESULT 30
O19718 PRELIMINARY; PRT; 11 AA.
AC O19718;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II antigen (Fragment).
GN HLA-DRB1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86206008; PubMed=3458223;
RA Gregersen P.K., Shen M., Song Q.-L., Merryman P., Degar S., Seki T.,
RA Maccari J., Goldberg D., Murphy H., Schwenzer J., Wang C.Y.,
RA Winchester R.J., Nepom G.T., Silver J.;
RT "Molecular diversity of HLA-DR4 haplotypes.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:2642-2646(1986).

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DR EMBL; M15074; AAA59810.1; --  
 FT NON\_TER 1 1  
 SQ SEQUENCE 11 AA; 1143 MW; 486AADA061B776D7 CRC64;

Query Match 16.7%; Score 3; DB 7; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQP 3  
 |||  
 Db 4 LQP 6

## RESULT 31

Q8UUP1 PRELIMINARY; PRT; 11 AA.  
 ID Q8UUP1  
 AC Q8UUP1  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Beta-TrCP protein (Fragment).  
 GN BETA-TRCP.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Carnevali F.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Ballarino M.;  
 RT "Analisi strutturale e funzionale del gene beta-TrCP in Xenopus laevis".  
 RL Thesis (2001), Department of Genetica e Biologia Molecolare, University of Rome La Sapienza, Rome, Italy.  
 DR EMBL; AJ428930; CAD21927.1; --  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1195 MW; CEB938BE35BEA5B9 CRC64;

Query Match 16.7%; Score 3; DB 13; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQP 3  
 |||  
 Db 8 LQP 10

## RESULT 32

Q9K7A4 PRELIMINARY; PRT; 11 AA.  
 ID Q9K7A4  
 AC Q9K7A4  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Hypothetical protein BH3464.  
 GN BH3464.  
 OS Bacillus halodurans.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=86665;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C-125 / JCM 9153;  
 RX MEDLINE=20512582; PubMed=11058132;  
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,  
 RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,  
 RA Horikoshi K.;  
 RT "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis.";  
 RL Nucleic Acids Res. 28:4317-4331(2000).

DR EMBL; AP001518; BAB07183.1; --  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 11 AA; 1219 MW; 5F7D235CB7272B13 CRC64;

Query Match 16.7%; Score 3; DB 16; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKE 13  
 |||  
 Db 3 VKE 5

## RESULT 33

Q9ICE5 PRELIMINARY; PRT; 12 AA.  
 ID Q9ICE5  
 AC Q9ICE5  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Envelope glycoprotein.  
 GN ENV.  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=546CP-H7, 546CP-E4, and 546CP-F5;  
 RA Gartner S., Liu Y., Tang X.P., McArthur J.C., Scott J.;  
 RT "Analysis of human immunodeficiency virus type 1 gp160 sequences from a patient with HIV dementia: evidence for monocyte trafficking into brain.";  
 RT J. Neurovirol. 0:0-0(2000).  
 RL EMBL; AF217155; AAF75497.1; --  
 DR EMBL; AF217153; AAF75495.1; --  
 DR EMBL; AF217154; AAF75496.1; --  
 SQ SEQUENCE 12 AA; 1636 MW; 7ED6A2917A24005B CRC64;

Query Match 16.7%; Score 3; DB 15; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 9.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKE 13  
 |||  
 Db 3 VKE 5

## RESULT 34

O31295 PRELIMINARY; PRT; 13 AA.  
 ID O31295  
 AC O31295  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE 2-isopropylmalate synthase (EC 4.1.3.12) (Fragment).  
 GN LEUA.  
 OS Buchnera aphidicola.  
 OG Plasmid pBt1.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Buchnera.  
 OX NCBI\_TaxID=9;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RP MEDLINE=97386415; PubMed=9244264;  
 RA Van Ham R.C.H.J., Moya A., Latorre A.;  
 RX "Putative origin of plasmids carrying the genes involved in leucine biosynthesis in Buchnera aphidicola (endosymbiont of aphids).";  
 RT J. Bacteriol. 179:4768-4777(1997).  
 RL EMBL; Y11966; CAA72696.1; --  
 KW Lyase; Plasmid.  
 FT NON\_TER 13 13  
 SQ SEQUENCE 13 AA; 1487 MW; 1BD1D3E72A9E2050 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKV 11  
 ||||  
 Db 3 PKV 5

## RESULT 35

Q9UE87 Q9UE87 PRELIMINARY; PRT; 13 AA.  
 AC Q9UE87;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE Transforming growth factor alpha (Fragment).  
 GN TGFA.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9219018; PubMed=2907605;  
 RA Jakobovits E.B., Schlokot U., Vannice J.L., Derynck R., Levinson A.D.;  
 RT "The human transforming growth factor alpha promoter directs  
 RT transcription initiation from a single site in the absence of a TATA  
 RT sequence.";  
 RL Mol. Cell. Biol. 8:5549-5554(1988).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92168034; PubMed=1791840;  
 RA Saeki T., Cristiano A., Lynch M.J., Brattain M., Kim N., Normanno N.,  
 RA Kenney N., Ciardiello F., Salomon D.S.;  
 RT "Regulation by estrogen through the 5'-flanking region of the  
 RT transforming growth factor alpha gene.";  
 RL Mol. Endocrinol. 5:1955-1963(1991).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93364904; PubMed=8358733;  
 RA Lynch M.J., Pelosi L., Carboni J.M., Merwin J., Coleman K., Wang R.C.,  
 RA Lin P.F., Henry D.L., Brattain M.G.;  
 RT "Transforming growth factor-beta 1 induces transforming growth factor-  
 RT alpha promoter activity and transforming growth factor-alpha secretion  
 RT in the human colon adenocarcinoma cell line FET.";  
 RL Cancer Res. 53:4041-4047(1993).  
 DR EMBL; M96868; AAA79958.1; -.  
 FT NON\_TER 13  
 SQ SEQUENCE 13 AA; 1318 MW; 2C6E4395FCE36D8 CRC64;

Query Match 16.7%; Score 3; DB 4; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 MVP 17  
 ||||  
 Db 1 MVP 3

## RESULT 36

Q8WEJ9 Q8WEJ9 PRELIMINARY; PRT; 13 AA.  
 AC Q8WEJ9;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE NADH dehydrogenase (Fragment).  
 GN NAD1.  
 OS Ginkgo biloba (Ginkgo).  
 OC Mitochondrion.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.

OX NCBI\_TaxID=3311;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21555473; PubMed=11697913;  
 RA Gugerli F., Sperisen C., Buchler U., Brunner I., Brodbeck S.,  
 RA Palmer J.D., Qiu Y.L.;  
 RT "The evolutionary split of pinaceae from other conifers: evidence from  
 RT an intron loss and a multigene phylogeny.";  
 RL Mol. Phylogenet. Evol. 21:167-175(2001).  
 DR EMBL; AF227466; AAL38910.1; -.  
 FT NON\_TER 1  
 KW Mitochondrion.  
 FT NON\_TER 13  
 SQ SEQUENCE 13 AA; 1419 MW; C00F6805F94945BD CRC64;

Query Match 16.7%; Score 3; DB 8; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 MVP 17  
 ||||  
 Db 1 MVP 3

## RESULT 37

Q39380 Q39380 PRELIMINARY; PRT; 13 AA.  
 ID Q39380;  
 AC Q39380;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE IFA binding protein (Sp10) (Fragment).  
 OS Brassica oleracea (Cauliflower).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Brassica.  
 OX NCBI\_TaxID=3712;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=DOK; TISSUE=Curd surface;  
 RA Willis G.;  
 RT "An investigation of nuclear lamin homologues in plants: an apparently  
 RT non-intermediate filament sequence that bind a polyclonal anti-lamin  
 RT antiserum.";  
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; X97678; CAA66268.1; -.  
 FT NON\_TER 1  
 SQ SEQUENCE 13 AA; 1413 MW; D1D4EA3926B42772 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VPK 10  
 ||||  
 Db 6 VPK 8

## RESULT 38

O88176 O88176 PRELIMINARY; PRT; 13 AA.  
 ID O88176;  
 AC O88176;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Neural cell adhesion molecule (Fragment).  
 GN NCAM1 OR NCAM.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.

```

RC STRAIN=Balb-c; TISSUE=Liver;
RX MEDLINE=98250618; PubMed=9582442;
RA Kawahigashi H., Harada Y., Asano A., Nakamura M.;
RT "A cis-acting regulatory element that affects the alternative splicing
of a muscle-specific exon in the mouse NCAM gene.";
RL Biochim. Biophys. Acta 1397:305-315(1998).
DR EMBL; AB001873; BAA31275.1; -.
DR MGD; MGI:97281; Ncam1.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1496 MW; CC6098E54C72D732 CRC64;

Query Match 16.7%; Score 3; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQP 3
DB 7 LQP 9

RESULT 39
Q9UWM2
ID Q9UWM2 PRELIMINARY; PRT; 14 AA.
AC Q9UWM2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE L-glutamate:NAD(P)+ oxidoreductase (EC 1.4.1.3) (Fragment).
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]
RP SEQUENCE.
RX MEDLINE=92247806; PubMed=1576153;
RA Robb F.T., Park J.B., Adams M.W.;
RT "Characterization of an extremely thermostable glutamate
dehydrogenase: a key enzyme in the primary metabolism of the
hyperthermophilic archaeobacterium, Pyrococcus furiosus.";
RL Biochim. Biophys. Acta 1120:267-272(1992).
SQ SEQUENCE 14 AA; 1684 MW; 1B8EF0500B25D50B CRC64;

Query Match 16.7%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKE 13
DB 1 VKE 3

RESULT 40
Q5326
ID Q5326 PRELIMINARY; PRT; 14 AA.
AC Q5326;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Putative ORF1 (Fragment).
OS Synecococcus sp. (strain PCC 7002) (Agmenellum quadruplicatum).
OC Bacteria; Cyanobacteria; Chroococcales; Synecococcus.
OX NCBI_TaxID=32049;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=PR6;
RX MEDLINE=92201692; PubMed=1551590;
RA Rhiel E., Stirewalt V.L., Gasparich G.E., Bryant D.A.;
RT "The psac genes of Synecococcus sp. PCC7002 and Cyanophora paradoxa:
cloning and sequence analysis.";
RL Gene 112:123-128(1992).
DR EMBL; M86238; AAA27351.1; -.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1632 MW; 47EB1EE28D59A8D7 CRC64;

Query Match 16.7%; Score 3; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ SEQUENCE 14 AA; 1590 MW; 9D5226BDCB998BCA CRC64;

Query Match 16.7%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQP 3
DB 12 LQP 14

RESULT 41
Q8JIG2
ID Q8JIG2 PRELIMINARY; PRT; 14 AA.
AC Q8JIG2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE YPLJ56 (Fragment).
GN YPLJ56.
OS Ashbya gossypii (Eremothecium gossypii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Ashbya.
OX NCBI_TaxID=33169;
RN [1]
RP SEQUENCE FROM N.A. Dietrich F., Philippsen P.;
RA Alberti-Segui C.;
RT "Identification of kinesin-related proteins in the filamentous fungus
Ashbya gossypii.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF378570; AAN87139.1; -.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1646 MW; 8C3A12EB808B1D15 CRC64;

Query Match 16.7%; Score 3; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKV 11
DB 3 PKV 5

RESULT 42
Q9P2A2
ID Q9P2A2 PRELIMINARY; PRT; 14 AA.
AC Q9P2A2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Truncated aldo-keto reductase (Fragment).
GN TRUNCATED AKR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
RX MEDLINE=20138537; PubMed=10672042;
RA Nishizawa M., Nakajima T., Yasuda K., Kanzaki H., Sasaguri Y.,
Watanabe K., Ito S.;
RA "Close kinship of human 20alpha-hydroxysteroid dehydrogenase gene with
three aldo-keto reductase genes.";
RL Genes Cells 5:111-125(2000).
DR EMBL; AB037903; BAA92888.1; -.
FT NON_TER 1 1
SQ SEQUENCE 14 AA; 1632 MW; 47EB1EE28D59A8D7 CRC64;

Query Match 16.7%; Score 3; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 LQP 3  
Db 7 LQP 9

## RESULT 43

Q16045 ID Q16045 PRELIMINARY; PRT; 14 AA.  
AC Q16045;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE D3 dopamine receptor (Fragment).  
GN D3R.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
[1]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Blood;  
RX MEDLINE=93326145; PubMed=7916609;  
RA Nagai Y., Ueno S., Saeiki Y., Soga F., Yanagihara T.;  
RT "Expression of the D3 dopamine receptor gene and a novel variant  
RT transcript generated by alternative splicing in human peripheral blood  
RT lymphocytes.";  
RL Biochem. Biophys. Res. Commun. 194:368-374 (1993).  
DR EMBL; S63845; AAB27543.2; -;  
KW Receptor.  
FT NON\_TER 1 1  
SQ SEQUENCE 14 AA; 1586 MW; EA310BEFE94CF1B1 CRC64;

Query Match 16.7%; Score 3; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQP 3  
Db 12 LQP 14

## RESULT 44

Q8HYM2 ID Q8HYM2 PRELIMINARY; PRT; 14 AA.  
AC Q8HYM2;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Interferon regulatory factor 6 (Fragment).  
GN IRF6.  
OS Felis silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
OX NCBI\_TaxID=9685;  
[1]  
RN SEQUENCE FROM N.A.  
RP Suscott E.E., Rollo W.A., Vento P.J., Ewart S.L.;  
RA "Characterization of 8 Feline Type I Markers.";  
RT Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF459807; AAO15587.1; -;  
FT NON\_TER 1 1  
FT NON\_TER 14 14  
SQ SEQUENCE 14 AA; 1684 MW; C593CC0754F47BB9 CRC64;

Query Match 16.7%; Score 3; DB 6; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KVK 12  
Db 3 KVK 5

## RESULT 45

P82341 ID P82341 PRELIMINARY; PRT; 14 AA.  
AC P82341;  
DT 01-JUN-2000 (TrEMBLrel. 14, Created)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
DE Unknown protein from 2D-page of thylakoid (SPOT251) (Fragment).  
OS Pisum sativum (Garden pea).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.  
OX NCBI\_TaxID=3888;  
[1]  
RN SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.  
RP STRAIN=cv. DE GRACE; TISSUE=LEAF;  
RX MEDLINE=20181728; PubMed=10715320;  
RA Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,  
RA Adamska I., van Wijk K.J.;  
RT "Proteomics of the chloroplast: systematic identification and  
RT targeting analysis of luminal and peripheral thylakoid proteins.";  
RL Plant Cell 12:319-341 (2000).  
CC -|- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN OR  
CC PERIPHERY.  
CC -|- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.  
CC -|- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 8.5, ITS MW IS: 16.9 KDA.  
KW Chloroplast; Thylakoid membrane.  
FT NON\_TER 14 14  
SQ SEQUENCE 14 AA; 1590 MW; 6D968D2994D0185B CRC64;

Query Match 16.7%; Score 3; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PEI 5  
Db 6 PEI 8

## RESULT 46

Q89818 ID Q89818 PRELIMINARY; PRT; 14 AA.  
AC Q89818;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
DE Hypothetical 1.9 kDa protein.  
OS Murine minute virus (Murine parvovirus).  
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.  
OX NCBI\_TaxID=10794;  
[1]  
RN SEQUENCE FROM N.A.  
RP STRAIN=LYMPHOTROPIC VARIANT;  
RX MEDLINE=86115415; PubMed=3502703;  
RA Astell C.R., Gardiner E.M., Tattersall P.;  
RT "DNA sequence of the lymphotropic variant of minute virus of mice,  
RT VMV(1), and comparison with the DNA sequence of the fibrotropic  
RT prototype strain.";  
RL J. Virol. 570:656-669 (1986).  
RN [2]  
RN SEQUENCE FROM N.A.  
RP STRAIN=MVM(P);  
RX MEDLINE=83143341; PubMed=6298737;  
RA Astell C.R., Thomson M., Merchlinsky M., Ward D.C.;  
RT "The complete DNA sequence of minute virus of mice, an autonomous  
RT parvovirus.";  
RL Nucleic Acids Res. 11:999-1018 (1983).  
RN [3]  
RN SEQUENCE FROM N.A.  
RP STRAIN=MVM(P);  
RX MEDLINE=86115415; PubMed=3502703;  
RA Astell C.R., Gardiner E.M., Tattersall P.;

RT "DNA sequence of the lymphotropic variant of minute virus of mice,  
 RT MVM(i), and comparison with the DNA sequence of the fibrotropic  
 RT prototype strain.",  
 RL J. Virol. 57:656-669 (1986).  
 RN [14]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MVM(P);  
 RX MEDLINE=87061199; PubMed=3783817;  
 RA Morgan W.R., Ward D.C.;  
 RT "three splicing patterns are used to excise the small intron common to  
 RT all minute virus of mice RNAs.";  
 RL J. Virol. 60:1170-1174 (1986).  
 DR EMBL; M12032; AA69571.1; -;  
 DR EMBL; J02275; AA67113.1; -;  
 DR EMBL; V01115; CAA24312.1; -;  
 KW Hypothetical protein.  
 SQ SEQUENCE 14 AA; 1927 MW; 12535381F864D1B CRC64;

Query Match 16.7%; Score 3; DB 12; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PEI 5  
 Db 9 PEI 11

RESULT 47  
 Q8AXO7  
 ID Q8AXO7 PRELIMINARY; PRT; 14 AA.  
 AC Q8AXO7;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Mannose-binding lectin-associated serine protease (Fragment).  
 GN MASP.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Endo Y., Nonaka M., Saiga H., Kakinuma Y., Takahashi M.,  
 RA Matsushita M., Fujita T.;  
 RT "Ancient origin and extensive distribution of mannose-binding lectin-  
 RT associated serine protease-3 in vertebrate lineage."  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB078909; BAC41345.1; -;  
 KW Lectin; Protease.  
 FT NON TER 1 1  
 FT NON TER 14 14  
 SQ SEQUENCE 14 AA; 1533 MW; 99DD285F40C2B15 CRC64;

Query Match 16.7%; Score 3; DB 13; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GVP 9  
 Db 2 GVP 4

RESULT 48  
 Q9UR63  
 ID Q9UR63 PRELIMINARY; PRT; 15 AA.  
 AC Q9UR63;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Beta-D-FRUCTOFURANOSIDE FRUCTOHYDROLASE 60 kDa high molecular weight  
 DE isoform (EC 3.2.1.26) (Fragment).  
 OS Emericella nidulans (Aspergillus nidulans).

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 OC Eurotiales; Trichocomaceae; Emericella.  
 OX NCBI\_TaxID=162425;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=96409246; PubMed=8814228;  
 RA Chen J.S., Saxton J., Hemming F.W., Peberdy J.F.;  
 RT "Purification and partial characterization of the high and low  
 RT molecular weight form (S- and F-form) of invertase secreted by  
 RT Aspergillus nidulans.";  
 RL Biochim. Biophys. Acta 1296:207-218 (1996).  
 SQ SEQUENCE 15 AA; 1588 MW; 2C992B42211366BB CRC64;

Query Match 16.7%; Score 3; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQP 3  
 Db 1 LQP 3

RESULT 49  
 Q9UE41  
 ID Q9UE41 PRELIMINARY; PRT; 15 AA.  
 AC Q9UE41;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Collagen.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=89325561; PubMed=2753125;  
 RA Vikkula M., Paltonen L.;  
 RT "Structural analyses of the polymorphic area in type II collagen  
 RT gene.";  
 RL FEBS Lett. 250:171-174 (1989).  
 DR EMBL; X16158; CAA34281.1; -;  
 SQ SEQUENCE 15 AA; 1334 MW; D6DC3824197ABEF6 CRC64;

Query Match 16.7%; Score 3; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GVP 9  
 Db 1 GVP 3

RESULT 50  
 Q9UCC7  
 ID Q9UCC7 PRELIMINARY; PRT; 15 AA.  
 AC Q9UCC7;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Midkine (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=94059921; PubMed=8241100;  
 RA Novotny W.F., Maffi T., Mehta R.L., Milner P.G.;  
 RT "Identification of novel heparin-releasable proteins, as well as the  
 RT cytokines midkine and pleiotrophin, in human postheparin plasma.";  
 RL Arterioscler. Thromb. 13:1798-1805 (1993).  
 SQ SEQUENCE 15 AA; 1527 MW; C34B6B9787474AC CRC64;



Query Match 16.7%; Score 3; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KVK 12  
|||  
DB 7 KVK 9

## RESULT 51

ID Q9UCY1 PRELIMINARY; PRT; 15 AA.  
AC Q9UCY1, (Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE Thromboxane A2 receptor isoform alpha (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96193877; PubMed=8613548;  
RA Hirata T., Ushikubi F., Kakizuka A., Okuma M., Narumiya S.;  
RT "Two thromboxane A2 receptor isoforms in human platelets. Opposite  
RT coupling to adenylyl cyclase with different sensitivity to Arg60 to Leu  
RT mutation.";  
RL J. Clin. Invest. 97:949-956(1996).  
SQ SEQUENCE 15 AA; 1656 MW; 5EC77C6E9E97FB78 CRC64;

Query Match 16.7%; Score 3; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQP 3  
|||  
DB 4 LQP 6

## RESULT 52

ID O46661 PRELIMINARY; PRT; 15 AA.  
AC O46661, (Created)  
DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Glucose-6-phosphate dehydrogenase (Fragment).  
GN G6PD.  
OS Macropus robustus robustus.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.  
OX NCBI\_TaxID=35580;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97224585; PubMed=9060417;  
RA Loebel D.A., Johnston P.G.;  
RT "Analysis of the intron-exon structure of the G6PD gene of the  
RT wallaroo (Macropus robustus) by polymerase chain reaction.";  
RL Mamm. Genome 8:146-147(1997).  
DR EMBL; U53768; AAC48786.1; -.  
DR InterPro; IPR001282; G6PD.  
DR Pfam; PF00479; G6PD; 1.  
FT NON\_TER 1 1  
FT NON\_TER 15 15  
SQ SEQUENCE 15 AA; 1704 MW; 039588640B5E671E CRC64;

Query Match 16.7%; Score 3; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5' IMG 7

Db 11 IMG 13  
|||

## RESULT 53

ID Q9TR64 PRELIMINARY; PRT; 15 AA.  
AC Q9TR64, (Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Nucleoside diphosphate kinase, NDK, P19=17.143 kDa A subunit  
DE (Fragment).  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE  
RX MEDLINE=95285334; PubMed=7767789;  
RA Weber B., Weber W., Buck F., Hilz H.;  
RT "Isolation of the myc transcription factor nucleoside diphosphate  
RT kinase and the multifunctional enzyme glyceraldehyde-3-phosphate  
RT dehydrogenase by cAMP affinity chromatography.";  
RL Int. J. Biochem. Cell Biol. 27:215-224(1995).  
FT NON\_TER 1 1  
FT NON\_TER 15 15  
SQ SEQUENCE 15 AA; 1820 MW; 2728CDB4FDAE6316 CRC64;

Query Match 16.7%; Score 3; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QPE 4  
|||  
DB 7 QPE 9

## RESULT 54

ID Q9MZRS PRELIMINARY; PRT; 15 AA.  
AC Q9MZRS, (Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE Interleukin 4 variant IL-4int2A (Fragment).  
GN IL-4.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX TISSUE=Spleen, and Lymph node;  
RX MEDLINE=20304414; PubMed=10843729;  
RA Perkins H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;  
RT "The complete cDNA sequences of IL-2, IL-4, IL-6 and IL-10 from the  
RT European rabbit (Oryctolagus cuniculus).";  
RL Cytokine 12:555-565(2000).  
DR EMBL; AF169172; AAF86656.1; -.  
FT NON\_TER 1 1  
FT NON\_TER 15 15  
SQ SEQUENCE 15 AA; 1586 MW; 876C50E85307B55 CRC64;

Query Match 16.7%; Score 3; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VPK 10  
|||  
DB 12 VPK 14

## RESULT 55

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Q9TH04
ID Q9TH04 PRELIMINARY; PRT; 15 AA.
AC Q9TH04;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE NADH dehydrogenase subunit 6 (Fragment).
GN ND6.
OS Grus americana (whooping crane).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Gruiformes; Gruidae; Grus.
OX NCBI_TaxID=91117;
[1] _TaxID=91117;
RP SEQUENCE FROM N.A.
RC STRAIN=LMS B3394;
RA Glenn T.C., Stephan W., Braun M.J.;
RT "Effects of a Population Bottleneck on Whooping Crane Mitochondrial
RT DNA Variation.";
RL Conserv. Biol. 0:0-0(1999).
DR EMBL; AF112373; AAD23994.1; -.
KW Mitochondrion.
FT NON TER 15 15
SQ SEQUENCE 15 AA; 1759 MW; A7F711A65E9F934F CRC64;

Query Match 16.7%; Score 3; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 MGW 8
DB 8 MGW 10

RESULT 56
Q9AT15
ID Q9AT15 PRELIMINARY; PRT; 15 AA.
AC Q9AT15;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Plasma membrane H+-ATPase (Fragment).
GN LHAI.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. VFNT Cherry;
RA Ewing N.N., Wimmers L.E., Meyer D.J., Chetelat R.T., Bennett A.B.;
RT "Molecular cloning of tomato plasma membrane H+-ATPase.";
RL Life Sci. Adv. Plant Physiol. 94:1874-1881(1990).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. VFNT Cherry;
RA Ewing N.N., Bennett A.B.;
RT "Assessment of the number and expression of P-type H(+) -ATPase genes
RT in tomato.";
RL Life Sci. Adv. Plant Physiol. 106:547-557(1994).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. VFNT Cherry;
RA Dahmani Z., Ewing N.N.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF353103; AAK31206.1; -.
FT NON TER 15 15
SQ SEQUENCE 15 AA; 1673 MW; 5F70477FC08C809E CRC64;

Query Match 16.7%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 12 KET 14
DB 13 KET 15

RESULT 57
P93515
ID P93515 PRELIMINARY; PRT; 15 AA.
AC P93515;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Copper amine oxidase (Fragment).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsia.
OX NCBI_TaxID=3702;
[1] _TaxID=3702;
RP SEQUENCE FROM N.A.
RX MEDLINE=96227319; PubMed=8654815;
RA Moller S.G., McPherson M.J.;
RT "Molecular and functional studies of copper amine oxidase from
RT Arabidopsis thaliana.";
RL Biochem. Soc. Trans. 23:630S-630S(1995).
DR EMBL; S82396; AAB37690.1; -.
DR InterPro; IPR000269; CuNH_oxidase.
DR Pfam; PF01179; Cu_amine_oxid; 1.
FT NON TER 1 1
SQ SEQUENCE 15 AA; 1842 MW; 12BF98E81198BC5CE CRC64;

Query Match 16.7%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 MVP 17
DB 2 MVP 4

RESULT 58
Q9S8N8
ID Q9S8N8 PRELIMINARY; PRT; 15 AA.
AC Q9S8N8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Protein E-22 (Fragment).
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
[1] _TaxID=4513;
RP SEQUENCE.
RX MEDLINE=94170739; PubMed=8125056;
RA Flegstrud R.;
RT "Separation of acidic barley endosperm proteins by two-dimensional
RT electrophoresis.";
RL Electrophoresis 14:1060-1066(1993).
SQ SEQUENCE 15 AA; 1752 MW; C7D693937E908B9E CRC64;

Query Match 16.7%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQP 3
DB 3 LQP 5

RESULT 59

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Q9PRZ0
ID Q9PRZ0 PRELIMINARY; PRT; 15 AA.
AC Q9PRZ0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Phospholipase A2 (EC 3.1.1.4) (Fragment).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Bothrops.
OC NCBI_TaxID=9724;
RN [1]
RN SEQUENCE.
RX MEDLINE=94080171; PubMed=8257916;
RA Machado O.L., Oliveira-Carvalho A.L., Zingali R.B., Carlini C.R.;
RT "Purification, physicochemical characterization and N-terminal-amino
RT acid sequence of a phospholipase A2 from Bothrops jararaca venom.";
RL Braz. J. Med. Biol. Res. 26:163-166(1993).
SQ SEQUENCE 15 AA; 1734 MW; AF893A50F081B0A0 CRC64;

Query Match 16.7%; Score 3; DB 13; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+04; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 0;

QY 13 ETM 15
Db 6 ETM 8
|||

RESULT 60
Q51950 PRELIMINARY; PRT; 16 AA.
ID Q51950
AC Q51950;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ORF E.
OS Staphylococcus aureus.
OG Plasmid pNS1.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OC NCBI_TaxID=1280;
RN [1]
RN SEQUENCE FROM N.A.
RA Nouchi N., Roki T., Sasatsu M., Kono M., Shishido K., Ando T.;
RT "Determination of the complete nucleotide sequence of pNS1, a
RT staphylococcal tetracycline-resistance plasmid propagated in Bacillus
RT subtilis.";
RL FEMS Microbiol. Lett. 37:283-288(1986).
DR EMBL; M16217; AAA19178.1; -.
KW Plasmid.
SQ SEQUENCE 16 AA; 1929 MW; 0F038C3A8B79F3B0 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 0;

QY 11 VKE 13
Db 14 VKE 16
|||

RESULT 61
Q9FIS7 PRELIMINARY; PRT; 16 AA.
ID Q9FIS7
AC Q9FIS7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Phosphoribosyl carboxyamido aminoimidazole transformylase (EC 6.3.2.6)
DE (Fragment).
GN PURH.
OS Streptococcus suis.

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OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OC NCBI_TaxID=1307;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=20576151; PubMed=11133943;
RA Sekizaki T., Otani Y., Osaki M., Takamatsu D., Shimoji Y.;
RT "Evidence for horizontal transfer of the SsuDAT1I restriction-
RT modification genes to the Streptococcus suis genome.";
RL J. Bacteriol. 183:500-511(2001).
DR EMBL; AB045610; BAB20834.1; -.
KW Ligase.
FT NON_TER
SQ SEQUENCE 16 AA; 1935 MW; 1FC8D8B8AE391D40 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 0;

QY 14 TMV 16
Db 5 TMV 7
|||

RESULT 62
Q9FIS4 PRELIMINARY; PRT; 16 AA.
ID Q9FIS4
AC Q9FIS4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Phosphoribosyl carboxyamido aminoimidazole transformylase (EC 6.3.2.6)
DE (Fragment).
GN PURH.
OS Streptococcus suis.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OC NCBI_TaxID=1307;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=20576151; PubMed=11133943;
RA Sekizaki T., Otani Y., Osaki M., Takamatsu D., Shimoji Y.;
RT "Evidence for horizontal transfer of the SsuDAT1I restriction-
RT modification genes to the Streptococcus suis genome.";
RL J. Bacteriol. 183:500-511(2001).
DR EMBL; AB045612; BAB20838.1; -.
KW Ligase.
FT NON_TER
SQ SEQUENCE 16 AA; 1949 MW; 6978D8B8AE391D44 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 0;

QY 14 TMV 16
Db 5 TMV 7
|||

RESULT 63
Q9TQZ7 PRELIMINARY; PRT; 16 AA.
ID Q9TQZ7
AC Q9TQZ7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Factor H (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.

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OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=96202005; PubMed=8615824;
RA Soames C.J., Day A.J., Sim R.B.;
RT "Prediction from sequence comparisons of residues of factor H involved
RT in the interaction with complement component C3b.";
RL Biochem. J. 315:523-531 (1996).
SQ SEQUENCE 16 AA; 1871 MW; 7052751E485EC825 CRC64;

Query Match 16.7%; Score 3; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 KET 14
Db 10 KET 12

RESULT 64
Q9QV11 ID Q9QV11 PRELIMINARY; PRT; 16 AA.
AC Q9QV11;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Hepatic glycoen associated protein phosphatase 1 (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=95237359; PubMed=7720853;
RA Moorhead G., MacKintosh C., Morrice N., Cohen P.;
RT "Purification of the hepatic glycoen-associated form of protein
RT phosphatase-1 by microcystin-Sepharose affinity chromatography.";
RL FEBS Lett. 362:101-105 (1995).
SQ SEQUENCE 16 AA; 1750 MW; F1CB6485F4B54AE1 CRC64;

Query Match 16.7%; Score 3; DB 11; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TMV 16
Db 13 TMV 15

RESULT 65
Q9QUW8 ID Q9QUW8 PRELIMINARY; PRT; 16 AA.
AC Q9QUW8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Protein isomerase-related protein precursor 71.5 kDa isoform
DE (Fragment).
OS Cavia (guinea pigs).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae.
OX NCBI_TaxID=10140;
RN [1]
RP SEQUENCE.
RX MEDLINE=96070119; PubMed=8535285;
RA Bonifacio M.D., Steeves T., Saunders D.M., Sinosich M.J.;
RT "Isolation of Exp72 from guinea pig term placenta using heparin
RT Sepharose affinity chromatography.";
RL Biochem. Mol. Biol. Int. 36:1143-1152 (1995).
SQ SEQUENCE 16 AA; 1880 MW; 21B44A5F5767CB17 CRC64;

Query Match 16.7%; Score 3; DB 11; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;

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Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKE 13
Db 11 VKE 13

RESULT 66
Q88250 ID Q88250 PRELIMINARY; PRT; 16 AA.
AC Q88250;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE F protein (Fragment).
OS Sendai virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Respirivirus.
OX NCBI_TaxID=11191;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91012818; PubMed=2170692;
RA Itoh M., Ming T.D., Hayashi T., Mochizuki Y., Homma M.;
RT "Pneumopathogenicity of a Sendai virus protease-activation mutant,
RT TCs, which is sensitive to trypsin and chymotrypsin.";
RL J. Virol. 64:5660-5664 (1990).
DR EMBL; M60152; AAA47808.1; -.
FT NON_TER 1
FT NON_TER 16
SQ SEQUENCE 16 AA; 1648 MW; 049B529F01B29066 CRC64;

Query Match 16.7%; Score 3; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GVP 9
Db 4 GVP 6

RESULT 67
Q04246 ID Q04246 PRELIMINARY; PRT; 16 AA.
AC Q04246;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE F protein (Fragment).
OS Sendai virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Respirivirus.
OX NCBI_TaxID=11191;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91012818; PubMed=2170692;
RA Itoh M., Ming T.D., Hayashi T., Mochizuki Y., Homma M.;
RT "Pneumopathogenicity of a Sendai virus protease-activation mutant,
RT TCs, which is sensitive to trypsin and chymotrypsin.";
RL J. Virol. 64:5660-5664 (1990).
DR EMBL; M60155; AAA47805.1; -.
FT NON_TER 1
FT NON_TER 16
SQ SEQUENCE 16 AA; 1634 MW; 73989D9F01B298D0 CRC64;

Query Match 16.7%; Score 3; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GVP 9
Db 4 GVP 6

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RESULT 68  
Q88249 ID Q88249 PRELIMINARY; PRT; 16 AA.  
AC Q88249;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE F protein (Fragment).  
OS Sendai virus.  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Paramyxoviridae; Paramyxovirinae; Respirovirus.  
OX NCBI\_TaxID=11191;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91012818; PubMed=2170692;  
RA Itoh M., Ming T.D., Hayashi T., Mochizuki Y., Homma M.;  
RT "Pneumopathogenicity of a Sendai virus protease-activation mutant,  
RT TCS, which is sensitive to trypsin and chymotrypsin.";  
RL J. Virol. 64:5660-5664(1990).  
DR EMBL; M60154; AAA47807.1; -.  
FT NON\_TER 1 16  
FT NON\_TER 16 16  
SQ SEQUENCE 16 AA; 1649 MW; 049B529F01B298C4 CRC64;  
  
Query Match 16.7%; Score 3; DB 12; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 7 GVP 9  
Db 4 GVP 6  
  
RESULT 69  
Q99154 ID Q99154 PRELIMINARY; PRT; 16 AA.  
AC Q99154;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE F protein (Fragment).  
OS Sendai virus.  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Paramyxoviridae; Paramyxovirinae; Respirovirus.  
OX NCBI\_TaxID=11191;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91012818; PubMed=2170692;  
RA Itoh M., Ming T.D., Hayashi T., Mochizuki Y., Homma M.;  
RT "Pneumopathogenicity of a Sendai virus protease-activation mutant,  
RT TCS, which is sensitive to trypsin and chymotrypsin.";  
RL J. Virol. 64:5660-5664(1990).  
DR EMBL; M60153; AAA47806.1; -.  
FT NON\_TER 1 16  
FT NON\_TER 16 16  
SQ SEQUENCE 16 AA; 1606 MW; 739B529F01B298D0 CRC64;  
  
Query Match 16.7%; Score 3; DB 12; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 7 GVP 9  
Db 4 GVP 6  
  
RESULT 70  
Q50842 ID Q50842 PRELIMINARY; PRT; 17 AA.  
AC Q50842;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last annotation update)  
RN [1]

DE RNA polymerase (Fragment).  
OS Methanococcus voltae.  
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;  
OC Methanococcaceae; Methanococcus.  
OX NCBI\_TaxID=2188;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85230552; PubMed=4006907;  
RA Bollschweiler C., Kuehn R., Klein A.;  
RT "Non-repetitive AT-rich sequences are found in intergenic regions of  
RT Methanococcus voltae DNA.";  
RL EMBO J. 4:805-809(1985).  
DR EMBL; X02517; CAA26352.1; -.  
FT NON\_TER 1 1  
FT NON\_TER 1 1  
SQ SEQUENCE 17 AA; 1954 MW; 65B6C6ED9F34B80DA CRC64;  
  
Query Match 16.7%; Score 3; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 8 VPK 10  
Db 8 VPK 10  
  
RESULT 71  
Q8VME2 ID Q8VME2 PRELIMINARY; PRT; 17 AA.  
AC Q8VME2;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE ParC protein (Fragment).  
GN PARC.  
OS Pseudomonas putida.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Pseudomonas.  
OX NCBI\_TaxID=303;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Great A., Lambertson L., Williams P.A., Thomas C.M.;  
RT "Complete nucleotide sequence of IncP-9 plasmid pW0.";  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ344068; CAC86875.1; -.  
KW Plasmid.  
FT NON\_TER 17 17  
FT NON\_TER 17 17  
SQ SEQUENCE 17 AA; 1903 MW; A58E0B85C365A999 CRC64;  
  
Query Match 16.7%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 LQP 3  
Db 13 LQP 15  
  
RESULT 72  
Q9EUB3 ID Q9EUB3 PRELIMINARY; PRT; 17 AA.  
AC Q9EUB3;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE CmlB (CmlA).  
GN CmlB OR CMLA.  
OS Corynebacterium striatum.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.  
OX NCBI\_TaxID=43770;  
RN [1]

```

RP SEQUENCE FROM N.A.
RC STRAIN=M82B; PLASMid=pTP10;
RX MEDLINE=20194806; PubMed=10732668;
RA Tauch A., Krieff S., Kalinowski J., Puhler A.;
RT "The 51,409-bp R-plasmid pTP10 from the multiresistant clinical
RT isolate Corynebacterium striatum M82B is composed of DNA segments
RT initially identified in soil bacteria and in plant, animal, and human
RT pathogens.";
RL Mol. Gen. Genet. 263:1-11(2000).
RN [2]

RP SEQUENCE FROM N.A.
RC STRAIN=M82B; PLASMid=pTP10;
RX MEDLINE=98414982; PubMed=9735314;
RA Tauch A., Zheng Z., Puhler A., Kalinowski J.;
RT "Corynebacterium striatum chloramphenicol resistance transposon
RT Tn5564: genetic organization and transposition in Corynebacterium
RT glutamicum.";
RL Plasmid 40:126-139(1998).
DR EMBL; AF024666; AAG03379.1; -.
DR EMBL; AF024666; AAG03369.1; -.
KW Plasmid.
SQ SEQUENCE 17 AA; 1715 MW; 13CA5DE6CA436B0F CRC64;

Query Match 16.7%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GVP 9
DB 3 GVP 5

RESULT 73
Q14001 PRELIMINARY; PRT; 17 AA.
ID Q14001
AC Q14001;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cyclic nucleotide phosphodiesterase (Fragment).
GN CGIPDE1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97079687; PubMed=8921398;
RA Loebbert R.W., Winterpacht A., Seipel B., Zabel B.U.;
RT "Molecular cloning and chromosomal assignment of the human homologue
RT of the rat cGMP-inhibited phosphodiesterase 1 (PDE3A)-A gene involved
RT in fat metabolism located at 11p15.1.";
RL Genomics 37:211-218(1996).
DR EMBL; X95522; CAA64776.1; -.
FT NON_TER 17
FT SEQUENCE 17 AA; 2057 MW; 69D117C4FAE11540 CRC64;

Query Match 16.7%; Score 3; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQP 3
DB 14 LQP 16

RESULT 74
Q9UCC6 PRELIMINARY; PRT; 17 AA.
ID Q9UCC6
AC Q9UCC6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)

```

```

DE Pleiotrophin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=94059921; PubMed=8241100;
RA Novotny M.F., Maffi T., Mehta R.L., Milner P.G.;
RT "Identification of novel heparin-releasable proteins, as well as the
RT cytokines midkine and pleiotrophin, in human postheparin plasma.";
RL Arterioscler. Thromb. 13:1798-1805(1993).
SQ SEQUENCE 17 AA; 1925 MW; 442BC8BEFD417ADD CRC64;

Query Match 16.7%; Score 3; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KVK 12
DB 9 KVK 11

RESULT 75
Q9XSG1 PRELIMINARY; PRT; 17 AA.
ID Q9XSG1
AC Q9XSG1;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE SMCX (Fragment).
GN SMCX.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Poloumienko A., Blecher S.;
RT "Exon-intron structure of SMCX and SMCY genes in bovine and swine.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF135448; AAD34440.1; -.
FT NON_TER 17
FT SEQUENCE 17 AA; 1927 MW; 10351B0D516D16F0 CRC64;

Query Match 16.7%; Score 3; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PEI 5
DB 2 PEI 4

Search completed: November 25, 2003, 19:33:59
Job time : 36.8023 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:16:09 ; Search time 45.9419 Seconds  
(without alignments)  
62.189 Million cell updates/sec

Title: US-09-641-801-21

Perfect score: 18

Sequence: 1 LQPEIMGVKPKETWPK 18

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	ID	Description
1	18	100.0	18 22	Colostrinin derive
2	18	100.0	18 22	Colostrinin peptid
3	18	100.0	18 22	Colostrinin peptid
4	18	100.0	18 22	Ewe colostrinin pe
5	18	100.0	18 23	Colostrinin consti
6	18	100.0	18 23	Colostrinin consti
7	18	100.0	18 23	Neural cell regula
8	5	27.8	10 21	Retinoblastoma bin
9	5	27.8	11 21	Retinoblastoma bin

10	5	27.8	12	22	AA887422	Human gene 3 encod
11	5	27.8	14	14	AA43871	OmpA2-R-7 signal p
12	5	27.8	16	24	AB282578	G protein-coupled
13	5	27.8	16	24	AB282609	G protein-coupled
14	4	22.2	4	20	AA93084	Human erythropoiet
15	4	22.2	4	23	AB32218	Sheep colostrinin
16	4	22.2	6	14	AA32746	PK40 TAU/neurofila
17	4	22.2	6	20	AAV27421	PK40 protein kinas
18	4	22.2	6	23	AA51129	Bovine TAU/neurofi
19	4	22.2	7	14	AA333159	HPV E7 protein - R
20	4	22.2	7	20	AA49017	Membrane dipeptida
21	4	22.2	7	21	AA35822	T7 phage coat prot
22	4	22.2	7	22	AA72261	Colostrinin derive
23	4	22.2	7	22	AA72514	Colostrinin peptid
24	4	22.2	7	22	AA72546	Colostrinin peptid
25	4	22.2	7	22	AA59317	Ewe colostrinin pe
26	4	22.2	7	23	AA20243	Colostrinin consti
27	4	22.2	7	23	AA51050	Colostrinin consti
28	4	22.2	7	23	AA014592	Neural cell regula
29	4	22.2	8	12	AA810631	Human Papilloma Vi
30	4	22.2	8	14	AA333158	HPV E7 protein - R
31	4	22.2	8	19	AAW77186	Pharmaceutically a
32	4	22.2	8	21	AA35995	Sorbitol dehydroge
33	4	22.2	8	22	AB314637	HIV A03 super moti
34	4	22.2	8	22	ABP17276	HIV B27 super moti
35	4	22.2	8	22	ABP21662	HIV A03 motif pol
36	4	22.2	8	22	AB23544	HIV A11 motif pol
37	4	22.2	8	22	AA62330	Casein-related pep
38	4	22.2	9	12	AA810635	Human Papilloma Vi
39	4	22.2	9	14	AA333157	HPV E7 protein - R
40	4	22.2	9	14	AA333163	HPV E7 protein - R
41	4	22.2	9	14	AA333170	HPV E7 protein - R
42	4	22.2	9	14	AA343741	MHC Class I allele
43	4	22.2	9	14	AA43742	MHC Class I allele
44	4	22.2	9	15	AA59257	Peptide fragment (
45	4	22.2	9	15	AA59246	Peptide fragment (
46	4	22.2	9	15	AA73799	Antigen fragment 1
47	4	22.2	9	15	AA73800	Antigen fragment 1
48	4	22.2	9	15	AA73796	Antigen fragment 1
49	4	22.2	9	16	AA80939	Peptide for increa
50	4	22.2	9	16	AA78889	HPV16 E7 11-19 cyt
51	4	22.2	9	16	AA78894	HPV16 E7 12-20 cyt
52	4	22.2	9	16	AA78851	HIV pol 185-193 cy
53	4	22.2	9	16	AA70601	HIV(B35)POL-9, hum
54	4	22.2	9	16	AA84331	HPV derived peptid
55	4	22.2	9	17	AA89363	Immunogenic peptid
56	4	22.2	9	18	AAW39661	HPV16/18 E7 peptid
57	4	22.2	9	18	AAW39662	HPV16/18 E7 peptid
58	4	22.2	9	18	AAW36590	Hepatitis B virus
59	4	22.2	9	18	AAW28811	HPV-16 derived pep
60	4	22.2	9	19	AAW78893	Human papillomavir
61	4	22.2	9	19	AAW54766	Peptide from HPV 1
62	4	22.2	9	19	AAW54767	Peptide from HPV 1
63	4	22.2	9	20	AAV53466	HIV-1 RT protein (
64	4	22.2	9	20	AAV55432	HLA binding plu-1
65	4	22.2	9	20	AAV40315	Amino acid sequenc
66	4	22.2	9	20	AAV26807	HIV-derived lipope
67	4	22.2	9	20	AAV10346	T cell epitope/MHC
68	4	22.2	9	20	AAV10511	HLA Class I motif
69	4	22.2	9	21	AA333705	MHC class I associ
70	4	22.2	9	21	AA318492	Peptide substrate
71	4	22.2	9	21	AAV96941	Processed N-termin
72	4	22.2	9	21	AAV66364	HLA-B7-binding HIV
73	4	22.2	9	21	AAV66378	HLA-B8-binding HIV
74	4	22.2	9	22	ABP11796	HIV A01 super moti
75	4	22.2	9	22	ABP16116	HIV A24 super moti
76	4	22.2	9	22	ABP16839	HIV B07 super moti
77	4	22.2	9	22	ABP21667	HIV A03 motif pol
78	4	22.2	9	22	ABP23548	HIV A11 motif pol
79	4	22.2	9	22	ABP24295	HIV A24 motif pol
80	4	22.2	9	22	AA931801	Human papilloma vi
81	4	22.2	9	22	AA886611	HER2/NEU DR superm
82	4	22.2	9	22	AA886725	HER2/NEU DR 3a mot



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83      4      22.2      9      22      AAB95951      MHC class-I associ
84      4      22.2      9      22      AAB95999      HPV 16 E7 A2 MHC-b
85      4      22.2      9      22      AAB96001      HPV 16 E7 A2 MHC-b
86      4      22.2      9      22      AAB96004      HPV 16 E7 A2 MHC-b
87      4      22.2      9      22      AAB20215      HPV strain 16 E7 p
88      4      22.2      9      22      AAB30975      HPV E7 peptide whi
89      4      22.2      9      22      AAB31056      Polyepitopic pep
90      4      22.2      9      22      AAB31145      A polyepitopic pep
91      4      22.2      9      22      AAB46273      HPV type 16 L1 pro
92      4      22.2      9      22      ABJ15172      Immunogenic HIV pe
93      4      22.2      9      23      ABG80028      MHC class I molecu
94      4      22.2      9      23      ABG80194      Human leukocyte an
95      4      22.2      9      23      ABG34185      Human leukocyte an
96      4      22.2      9      23      ABG34191      Human leukocyte an
97      4      22.2      9      23      ABG34256      Human leukocyte an
98      4      22.2      9      23      ABG34370      Human leukocyte an
99      4      22.2      9      23      ABG34387      Human leukocyte an
100     4      22.2      9      23      ABG34388      Human leukocyte an
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## ALIGNMENTS

```
RESULT 1
AAB72266
ID AAB72266 standard; peptide; 18 AA.
XX
AC AAB72266;
XX
DT 14-MAY-2001 (first entry)
XX
DE Colostrinin derived cytokine inducing peptide SEQ ID 21.
XX
KW Colostrinin; immune response; cytokine; blood cell proliferation;
KW central nervous system disorder; neurological disorder; mental disorder;
KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
KW neurosis; infection.
XX
OS Synthetic.
XX
PW WO20011937-A2.
XX
PD 22-FEB-2001.
XX
PF 17-AUG-2000; 2000WO-US22818.
XX
PR 17-AUG-1999; 99US-0149311.
XX
PA (TEXA ) UNIV TEXAS SYSTEM.
PA (REG- ) REGEN THERAPEUTICS PLC.
XX
PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
XX
PS WPI; 2001-202804/20.
XX
PT Inducing a cytokine and modulating an immune response, useful for
PT treating central nervous system diseases and bacterial and viral
PT infections, comprises administering colostrinin as an immunological
PT regulator -
XX
PS Claim 1; Page 34; 50pp; English.
XX
CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,
CC a proline rich polypeptide aggregate contained in colostrum. The
CC peptides have immune response modulatory activity, and are capable of
CC inducing cytokines. Colostrinin and its derived peptides are useful for
CC inducing cytokine production, for modulating an immunological response
CC and for inducing blood cell proliferation. The peptides are useful in the
CC treatment of disorders of the central nervous system, neurological
CC disorders, mental disorders, dementia, neurodegenerative diseases,
CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
CC disorders of the immune system, bacterial and viral infections and
CC acquired immunological deficiencies.
```

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XX      SQ      Sequence      18 AA;
SQ
Query Match      100.0%; Score 18; DB 22; Length 18;
Best Local Similarity      100.0%; Pred. No. 2.3e-12;
Matches      18; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 LQPEIMGVPKVKETWVPK 18
      |||||
DB      1 LQPEIMGVPKVKETWVPK 18
      |||||

RESULT 2
AAB72519
ID AAB72519 standard; Peptide; 18 AA.
XX
AC AAB72519;
XX
DT 09-MAY-2001 (first entry)
XX
DE Colostrinin peptide #20.
XX
KW Dermatological; oxidative stress regulator; colostrinin.
XX
OS Unidentified.
XX
PN WO200112650-A2.
XX
PD 22-FEB-2001.
XX
PF 17-AUG-2000; 2000WO-US22665.
XX
PR 17-AUG-1999; 99US-0149310.
XX
PA (TEXA ) UNIV TEXAS SYSTEM.
XX
PI Stanton GJ, Hughes TK, Boldogh I;
XX
PS WPI; 2001-218342/22.
XX
PT Modulating oxidative stress level in a cell, involves contacting the
PT cell with an oxidative stress regulator selected from colostrinin, its
PT constituent peptide, analog or their combinations -
XX
PS Claim 6; Page 25; 48pp; English.
XX
CC The present invention relates to a method for modulating the oxidative
CC stress level in a cell or a patient, comprising contacting the cell with,
CC or administering to the patient, an oxidative stress regulator selected
CC from colostrinin, or its constituent peptide (e.g. the present peptide),
CC to change the level of an oxidising species in the cell. The method can
CC be used to treat oxidative damage to skin, by decreasing or preventing an
CC increase in the level of damage to a biomolecule of the patient.
XX
SQ      Sequence      18 AA;
SQ
Query Match      100.0%; Score 18; DB 22; Length 18;
Best Local Similarity      100.0%; Pred. No. 2.3e-12;
Matches      18; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 LQPEIMGVPKVKETWVPK 18
      |||||
DB      1 LQPEIMGVPKVKETWVPK 18
      |||||

RESULT 3
AAB72551
ID AAB72551 standard; Peptide; 18 AA.
XX
AC AAB72551;
XX
DT 09-MAY-2001 (first entry)
XX
```

DE Colostrinin peptide #20.  
 XX Neuroprotective; neural cell differentiation regulator; colostrinin;  
 KW colostrum.  
 XX Unidentified.  
 OS  
 XX WO200112651-A2.  
 PN  
 XX 22-FEB-2001.  
 PD  
 XX 17-AUG-2000; 2000WO-US22774.  
 PF  
 XX 17-AUG-1999; 99US-0149633.  
 PR  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA  
 XX Boldogh I;  
 PI  
 XX WPI; 2001-226545/23.  
 DR  
 XX Use of colostrinin, its constituent peptide or analog as a neural cell  
 PT regulator, for promoting neural cell differentiation and treating  
 PT damaged neural cells in a patient -  
 PT  
 XX Claim 6; Page 21; 35pp; English.  
 PS  
 XX The present invention relates to a method for promoting neural cell  
 CC differentiation and treating damaged neural cells, using colostrinin and  
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural  
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.  
 CC  
 XX SQ Sequence 18 AA;  
 DE Query Match 100.0%; Score 18; DB 22; Length 18;  
 XX Best Local Similarity 100.0%; Pred. No. 2.3e-12;  
 KW Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 OY 1 LQPEIMGVPKVKTWPK 18  
 DB 1 LQPEIMGVPKVKTWPK 18  
 DE  
 XX  
 AC AAB59329 standard; Peptide; 18 AA.  
 XX  
 AC AAB59329;  
 XX  
 DT 21-MAR-2001 (first entry)  
 XX  
 DE Ewe colostrinin peptide fragment C-4.  
 XX  
 XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.  
 XX  
 OS Ovis sp.  
 XX  
 PN WO200075173-A2.  
 XX  
 PD 14-DEC-2000.  
 XX  
 PF 02-JUN-2000; 2000WO-GB02128.  
 PP  
 XX 02-JUN-1999; 99GB-0012852.  
 PR  
 XX (REGE-) REGEN THERAPEUTICS PLC.  
 PA  
 XX Georgiades JA;  
 PI  
 XX WPI; 2001-071058/08.  
 DR  
 XX Peptides having an N-terminal amino acid sequence isolated from  
 PT

PT colostrinin for treating e.g. disorders of the central nervous system  
 PT and immune system, viral and bacterial infections, and diseases  
 PT characterized by amyloid plaques -  
 XX  
 PS Claim 7; Page 27; 63pp; English.  
 XX  
 CC The present invention provides the sequences of a number of peptides  
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
 CC fragment of colostrum. These peptides can be used in the treatment of  
 CC central nervous system disorders such as senile dementia, Parkinson's  
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
 CC disorders such as bacterial and viral infections, to improve the  
 CC development of a child's immune system, as a dietary supplement, and to  
 CC promote the dissolution of beta-amyloid plaques.  
 XX  
 SQ Sequence 18 AA;  
 DE Query Match 100.0%; Score 18; DB 22; Length 18;  
 XX Best Local Similarity 100.0%; Pred. No. 2.3e-12;  
 KW Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 OY 1 LQPEIMGVPKVKTWPK 18  
 DB 1 LQPEIMGVPKVKTWPK 18  
 DE  
 XX  
 AC AAE20248 standard; peptide; 18 AA.  
 XX  
 AC AAE20248;  
 XX  
 DT 18-JUN-2002 (first entry)  
 XX  
 DE Colostrinin constituent peptide #20.  
 XX  
 KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;  
 KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;  
 KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;  
 KW transplantation; implantation; dermatological; vulnary.  
 XX  
 OS Unidentified.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 18  
 FT /note= "Optionally C-terminal amide"  
 XX  
 PN WO200213850-A1.  
 XX  
 PD 21-FEB-2002.  
 XX  
 PF 17-AUG-2000; 2000WO-US22776.  
 XX  
 PR 17-AUG-2000; 2000WO-US22776.  
 PP  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA  
 XX Stanton GJ, Hughes TK, Boldogh I;  
 PI  
 XX WPI; 2002-269151/31.  
 DR  
 XX Composition useful for the modulation of blood cell proliferation in a  
 PT patient comprises a blood cell regulator selected from colostrinin, its  
 PT constituent peptide and/or analog -  
 XX  
 PS Claim 6; Page 25; 51pp; English.  
 XX  
 CC The invention relates to a composition which comprises a blood cell  
 CC regulator selected from colostrinin, its constituent peptide and/or  
 CC analogue. The invention is used for modulating the oxidative stress  
 CC level in a cell e.g. mammalian or human cell present in a cell culture,  
 CC tissue, organ, or organism; or for treating oxidative damage to the skin  
 CC of a patient e.g. animal or human; to modulate oxidative stress during/

CC after a premature birth or normal birth, preventing/delaying aging in a  
 CC patient, enhancing wound healing, and the reduction of side effects of  
 CC cosmetic procedures. The method changes the level of an oxidising species  
 CC in the cell, such as decreases or prevents increase in the level of  
 CC damage to a biomolecule of the patient selected from DNA, protein and/or  
 CC lipid, compared to the same conditions when the oxidative stress  
 CC regulator is not present. The modulation of oxidative stress results in  
 CC enhanced repair, regeneration, and replacement of cells, tissues and  
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
 CC external organs), as well as enhanced preservation of such organs for  
 CC transplantation, implantation, or scientific research. The present  
 CC sequence is a colostrinin constituent peptide.

SQ Sequence 18 AA;  
 Query Match 100.0%; Score 18; DB 23; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-12;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPEIMGVPKVKETWVPK 18  
 |||||  
 Db 1 LQPEIMGVPKVKETWVPK 18  
 |||||

## RESULT 6

AA051055  
 ID AAMS1055 standard; Peptide; 18 AA.

XX AC AAMS1055;

XX DT 30-MAY-2002 (first entry)

XX DE Colostrinin constituent peptide (casein amino acids 103-120).

XX KW Colostrinin; colostrum; immunomodulator; cardiovascular;

XX KW blood cell regulator; cytokine inducer; beta-casein; human.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Modified-site 18  
 FT /note= "optional C-terminal amidation"

XX XN WO200213849-A1.

XX PD 21-FEB-2002.

XX PF 17-AUG-2000; 2000WO-US22775.

XX PR 17-AUG-2000; 2000WO-US22775.

XX PA (TEXA ) UNIV TEXAS SYSTEM.

XX PA (REGF-) REGEN THERAPEUTICS PLC.

XX PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX DR WPI; 2002-269150/31.

XX PT Modulation of blood cell proliferation in a patient involves use of  
 PT blood cell regulator selected from colostrinin, its constituent peptide  
 PT and/or analogue -

XX PS Claim 1; Page 34; 54pp; English.

XX CC The present sequence is that of a colostrinin constituent peptide  
 CC that is used as an immunological regulator and as a blood cell  
 CC regulator in claimed methods of the invention. It is classified  
 CC as having a beta-casein homologue precursor, and corresponds to  
 CC casein amino acids 103-120. Methods are claimed for: inducing a  
 CC cytokine in a cell by contact with an immunological regulator,  
 CC where the cell is present in a cell culture, a tissue, an organ  
 CC or an organism, and the cell is mammalian, including human;  
 CC modulating an immune response in a cell by contact with the

CC immunological regulator under conditions effective to induce a  
 CC cytokine; modulating an immune response in a patient by administering  
 CC an immunological regulator under conditions effective to induce a  
 CC cytokine, where the immunological regulator is administered topically  
 CC or as part of a dietary supplement, and where the immune response is  
 CC specific or non specific, an interferon response or an antibody  
 CC response; modulating blood cell proliferation by contacting blood  
 CC cells with a blood cell regulator, where the blood cells are present  
 CC in a cell culture or an organism, are mammalian or human, and where  
 CC the blood cells are increased in number or differentiated; and a  
 CC method for modulating blood cell proliferation in a patent. A  
 CC claimed cytokine-inducing composition comprises a pharmaceutical  
 CC carrier and an active agent such as the present peptide.

XX SQ Sequence 18 AA;

Query Match 100.0%; Score 18; DB 23; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-12;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPEIMGVPKVKETWVPK 18  
 |||||  
 Db 1 LQPEIMGVPKVKETWVPK 18  
 |||||

## RESULT 7

AA014597  
 ID AA014597 standard; peptide; 18 AA.

XX AC AA014597;

XX DT 27-MAY-2002 (first entry)

XX DE Neural cell regulatory colostrinin peptide 20.

XX KW Neural cell differentiation; neural cell regulator; colostrinin peptide;

XX KW neural cell formation; proline-rich polypeptide aggregate; colostrum;

XX KW neural cell treatment.

XX OS Unidentified.

XX FH Key Location/Qualifiers

FT Modified-site 18  
 FT /note= "Optional C-terminal amide"

XX XN WO200213851-A1.

XX PD 21-FEB-2002.

XX PF 17-AUG-2000; 2000WO-US22777.

XX PR 17-AUG-2000; 2000WO-US22777.

XX PA (TEXA ) UNIV TEXAS SYSTEM.

XX PI Boldogh I, Stanton JG, Hughes TK;

XX DR WPI; 2002-269152/31.

XX PT Promoting cell differentiation in a patient involves use of blood cell  
 PT regulator selected from colostrinin, its constituent peptide and/or  
 PT analog -

XX PS Claim 7; Page 21; 37pp; English.

XX CC The invention comprises a method for promoting cell differentiation (e.g.  
 CC neural cell differentiation). The method involves contacting cells with a  
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the  
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich  
 CC polypeptide aggregate that is present in colostrum. The method of the  
 CC invention is useful for promoting the differentiation of cells and for  
 CC treating damaged neural cells in a patient. The present amino acid  
 CC sequence represents a specifically claimed colostrinin peptide used in

```
CC the method of the invention.
XX
SQ Sequence 18 AA;
    Query Match      100.0%; Score 18; DB 23; Length 18;
    Best Local Similarity 100.0%; Pred. No. 2.3e-12;
    Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LQPEIMGVPKVKETWVPK 18
    |||||
Db 1 LQPEIMGVPKVKETWVPK 18

RESULT 8
AAAY5836
ID AAY5836 standard; Peptide; 10 AA.
XX
AC AAY5836;
XX
DT 10-FEB-2000 (first entry)
XX
DE Retinoblastoma binding protein 1 isoform I mutant peptide 6.
XX
KW Human; frameshift mutant; T cell response; tumour; treatment; cancer;
KW muten.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9958552-A2.
XX
PD 18-NOV-1999.
XX
PF 03-MAY-1999; 99WO-NO00143.
XX
PR 08-MAY-1998; 98NO-0002097.
XX
PA (NHYD ) NORSK HYDRO AS.
XX
PI Gaudernack G, Eriksen JA, Moller M, Gjertsen MK, Saeterdal I;
XX
DR WPI; 2000-039064/03.
XX
PT New peptides derived from genes with frameshift mutations, used to
PT develop products for the treatment and prophylaxis of cancers -
XX
PS Claim 13; Page 28; 166pp; English.
XX
CC Peptides AAY5684-Y66142 are fragments of mutant proteins arising from a
CC frameshift mutation in a gene from a cancer cell. The peptides are
CC characterised in that they:
CC (i) are at least 8 amino acids long and a fragment of a mutant protein
CC arising from a frameshift mutation in a gene of a cancer cell;
CC (ii) consist of at least one amino acid of the mutant part of a protein
CC sequence encoded by the gene;
CC (iii) comprise 0-10 amino acid from the carboxyl terminus of the normal
CC part of the protein sequence preceding the amino terminus of the mutant
CC sequence and may further extend to the carboxyl terminus of the mutant
CC part of the protein as determined by a new stop codon generated by the
CC frameshift mutation; and
CC (iv) induce, either in their full lengths or after processing by an
CC antigen presenting cell (APC), T cell responses.
CC The genes that the peptides are derived from, are characterised as
CC susceptible to frameshift mutation by having a mono nucleoside base
CC repeat sequence of at least 5 residues, or a di-nucleoside base repeat
CC sequence of at least 4 di-nucleoside base units. The peptides are
CC created by the addition or deletion of 1 or 2 nucleoside base residues
CC from the repeat sequence. The novel peptides can elicit T cell responses
CC and toxicity against tumours and cancer cells carrying genes with
CC frameshift mutations. The novel peptides and DNA sequences can be used
CC for the preparation of a composition for the treatment or prophylaxis of
CC cancer.
XX

CC the method of the invention.
XX
SQ Sequence 10 AA;
    Query Match      27.8%; Score 5; DB 21; Length 10;
    Best Local Similarity 100.0%; Pred. No. 63;
    Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 PKVKE 13
    |||||
Db 2 PKVKE 6

RESULT 9
AAAY5837
ID AAY5837 standard; Peptide; 11 AA.
XX
AC AAY5837;
XX
DT 10-FEB-2000 (first entry)
XX
DE Retinoblastoma binding protein 1 isoform I mutant peptide 7.
XX
KW Human; frameshift mutant; T cell response; tumour; treatment; cancer;
KW muten.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9958552-A2.
XX
PD 18-NOV-1999.
XX
PF 03-MAY-1999; 99WO-NO00143.
XX
PR 08-MAY-1998; 98NO-0002097.
XX
PA (NHYD ) NORSK HYDRO AS.
XX
PI Gaudernack G, Eriksen JA, Moller M, Gjertsen MK, Saeterdal I;
XX
DR WPI; 2000-039064/03.
XX
PT New peptides derived from genes with frameshift mutations, used to
PT develop products for the treatment and prophylaxis of cancers -
XX
PS Claim 13; Page 28; 166pp; English.
XX
CC Peptides AAY5684-Y66142 are fragments of mutant proteins arising from a
CC frameshift mutation in a gene from a cancer cell. The peptides are
CC characterised in that they:
CC (i) are at least 8 amino acids long and a fragment of a mutant protein
CC arising from a frameshift mutation in a gene of a cancer cell;
CC (ii) consist of at least one amino acid of the mutant part of a protein
CC sequence encoded by the gene;
CC (iii) comprise 0-10 amino acid from the carboxyl terminus of the normal
CC part of the protein sequence preceding the amino terminus of the mutant
CC sequence and may further extend to the carboxyl terminus of the mutant
CC part of the protein as determined by a new stop codon generated by the
CC frameshift mutation; and
CC (iv) induce, either in their full lengths or after processing by an
CC antigen presenting cell (APC), T cell responses.
CC The genes that the peptides are derived from, are characterised as
CC susceptible to frameshift mutation by having a mono nucleoside base
CC repeat sequence of at least 5 residues, or a di-nucleoside base repeat
CC sequence of at least 4 di-nucleoside base units. The peptides are
CC created by the addition or deletion of 1 or 2 nucleoside base residues
CC from the repeat sequence. The novel peptides can elicit T cell responses
CC and toxicity against tumours and cancer cells carrying genes with
CC frameshift mutations. The novel peptides and DNA sequences can be used
CC for the preparation of a composition for the treatment or prophylaxis of
CC cancer.
XX
SQ Sequence 11 AA;
```

Query Match 27.8%; Score 5; DB 21; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 69; Mismatches 0; Indels 0; Gaps 0;  
 Matches 5; Conservative 0;

QY 9 PKVKE 13  
 DB 2 PKVKE 6

RESULT 10  
 AAB87422 ID AAB87422 standard; peptide; 12 AA.  
 XX AC AAB87422;  
 XX DT 22-MAY-2001 (first entry)  
 XX DE Human gene 3 encoded secreted protein fragment, SEQ ID NO:163.  
 XX KW Human; secreted protein; proliferative disorder; cancer; tumour;  
 KW foetal abnormality; developmental abnormality; haematopoietic disorder;  
 KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;  
 KW inflammation; allergy; neurological disorder; Alzheimer's disease;  
 KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;  
 KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;  
 KW cardiovascular disorder; angiogenic disorder; kidney disorder;  
 KW gastrointestinal disorder; pregnancy-related disorder;  
 KW endocrine disorder; infection; wound healing; vulnery;  
 KW cell culture; chemotaxis; food additive;  
 KW binding partner identification.  
 XX KW Homo sapiens.  
 OS WO200118022-A1.  
 XX PN 15-MAR-2001.  
 XX PD 31-AUG-2000; 2000WO-US24008.  
 XX PF 03-SEP-1999; 99US-0152315.  
 XX PR 03-SEP-1999; 99US-0152317.  
 XX FA (HUMA-) HUMAN GENOME SCI INC.  
 XX NI J, Baker KP, Birse CE, Fiscella M, Komatsoulis GA, Rosen CA;  
 PI Soppet DR, Young PE, Ebner R, Duan DR, Olsen HS, Lafleur DW;  
 PI Moore PA, Shi Y, Wei Y, Florence KA;  
 XX WPI; 2001-203081/20.  
 XX Nucleic acid molecules encoding human secreted proteins, used in  
 PT preventing, treating or ameliorating a disorder, e.g. Alzheimer's and  
 PT Parkinson's diseases and cancers -  
 PS Disclosure; Page 18; 607pp; English.

AAF91858-AAF91929 represent cDNAs corresponding to 52 human secreted  
 protein genes, and AAB87342-AAB87413 represent the proteins they encode.  
 AAB87414-AAB87454 represent human secreted protein fragments. The genes  
 and their corresponding secreted proteins are useful for preventing,  
 treating or ameliorating medical conditions, e.g., by protein or gene  
 therapy. Pathological conditions can be diagnosed by determining the  
 amount of the new protein in a sample or by determining the presence of  
 mutations in the new genes. Specific uses are described for each of the  
 52 genes, based on the tissues in which they are most highly expressed,  
 and include developing products for the diagnosis or treatment of  
 proliferative disorders, cancer, tumours, foetal and developmental  
 abnormalities, haematopoietic disorders, diseases of the immune system,  
 AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,  
 allergies, neurological disorders (e.g., Alzheimer's disease,  
 Parkinson's disease), cognitive disorders, schizophrenia, asthma,  
 skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,  
 cardiovascular disorders, angiogenic disorders, kidney disorders,

CC gastrointestinal disorders, pregnancy-related disorders, endocrine  
 CC disorders, and infections. The proteins can also be used to aid wound  
 CC healing and epithelial cell proliferation, to prevent skin aging due to  
 CC sunburn, to maintain organs before transplantation, for supporting cell  
 CC culture of primary tissues, to regenerate tissues, to identify their  
 CC cognate ligands or binding partners, and in chemotaxis, and can be used  
 CC as a food additive or preservative to modify storage properties.  
 CC Antibodies specific for a protein of the invention can be used in  
 CC alleviating symptoms associated with the disorders mentioned above, and  
 CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked  
 CC immunosorbent assay (ELISA). The present sequence represents a human  
 CC secreted protein fragment referred to in the disclosure of the invention.  
 XX Sequence 12 AA;  
 SQ Query Match 27.8%; Score 5; DB 22; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 74;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GVPKV 11  
 DB 1 GVPKV 5

RESULT 11  
 AAR43871 ID AAR43871 standard; Protein; 14 AA.  
 XX AC AAR43871;  
 XX DT 25-MAR-2003 (updated)  
 XX DT 23-DEC-1993 (first entry)  
 XX DE OmpA2-R-7 signal peptide.  
 XX KW Polypeptide; antibodies; HTLV; AIDS; vaccine.  
 XX OS Human T-cell lymphotropic virus.  
 XX PN EP552850-A1.  
 XX PD 28-JUL-1993.  
 XX PF 10-OCT-1985; 93EP-0200929.  
 XX PR 10-OCT-1984; 84US-0659339.  
 XX PR 23-JAN-1985; 85US-0693866.  
 XX PR 10-OCT-1985; 85EP-0307260.  
 XX FA (CENZ ) CENTOCOR INC.  
 XX CH Chang NT, Gallo RC, Wong-staal F;  
 XX WPI; 1993-236543/30.  
 XX DR N-PSDB; AAQ45924.  
 XX PS Disclosure; Figure 6a; 31pp; English.  
 XX A fragment of DNA approximately 200-500 base pairs in length is  
 CC ligated into a recombinant vector (ompA1-R-6; ompA2-R-7 or ompA3-R-3)  
 CC and used to transform E.coli. These cells then express a polypeptide  
 CC which is immunoreactive with HTLV-III-specific antibody. The  
 CC HTLV-III polypeptides can be used for the production  
 CC of antibodies, in immunoassays for the detection of HTLV-  
 CC III-specific antibodies and in vaccines for the prevention of AIDS.  
 CC The antibodies can also be used to detect HTLV-III polypeptides.  
 CC (Updated on 25-MAR-2003 to correct PF field.)  
 CC (Updated on 25-MAR-2003 to correct PR field.)  
 CC (Updated on 25-MAR-2003 to correct PR field.)



an antibody against a particular GPCR, and in the production of specific antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, growth-related diseases, cell regeneration-related disease, immunological-related cell proliferative diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease, atherosclerosis, bacterial, fungal, protozoan or viral infections, osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies. Crohn's disease, diabetes, graft versus host disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, anxiety, depression, schizophrenia, dementia, mental retardation, memory loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode GPCR proteins given in ABP81675 to ABP82018, which are used in the exemplification of the present invention.

XX SQ Sequence 16 AA;

Query Match 27.8%; Score 5; DB 24; Length 16;  
Best Local Similarity 100.0%; Pred. No. 93;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVKE 13  
|||||  
Db 8 PKVKE 12

RESULT 14

AAW93084  
ID AAW93084 standard; Protein; 4 AA.

XX AC AAW93084;

XX DT 19-MAY-1999 (first entry)

XX DE Human erythropoietin modified signal peptide N-terminal #3.

XX XX Erythropoietin; human; EPO; therapy; erythrocyte production; stimulation.

XX KW Synthetic.

OS Homo sapiens.

XX PN WO9905268-A1.

XX XX 04-FEB-1999.

XX PF 22-JUL-1998; 98WO-EP04590.

XX PR 10-JUL-1998; 98US-0113692.

XX PR 23-JUL-1997; 97EP-0112640.

XX PR 03-DEC-1997; 97DE-1053681.

XX XX (BOEF ) BOEHRINGER MANNHEIM GMBH.

XX XX Auer J, Brandt M, Honold K, Koll H, Stern A;

XX DR WPI; 1999-142926/12.

XX DR N-PSDB; AAX22430.

XX PT New human cells containing erythropoietin gene controlled by heterologous promoter - for large scale production of pure, glycosylated erythropoietin

XX PS Claim 11; Page 32; 70pp; German.

XX CC This invention describes human cells containing a copy of an endogenous gene for erythropoietin (EPO) linked to a heterologous promoter, CC functional in human cells, and capable of producing at least 200 ng EPO/million cells/24 hr. The invention also describes a DNA construct for activating an endogenous EPO gene in a human cell comprising (i) two

CC flanking sequences, homologous to regions (i.e. the 5'-untranslated region, exon 1 or intron 1) of the human EPO gene locus and capable of homologous recombination, including in the exon 1 region a modified sequence encoding Met-X1-X2-X3 where X1 = Gly or Ser; X2 = Ala, Val, Leu, Ile, Ser or Pro; X3 = Pro, Arg, Cys or His; but X1-X2-X3 is not CC Gly-Val-His (ii) a positive selection marker gene (iii) a heterologous expression control sequence and (iv) optionally an amplification gene. CC The method of the invention can be used to produce EPO for therapeutic use (stimulation of erythrocyte production). The new cells make possible CC economical, large scale production of pure human EPO, and are CC significantly more productive than transformed CHO cells. Altering the CC signal sequence and/or the distance between promoter and start signal CC optimises EPO expression.

XX SQ Sequence 4 AA;

Query Match 22.2%; Score 4; DB 20; Length 4;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 MGVP 9

|||||

Db 1 MGVP 4

RESULT 15

ABG32218

ID ABG32218 standard; peptide; 4 AA.

XX AC ABG32218;

XX DT 05-NOV-2002 (first entry)

XX DE Sheep colostrinin derived peptide #12.

XX KW Sheep; colostrinin; colostrum; cytokine inducer; antigen; dementia; central nervous system disorder; neurological disorder; neurosis; mental disorder; psychosis; neurodegenerative disorder; Alzheimer's disease; motor neuron disease; immune system disorder; acquired immunological deficiency; bacterial infection; viral infection; amyloid plaque; dietary supplement; cachexia; weight loss; senile dementia; Parkinson's disease; emotional disturbance; depression; drug addiction; drug withdrawal.

XX OS Ovis aries.

XX PN WO200246211-A2.

XX PD 13-JUN-2002.

XX PF 05-DEC-2001; 2001WO-GB05376.

XX PR 06-DEC-2000; 2000GB-0029777.

XX XX (REGF-) REGEN THERAPEUTICS PLC.

XX XX Georgiades JA;

XX XX WPI; 2002-619016/66.

XX PT Novel peptides isolated from colostrinin polypeptide, useful for treating viral and bacterial infections, disorders of immune system and central nervous system e.g., Alzheimer's disease, dementia, and as food additive

XX PS Claim 1; Page 8; 16pp; English.

XX CC The invention relates to a peptide derived from colostrinin (a colostrum protein known to be a cytokine inducer) substantially entirely consists of the peptide sequences appearing as ABG32207-ABG32223. Also included CC are a composition comprising two or more of the peptides in combination with a carrier, a dietary supplement comprising an orally ingestible combination of the peptide in combination with a carrier and an antibody

CC which binds to the peptide, and which is obtainable by using peptide as  
 CC an antigen. The peptide is useful as a medicament for treating chronic  
 CC disorders of central nervous system e.g., neurological disorders and/or  
 CC mental disorders such as psychosis and/or neurosis, dementia,  
 CC neurodegenerative disorders such as Alzheimer's disease, motor  
 CC neuron disease, chronic disorders of immune system, diseases  
 CC with bacterial and viral etiology, acquired immunological deficiencies,  
 CC chronic bacterial, viral infections. The peptide is also useful for  
 CC treating diseases characterised by presence of amyloid plaque. The  
 CC peptide is also useful as a dietary supplement for babies, small  
 CC children, adults who have been subjected to chemotherapy and/or  
 CC adults who have suffered from cachexia or weight loss due to chronic  
 CC disease. The peptide is also useful for treating senile dementia.  
 CC Parkinson's disease, emotional disturbances and depression. The peptides  
 CC may also be used as an auxiliary withdrawal treatment for drug addicts,  
 CC after a period of detoxification, and in persons dependent on stimulants.  
 CC The present sequence is a colostrin derived peptide of the invention.

XX Sequence 4 AA;

Query Match 22.2%; Score 4; DB 23; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PKVK 12  
 Db 1 PKVK 4

# RESULT 16

AA32746

ID AAR32746 standard; peptide; 6 AA.

XX AC

XX AAR32746;

XX 25-MAR-2003 (updated)

DT 18-JUN-1993 (first entry)

DE PK40 TAU/neurofilament protein kinase tryptic peptide.

XX Neurodegenerative disease; treatment; diagnosis; Alzheimer's;

KW Kinase inhibitor; paired helical fragments; PHF; tangles; formation.

XX Homo sapiens.

XX WO9303148-A2.

XX 18-FEB-1993.

XX 10-JUL-1992; 92WO-US05825.

XX 09-AUG-1991; 91US-0742880.

XX (MASI ) MASSACHUSETTS INST TECHNOLOGY.

XX Ingram VM, Roder HM;

XX WPI; 1993-076505/09.

PT Prepn. contg. isolated, pure non-skeletal associated kinase -  
 PT used in treatment and diagnosis of neurodegenerative conditions  
 PT e.g. Alzheimer's disease

XX Example; Page 76; 88pp; English.

XX The sequence is that of a tryptic peptide of TAU/neurofilament  
 CC protein kinase PK40. Antibodies (monoclonal or polyclonal) specific  
 CC for PK40 which are capable of binding to and inhibiting the kinase  
 CC activity of PK 40 may be used to reduce phosphorylation activity in  
 CC the cell, and to reduce or prevent formation of paired helical  
 CC fragments (PHF) or tangles. This allows investigation e.g. of the  
 CC contribution of such phosphorylation activity to cell maintenance  
 CC and to neurocellular states characteristic of neurodegenerative

CC diseases, partic. Alzheimer's and ageing. The sequence shows a very  
 CC close match to the ERK-kinase family proteins and so PK40 can be  
 CC considered to be a member of the cell cycle-associated ERK kinase  
 CC family.  
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 6 AA;

Query Match 22.2%; Score 4; DB 14; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PEIM 6  
 Db 2 PEIM 5

# RESULT 17

AA27421

ID AAY27421 standard; peptide; 6 AA.

XX AC

XX AAY27421;

DT 26-NOV-1999 (first entry)

DE PK40 protein kinase tryptic peptide.

XX TAU hyper-phosphorylation; adenosine triphosphate; ATP binding site;  
 KW PK40; TAU kinase; neurofilament protein kinase; Alzheimer's disease;  
 KW tryptic peptide; ERK-Kinase.

XX Homo sapiens.

XX US5955444-A.

XX 21-SEP-1999.

XX 07-JUN-1995; 95US-0480793.

XX 10-JUL-1992; 92US-0912293.

XX 09-AUG-1991; 91US-0742880.

XX (MASI ) MASSACHUSETTS INST TECHNOLOGY.

XX Roder HM, Ingram VM;

XX WPI; 1999-560501/47.

PT Inhibiting abnormal TAU hyper-phosphorylation in cells for the  
 PT treatment of Alzheimer's disease -

XX Example 11; Columns 33-34; 19pp; English.

XX The invention relates to a new method for inhibiting abnormal TAU hyper-  
 CC phosphorylation activity in cells. The method comprises contacting a  
 CC cell with an inhibitor which binds to an adenosine triphosphate (ATP)  
 CC binding site on PK40 (a TAU/neurofilament protein kinase) and therefore  
 CC inhibits the phosphorylation activity of PK40 (which is characteristic of  
 CC abnormal TAU hyper-phosphorylation in Alzheimer's disease). The method  
 CC may be used for inhibiting TAU hyper-phosphorylation activity in cells.  
 CC In particular, it may be used for inhibiting the phosphorylating activity  
 CC of PK40 which is characteristic of abnormal TAU hyper-phosphorylation in  
 CC Alzheimer's disease. Sequences AAY27408-422 represent peptides obtained  
 CC by tryptic digestion of PK40 kinase. Peptides AAY27410-422 has high  
 CC homology to the ERK-kinase family proteins.

XX Sequence 6 AA;

Query Match 22.2%; Score 4; DB 20; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PEIM 6



Db |||||  
2 PEIM 5

## RESULT 18

AAM51129  
ID AAM51129 standard; Peptide; 6 AA.

XX AAM51129;

XX 06-JUN-2002 (first entry)

XX Bovine TAU/neurofilament protein kinase PK40 tryptic peptide 14.

XX PK40; TAU; neurofilament; protein kinase; enzyme; human;

XX ERK kinase; phosphorylation; ageing; Alzheimer's disease;

XX Parkinson's disease; Huntington's disease; brain infarct;

XX neurotropic; neuroprotective; diagnosis; therapy.

XX Bos taurus.

XX US2002025942-A1.

XX 28-FEB-2002.

XX 20-MAR-1998; 98US-0045020.

XX 10-JUL-1992; 92US-0912293.

XX 07-JUN-1995; 95US-0480793.

XX 09-AUG-1991; 91US-0742880.

XX (INGR/) INGRAM V M.

XX (RODE/) RODER H M.

XX Ingram VM, Roder HM;

XX WPI; 2002-255975/30.

XX Preparation for phosphorylating dephosphorylated neurofilament-M,  
comprises isolated, pure, nonskeletal-associated kinase -

XX Example 11; Page 17; 21pp; English.

XX The present sequence is that of tryptic peptide 14, which is 1 of  
15 peptides (see AAM51116-30) obtained by trypsin digestion of a  
novel TAU/neurofilament protein kinase, termed PK40, isolated from  
bovine brain. PK40 is capable of phosphorylating completely  
dephosphorylated (cd) neurofilament-M (NF-M) so as to cause a  
complete shift on SDS-PAGE of the apparent Kr to that of native  
NF-M. It also causes a partial shift of cdNF-H. PK40 is capable  
of causing a complete shift of bovine cdTAU or human TAU isoform  
expressed in Escherichia coli. Under saturation phosphorylation  
conditions, PK40 causes a change in the isoform pattern that  
closely resembles the pattern of human TAU proteins extracted from  
paired helical filaments. PK40 also phosphorylates both KSP sites  
of TAU and abolishes the TAU 1 epitope. PK40 was identified using  
a novel kinase immunoassay of the invention. Peptides 3-15 show  
homology to ERK1 and ERK2, suggesting that PK40 is a member of the  
cell cycle-associated ERK kinase family. A novel assay that can be  
used as a diagnostic test for early Alzheimer's disease measures  
the level of neuroprotein phosphorylation activity in a human cell  
by PK40 or PK36. The assay can also be used to diagnose other  
conditions affected by neuronal degeneration such as Parkinson's  
disease, Huntington's disease, normal ageing and brain infarcts.  
An inhibitor of PK40 (e.g. an antibody or ATP) may be useful in the  
treatment of these conditions.

XX Sequence 6 AA;

XX Query Match 22.2%; Score 4; DB 23; Length 6;

XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;

XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PEIM 6  
Db |||||  
2 PEIM 5

## RESULT 19

AAR33159  
ID AAR33159 standard; peptide; 7 AA.

XX AAR33159;

XX 25-MAR-2003 (updated)

XX 25-JUN-1993 (first entry)

XX HPV E7 protein - RSG protein binding inhibitor peptide.

XX Human papilloma virus; retinoblastoma gene; genital warts;

XX cervical cancer; treatment.

XX Synthetic.

XX EP531080-A2.

XX 10-MAR-1993.

XX 01-SEP-1992; 92EP-0307905.

XX 04-SEP-1991; 91US-0754829.

XX (MERI ) MERCK & CO INC.

XX Oliff AI, Riemen MW;

XX WPI; 1993-078581/10.

XX New polypeptide(s) which inhibit human papilloma virus binding to  
RBG protein - useful for treating genital warts and cervical cancer

XX Claim 7; Page 15; 15pp; English.

XX The sequence is that of a peptide which inhibits binding of human  
papilloma virus (HPV) E7 protein to the retinoblastoma gene (RBG)  
protein. It can be used in the treatment of conditions caused by HPV,  
esp. genital warts and cervical cancer.

XX (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 7 AA;

XX Query Match 22.2%; Score 4; DB 14; Length 7;

XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;

XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4  
Db |||||  
2 LOPE 5

## RESULT 20

AAV49017  
ID AAY49017 standard; Peptide; 7 AA.

XX AAY49017;

XX 20-MAR-2003 (updated)

XX 10-DEC-1999 (first entry)

XX Membrane dipeptidase-binding adrenal gland homing peptide #16.

XX Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP;

XX prostate; ovary; lymph node; adrenal gland; liver; gut; tumour;

XX membrane dipeptidase.

XX Synthetic.

OS Homo sapiens.  
 PN WO9946284-A2.  
 XX  
 PD 16-SEP-1999.  
 XX  
 XX 10-MAR-1999; 99WO-US05284.  
 XX  
 PR 13-MAR-1998; 98US-0042107.  
 PR 26-FEB-1999; 99US-0258754.  
 XX  
 PA (BURN-) BURNHAM INST.  
 XX  
 PI Rajotte D, Pasqualini R, Ruoslahti E;  
 XX WPI; 1999-571717/48.  
 XX  
 PT New peptides which selectively home to organs or tissues, used for,  
 PT e.g. identifying target ligands and for therapy of pathological  
 PT conditions -  
 XX  
 PS Claim 65; Page 155; 193pp; English.  
 XX  
 CC The present invention describes peptides that selectively home to a  
 CC tissue or organ. The peptides can be used for identifying an organ  
 CC or tissue, for identifying a target molecule expressed by an organ or  
 CC tissue or for treating an organ or tissue pathology, where the organ or  
 CC tissue is selected from prostate, lung, skin, retina, pancreas, gut,  
 CC ovary, adrenal gland, liver, and lymph node. The peptide bind to the  
 CC membrane dipeptidase (MDP). AAY48618 to AAY49066 represent sequences  
 CC which are used in the exemplification of the present invention.  
 CC (Updated on 20-MAR-2003 to correct PR field.)  
 XX  
 SQ Sequence 7 AA;  
 Query Match 22.2%; Score 4; DB 20; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 0;  
 QY 9 PKVK 12  
 Db |||||  
 1 PKVK 4  
 RESULT 22  
 AAB35822  
 ID AAB35822 standard; peptide; 7 AA.  
 XX  
 AC AAB35822;  
 XX  
 DT 26-FEB-2001 (first entry)  
 XX  
 DE T7 phage coat protein C-terminus modification K+ peptide.  
 XX  
 XX Epitope identification; display system; gene delivery; drug delivery;  
 KW bacteriophage T7.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200065350-A1.  
 XX  
 PD 02-NOV-2000.  
 XX  
 XX 27-APR-2000; 2000WO-US11270.  
 XX  
 PR 27-APR-1999; 99US-0131151.  
 PR 07-JUN-1999; 99US-0139431.  
 XX  
 PA (MIRU-) MIRUS CORP.  
 XX  
 PI Wolff JA;  
 XX  
 DR WPI; 2000-687379/67.

XX Identifying new peptide ligands that protect phage which delivers drugs  
 PT and genes in vivo, by binding to blood proteins, comprises exposing an  
 PT epitope display system to blood products -  
 XX  
 PS Example 1; Page 55; 87pp; English.  
 XX  
 CC This invention relates to a process comprising exposing an epitope  
 CC display system to blood products to identify useful epitopes. The process  
 CC is useful for identifying new peptide ligands that protect the display  
 CC system e.g. phage, which delivers drugs and genes in vivo. The delivery  
 CC system may be inhibited through binding to complement, the process  
 CC reveals peptides which may be used to protect the system from this  
 CC inhibition. The present sequence represents a peptide which can be used  
 CC to modify the C-terminal of a T7 phage coat protein. The peptide protects  
 CC against inactivation.  
 XX  
 SQ Sequence 7 AA;  
 Query Match 22.2%; Score 4; DB 21; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 0;  
 QY 9 PKVK 12  
 Db |||||  
 4 PKVK 7  
 RESULT 22  
 AAB72261  
 ID AAB72261 standard; peptide; 7 AA.  
 XX  
 AC AAB72261;  
 XX  
 DT 14-MAY-2001 (first entry)  
 XX  
 DE Colostrin derived cytokine inducing peptide SEQ ID 16.  
 XX  
 KW Colostrin; immune response; cytokine; blood cell proliferation;  
 KW central nervous system disorder; neurological disorder; mental disorder;  
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;  
 KW neurosis; infection.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200111937-A2.  
 XX  
 XX 22-FEB-2001.  
 PD  
 XX 17-AUG-2000; 2000WO-US22818.  
 PF  
 XX 17-AUG-1999; 99US-0149311.  
 PR  
 XX (TEXA) UNIV TEXAS SYSTEM.  
 PA (REG-) REGEN THERAPEUTICS PLC.  
 XX  
 PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
 XX WPI; 2001-202804/20.  
 DR  
 XX Inducing a cytokine and modulating an immune response, useful for  
 PT treating central nervous system diseases and bacterial and viral  
 PT infections, comprises administering colostrin as an immunological  
 PT regulator -  
 XX  
 PS Claim 1; Page 34; 50pp; English.  
 XX  
 CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrin,  
 CC a proline rich polypeptide aggregate contained in colostrum. The  
 CC peptides have immune response modulatory activity, and are capable of  
 CC inducing cytokines. Colostrin and its derived peptides are useful for  
 CC inducing cytokine production, for modulating an immunological response  
 CC and for inducing blood cell proliferation. The peptides are useful in the

CC treatment of disorders of the central nervous system, neurological  
 CC disorders, mental disorders, dementia, neurodegenerative diseases,  
 CC Alzheimer's disease, motor neuron disease, psychosis, neurosis, chronic  
 CC disorders of the immune system, bacterial and viral infections and  
 CC acquired immunological deficiencies.

XX SQ Sequence 7 AA;

Query Match 22.2%; Score 4; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQPE 4  
 ||||  
 Db 4 LQPE 7

# RESULT 23

AAB72514  
 ID AAB72514 standard; Peptide; 7 AA.

XX AC AAB72514;

XX DT 09-MAY-2001 (first entry)

XX DE Colostrinin peptide #15.

XX KW Dermatalogical; oxidative stress regulator; colostrinin.

XX OS Unidentified.

XX FN WO200112650-A2.

XX XX 22-FEB-2001.

XX PF 17-AUG-2000; 2000WO-US22665.

XX XX 17-AUG-1999; 99US-0149310.

XX PA (TEXA ) UNIV TEXAS SYSTEM.

XX PI Stanton GJ, Hughes TK, Boldogh I;

XX DR WPI; 2001-218342/22.

XX PT Modulating oxidative stress level in a cell, involves contacting the  
 cell with an oxidative stress regulator selected from colostrinin, its  
 constituent peptide, analog or their combinations -

XX PS Claim 6; Page 25; 48pp; English.

XX The present invention relates to a method for modulating the oxidative  
 stress level in a cell or a patient, comprising contacting the cell with,  
 or administering to the patient, an oxidative stress regulator selected  
 from colostrinin, or its constituent peptide (e.g. the present peptide),  
 to change the level of an oxidising species in the cell. The method can  
 be used to treat oxidative damage to skin, by decreasing or preventing an  
 increase in the level of damage to a biomolecule of the patient.

XX SQ Sequence 7 AA;

Query Match 22.2%; Score 4; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQPE 4  
 ||||  
 Db 4 LQPE 7

# RESULT 24

AAB72546  
 ID AAB72546 standard; Peptide; 7 AA.

XX AAB72546;  
 XX DT 09-MAY-2001 (first entry)  
 XX DE Colostrinin peptide #15.

XX KW Neuroprotective; neural cell differentiation regulator; colostrinin;  
 colostrinum.

XX OS Unidentified.

XX PN WO200112651-A2.

XX PD 22-FEB-2001.

XX PF 17-AUG-2000; 2000WO-US22774.

XX PR 17-AUG-1999; 99US-0149633.

XX PA (TEXA ) UNIV TEXAS SYSTEM.

XX PI Boldogh I;

XX DR WPI; 2001-226545/23.

XX PT Use of colostrinin, its constituent peptide or analog as a neural cell  
 regulator, for promoting neural cell differentiation and treating  
 PT damaged neural cells in a patient -

XX PS Claim 6; Page 21; 35pp; English.

XX CC The present invention relates to a method for promoting neural cell  
 differentiation and treating damaged neural cells, using colostrinin and  
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural  
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.

XX SQ Sequence 7 AA;

Query Match 22.2%; Score 4; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQPE 4  
 ||||  
 Db 4 LQPE 7

# RESULT 25

AAB59317  
 ID AAB59317 standard; Peptide; 7 AA.

XX AC AAB59317;

XX DT 21-MAR-2001 (first entry)

XX DE Ewe colostrinin peptide fragment B-2.

XX KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
 central nervous system disorder; dietary supplement; beta-amyloid plaque.

XX OS Ovis sp.

XX PN WO200075173-A2.

XX PD 14-DEC-2000.

XX PF 02-JUN-2000; 2000WO-GB02128.

XX PR 02-JUN-1999; 99GB-0012852.

XX PA (REGG-) REGEN THERAPEUTICS PLC.

PI Georgiades JA;  
 DR WPI; 2001-071058/08.  
 XX  
 PT Peptides having an N-terminal amino acid sequence isolated from  
 PT colostrinin for treating e.g. disorders of the central nervous system  
 PT and immune system, viral and bacterial infections, and diseases  
 PT characterized by amyloid plaques -  
 XX  
 PS Claim 7; Page 27; 63pp; English.  
 XX  
 CC The present invention provides the sequences of a number of peptides  
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
 CC fragment of colostrum. These peptides can be used in the treatment of  
 CC central nervous system disorders such as senile dementia, Parkinson's  
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
 CC disorders such as bacterial and viral infections, to improve the  
 CC development of a child's immune system, as a dietary supplement, and to  
 CC promote the dissolution of beta-amyloid plaques.  
 XX  
 SQ Sequence 7 AA;  
 Query Match 22.2%; Score 4; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LOPE 4  
 Db ||||  
 4 LOPE 7  
 RESULT 26  
 AAE20243  
 ID AAE20243 standard; peptide; 7 AA.  
 AC  
 XX  
 DT 18-JUN-2002 (first entry)  
 XX  
 DE Colostrinin constituent peptide #15.  
 DE  
 KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;  
 KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;  
 KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;  
 KW transplantation; implantation; dermatological; vulnery.  
 XX  
 OS Unidentified.  
 XX  
 PH Key Location/Qualifiers  
 FT Modified-site 7 /note= "Optionally C-terminal amide"  
 FT  
 XX  
 PN WO200213850-A1.  
 XX  
 PD 21-FEB-2002.  
 XX  
 XX 17-AUG-2000; 2000WO-US22776.  
 XX  
 XX 17-AUG-2000; 2000WO-US22776.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Stanton GJ, Hughes TK, Boldogh I;  
 XX WPI; 2002-269151/31.  
 DR  
 XX Composition useful for the modulation of blood cell proliferation in a  
 PT patient comprises a blood cell regulator selected from colostrinin, its  
 PT constituent peptide and/or analog -  
 PT  
 PS Claim 6; Page 25; 51pp; English.  
 XX  
 CC The invention relates to a composition which comprises a blood cell

CC regulator selected from colostrinin, its constituent peptide and/or  
 CC analogue. The invention is used for modulating the oxidative stress  
 CC level in a cell e.g. mammalian or human cell present in a cell culture,  
 CC tissue, organ, or organism; or for treating oxidative damage to the skin  
 CC of a patient e.g. animal or human; to modulate oxidative stress during/  
 CC after a premature birth or normal birth, preventing/delaying aging in a  
 CC patient, enhancing wound healing, and the reduction of side effects of  
 CC cosmetic procedures. The method changes the level of an oxidising species  
 CC in the cell, such as decreases or prevents increase in the level of  
 CC damage to a biomolecule of the patient selected from DNA, protein and/or  
 CC lipid, compared to the same conditions when the oxidative stress  
 CC regulator is not present. The modulation of oxidative stress results in  
 CC enhanced repair, regeneration, and replacement of cells, tissues and  
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
 CC external organs), as well as enhanced preservation of such organs for  
 CC transplantation, implantation, or scientific research. The present  
 CC sequence is a colostrinin constituent peptide.  
 XX  
 SQ Sequence 7 AA;  
 Query Match 22.2%; Score 4; DB 23; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LOPE 4  
 Db ||||  
 4 LOPE 7  
 RESULT 27  
 AAM51050  
 ID AAM51050 standard; Peptide; 7 AA.  
 AC  
 XX  
 DT 30-MAY-2002 (first entry)  
 XX  
 DE Colostrinin constituent peptide.  
 XX  
 KW Colostrinin; colostrum; immunomodulator; cardiovascular;  
 KW blood cell regulator; cytokine inducer; beta-casein; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PH Key Location/Qualifiers  
 FT Modified-site 7 /note= "optional C-terminal amidation"  
 FT  
 XX  
 PN WO200213849-A1.  
 XX  
 PD 21-FEB-2002.  
 XX  
 XX 17-AUG-2000; 2000WO-US22775.  
 XX  
 XX 17-AUG-2000; 2000WO-US22775.  
 XX  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA (REGE-) REGEN THERAPEUTICS PLC.  
 XX  
 PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
 XX WPI; 2002-269150/31.  
 DR  
 XX Modulation of blood cell proliferation in a patient involves use of  
 PT blood cell regulator selected from colostrinin, its constituent peptide  
 PT and/or analogue -  
 PT  
 XX Claim 1; Page 34; 54pp; English.  
 PS  
 XX The present sequence is that of a colostrinin constituent peptide  
 CC that is used as an immunological regulator and as a blood cell  
 CC regulator in claimed methods of the invention. The peptide is  
 CC classified as having a beta-casein homologue precursor. Methods

are claimed for: inducing a cytokine in a cell by contact with an immunological regulator, where the cell is present in a cell culture, a tissue, an organ or an organism, and the cell is mammalian, including human; modulating an immune response in a cell by contact with the immunological regulator under conditions effective to induce a cytokine; modulating an immune response in a patient by administering an immunological regulator under conditions effective to induce a cytokine, where the immunological regulator is administered topically or as part of a dietary supplement, and where the immune response is specific or non specific, an interferon response or an antibody response; modulating blood cell proliferation by contacting blood cells with a blood cell regulator, where the blood cells are present in a cell culture or an organism, are mammalian or human, and where the blood cells are increased in number or differentiated; and a method for modulating blood cell proliferation in a patent. A claimed cytokine-inducing composition comprises a pharmaceutical carrier and an active agent such as the present peptide.

SQ Sequence 7 AA;

Query Match 22.2%; Score 4; DB 23; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOPE 4  
|  
|  
|  
|  
Db 4 LOPE 7

RESULT 28  
AAO14592  
ID AAO14592 standard; peptide; 7 AA.  
AC AAO14592;  
XX  
DT 27-MAY-2002 (first entry)  
XX  
DE Neural cell regulatory colostrinin peptide 15.  
XX  
KW Neural cell differentiation; neural cell regulator; colostrinin peptide;  
KW neural cell formation; proline-rich polypeptide aggregate; colostrinum;  
KW neural cell treatment.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 7 /note="Optional C-terminal amide"  
FT  
PN WO200213851-A1.  
XX  
XX  
PD 21-FEB-2002.  
XX  
PF 17-AUG-2000; 2000WO-US22777.  
XX  
PR 17-AUG-2000; 2000WO-US22777.  
XX  
XX (TEXA ) UNIV TEXAS SYSTEM.  
XX  
XX Boldogh I, Stanton JG, Hughes TK;  
XX WPI; 2002-269152/31.  
XX  
XX Promoting cell differentiation in a patient involves use of blood cell  
PT regulator selected from colostrinin, its constituent peptide and/or  
PT analog -  
XX  
XX Claim 7; Page 21; 37pp; English.  
PS  
XX The invention comprises a method for promoting cell differentiation (e.g.  
CC neural cell differentiation). The method involves contacting cells with a  
CC neural cell regulator (i.e. a colostrinin peptide) in order to change the

cells in morphology to form neural cells. Colostrinin is a proline-rich polypeptide aggregate that is present in colostrum. The method of the invention is useful for promoting the differentiation of cells and for treating damaged neural cells in a patient. The present amino acid sequence represents a specifically claimed colostrinin peptide used in the method of the invention.

SQ Sequence 7 AA;

Query Match 22.2%; Score 4; DB 23; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOPE 4  
|  
|  
|  
|  
Db 4 LOPE 7

RESULT 29  
AAR10631  
ID AAR10631 standard; Protein; 8 AA.  
XX  
AC AAR10631;  
XX  
DT 25-MAR-2003 (updated)  
DT 18-APR-1991 (first entry)  
XX  
DE Human Papilloma Virus-16 "[Gln27]-E7-(20-27)-AMIDE" peptide.  
XX  
KW papilloma virus; retinoblastoma gene-binding protein; genital warts;  
KW cervical cancer.  
XX  
OS Synthetic.  
XX  
PN EP412762-A.  
XX  
PD 13-FEB-1991.  
XX  
PF 06-AUG-1990; 90EP-0308652.  
XX  
PR 09-APR-1990; 90US-0506981.  
PR 07-AUG-1989; 89US-0390569.  
XX  
PA (MERI ) MERCK & CO INC.  
PA (OLIF/) OLIFF A I.  
XX  
XX Oliff AI, Riemen MW;  
XX  
DR WPI; 1991-045887/07.  
XX  
PT Papilloma virus and retinoblastoma gene-binding protein  
PT inhibitors - involves a specified aminoacid sequence contg. 13  
PT residues for treatment of genital warts and cervical cancer  
XX  
XX Claim 12; Page 11; 11pp; English.  
XX  
CC The peptide carries an amide group at the C-terminus. The sequence  
CC comprises residues 20 to 27 of the deduced HPV-16 E7 protein  
CC sequence (N.Salzman and P.Howley, "The Papovaviridae", Vol 2,p.379,  
CC Plenum Press, N.Y. 1987) but with Gln replacing Asp at position 27.  
CC The peptides are used as screening tools and in the prevention,  
CC therapy, prophylaxis and treatment of HPV-induced diseases. They  
CC can also be used to raise antibodies either as vaccines or to  
CC heighten the immune response to an HPV infection all ready present.  
CC See also AAR10628-R10630, AAR10632-7.  
CC (Updated on 25-MAR-2003 to correct PA field.)  
XX  
SQ Sequence 8 AA;

Query Match 22.2%; Score 4; DB 12; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 LOPE 4
Db      ||||
        2 LOPE 5

RESULT 30
AAR33158
ID AAR33158 standard; peptide; 8 AA.
AC AAR33158;
XX
DT 25-MAR-2003 (updated)
DT 25-JUN-1993 (first entry)
XX
DE HPV E7 protein - RBG protein binding inhibitor peptide.
XX
KW Human papilloma virus; retinoblastoma gene; genital warts;
KW cervical cancer; treatment.
XX
OS Synthetic.
XX
PN EP531080-A2.
XX
PD 10-MAR-1993.
XX
PF 01-SEP-1992; 92EP-0307905.
XX
PR 04-SEP-1991; 91US-0754829.
XX
PA (MERI ) MERCK & CO INC.
XX
PI Oliff AI, Riemen MW;
XX
DR WPI; 1993-078581/10.
XX
PT New polypeptide(s) which inhibit human papilloma virus binding to
PT RBG protein - useful for treating genital warts and cervical cancer
PS Claim 7; Page 15; 15pp; English.
XX
CC The sequence is that of a peptide which inhibits binding of human
CC papilloma virus (HPV) E7 protein to the retinoblastoma gene (RBG)
CC protein. It can be used in the treatment of conditions caused by HPV,
CC esp. genital warts and cervical cancer.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 8 AA;
    Query Match      22.2%; Score 4; DB 14; Length 8;
    Best Local Similarity 100.0%; Pred. No. 9.3e+05;
    Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LOPE 4
Db      ||||
        2 LOPE 5

RESULT 31
AAW77186
ID AAW77186 standard; peptide; 8 AA.
XX
AC AAW77186;
XX
DT 23-NOV-1998 (first entry)
XX
DE Pharmaceutically active peptide 27.
XX
KW Pharmaceutically active peptide; target; organ; lymphocyte; treatment;
KW pharmaceutical agent; disease; radioactive isotope; imaging agent.
XX
OS Synthetic.
OS Homo sapiens.
XX

QY      1 LOPE 4
Db      ||||
        2 LOPE 5

RESULT 32
AAB35995
ID AAB35995 standard; Protein; 8 AA.
XX
AC AAB35995;
XX
DT 01-MAR-2001 (first entry)
XX
DE Sorbitol dehydrogenase subunit 3 internal peptide.
XX
KW Sorbitol dehydrogenase; SDH; Gluconobacter oxydans; D-sorbitol;
KW L-sorbose production; 2-keto-L-gulonic acid.
XX
OS Gluconobacter oxydans.
XX
PN WO200065066-A1.
XX
PD 02-NOV-2000.
XX
PF 23-APR-1999; 99WO-IB00736.
XX
PR 23-APR-1999; 99WO-IB00736.
XX
PA (CHOI/) CHOI E.
PA (RHEE/) RHEE S.
PA (LEEE/) LEE E.
XX
PI Choi E, Rhee S, Lee E;
XX

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PN WO9839469-A1.
XX
PD 11-SEP-1998.
XX
PF 04-MAR-1998; 98WO-US04188.
XX
PR 04-MAR-1997; 97US-0810074.
PR 04-MAR-1997; 97US-0039509.
XX
PA (BIOT-) BIO-TECHNOLOGY GENERAL CORP.
XX
PI Belkind A, Golan I, Hagai Y, Lazarovits J, Levanon A;
PI Nimrod A, Panet A, Vogel T, Zeelon E;
XX
DR WPI; 1998-495863/42.
XX
PT New peptide(s) binding targets in organs and lymphocytes - for the
PT targetted delivery of toxins, anti-cancer drugs and cardiovascular
PT agents to arteries, veins, placenta, liver
XX
PS Claim 54; Page 97; 114pp; English.
XX
CC Sequences shown in AAW77160 to AAW77214 and AAW79167 represent
CC non-naturally- occurring pharmacuetically active peptides. These novel
CC peptides specifically bind to undetermined and determined targets in
CC various organs and in lymphocytes. The peptides can be used in
CC compositions, where they can be linked to pharmaceutical agents, to treat
CC various diseases and conditions. The peptides or chimeric polypeptides
CC comprising these pharmacuetically active peptides and a second peptide
CC may be labelled with a marker (radioactive isotope, etc) to form an
CC imaging agent. This agent is used to bind an organ so that the organ can
CC be imaged.
XX
SQ Sequence 8 AA;
    Query Match      22.2%; Score 4; DB 19; Length 8;
    Best Local Similarity 100.0%; Pred. No. 9.3e+05;
    Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PKVK 12
Db      ||||
        3 PKVK 6

RESULT 33
AAB35995
ID AAB35995 standard; Protein; 8 AA.
XX
AC AAB35995;
XX
DT 01-MAR-2001 (first entry)
XX
DE Sorbitol dehydrogenase subunit 3 internal peptide.
XX
KW Sorbitol dehydrogenase; SDH; Gluconobacter oxydans; D-sorbitol;
KW L-sorbose production; 2-keto-L-gulonic acid.
XX
OS Gluconobacter oxydans.
XX
PN WO200065066-A1.
XX
PD 02-NOV-2000.
XX
PF 23-APR-1999; 99WO-IB00736.
XX
PR 23-APR-1999; 99WO-IB00736.
XX
PA (CHOI/) CHOI E.
PA (RHEE/) RHEE S.
PA (LEEE/) LEE E.
XX
PI Choi E, Rhee S, Lee E;
XX

```

DR WPI; 2000-687351/67.

XX Novel membrane-bound sorbitol dehydrogenase nucleic acid molecule

PT isolated from Gluconobacter suboxydans useful for the fermentative

PT production of 2-keto-L-gulononic acid and L-sorbose from D-sorbitol

XX

XX Example 2; Page 37; 96pp; English.

PS This invention relates to an isolated membrane-bound sorbitol

CC dehydrogenase (SDH) from Gluconobacter oxydans. The invention includes

CC polynucleotides (AAC83153 - AAC83154) encoding the 3 subunits of SDH

CC (AA835987 - AA835989). Also included in the invention are two

CC polynucleotide sequences AAC83156 and AAC83157 which contain the subunit

CC coding regions. The sorbitol dehydrogenase polynucleotide sequences are

CC useful for producing L-sorbose from D-sorbitol and for increasing the

CC production of 2-keto-L-gulononic acid by transforming a host cell.

CC especially Gluconobacter with the DNA and selecting the transformed host

CC cell. The present sequence represents the SDH subunit 3 internal

CC peptide.

XX

SQ Sequence 8 AA;

Query Match 22.2%; Score 4; DB 21; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GVPK 10

Db |||||

5 GVPK 8

RESULT 33

ABP14637

ID ABP14637 standard; Peptide; 8 AA.

XX

AC ABP14637;

XX

XX 15-JUL-2002 (first entry)

XX

DE HIV A03 super motif pol peptide #11.

XX

XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;

KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;

KW antigen; vaccine; HIV infection; immunisation; virucide.

XX

OS Human immunodeficiency virus type 1.

XX

PN WO200124810-A1.

XX

PD 12-APR-2001.

XX

PF 05-OCT-2000; 2000WO-US27766.

XX

PR 05-OCT-1999; 99US-0412863.

XX

PA (EPIM-) EPIMMUNE INC.

XX

XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Celis E, Kubo RT, Grey HM;

XX

XX WPI; 2001-354887/37.

DR

XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)

PT peptide groups, useful for vaccinating against HIV-1 -

PT

PS Claim 32; Page 168; 448pp; English.

XX

CC The present invention describes a composition (I) comprising a prepared

CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid

CC sequence selected from 51 defined amino acid sequences (ABL25347 to

CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)

CC may be used for immunising subjects against HIV-1 infections. The use of

CC group-based vaccines has several advantages over traditional vaccines,

CC particularly when compared to the use of whole antigens in vaccine

CC compositions. There is evidence that the immune response to whole

CC antigens is directed largely toward variable regions of the antigen,

CC particularly when compared to the use of whole antigens in vaccine

CC compositions. There is evidence that the immune response to whole

CC antigens is directed largely toward variable regions of the antigen,

CC allowing for immune escape due to mutations. The groups for inclusion in

CC an group-based vaccine may be selected from conserved regions of viral or

CC tumour-associated antigens, which therefore reduces the likelihood of

CC escape mutants. Furthermore, immunosuppressive groups that may be present

CC in whole antigens can be avoided with the use of group-based vaccines.

CC An additional advantage of an group-based vaccine approach is the ability

CC to combine selected groups (CTL and HTL), and further, to modify the

CC composition of the groups, achieving, for example, enhanced

CC immunogenicity. Accordingly, the immune response can be modulated, as

CC appropriate, for the target disease. Similar engineering of the response

CC is not possible with traditional approaches. ABP1501 to ABP25412

CC represent peptide sequences used in the exemplification of the present

XX invention.

XX

SQ Sequence 8 AA;

Query Match 22.2%; Score 4; DB 22; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PKVK 12

Db |||||

5 PKVK 8

RESULT 34

ABP17276

ID ABP17276 standard; Peptide; 8 AA.

XX

AC ABP17276;

XX

XX 15-JUL-2002 (first entry)

XX

DE HIV B27 super motif pol peptide #10.

XX

XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;

KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;

KW antigen; vaccine; HIV infection; immunisation; virucide.

XX

OS Human immunodeficiency virus type 1.

XX

PN WO200124810-A1.

XX

PD 12-APR-2001.

XX

PF 05-OCT-2000; 2000WO-US27766.

XX

PR 05-OCT-1999; 99US-0412863.

XX

PA (EPIM-) EPIMMUNE INC.

XX

XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Celis E, Kubo RT, Grey HM;

XX

XX WPI; 2001-354887/37.

DR

XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)

PT peptide groups, useful for vaccinating against HIV-1 -

PT

PS Claim 32; Page 223; 448pp; English.

XX

CC The present invention describes a composition (I) comprising a prepared

CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid

CC sequence selected from 51 defined amino acid sequences (ABL25347 to

CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)

CC may be used for immunising subjects against HIV-1 infections. The use of

CC group-based vaccines has several advantages over traditional vaccines,

CC particularly when compared to the use of whole antigens in vaccine

CC compositions. There is evidence that the immune response to whole

CC antigens is directed largely toward variable regions of the antigen,

CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP11501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.

XX SQ Sequence 8 AA;  
 Query Match 22.2%; Score 4; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PKVK 12  
 Db 1 PKVK 4

RESULT 35  
 ABP21662  
 ID ABP21662 standard; Peptide; 8 AA.

XX AC ABP21662;

XX DT 15-JUL-2002 (first entry)

XX DE HIV A03 motif pol peptide #657.

XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.

XX OS Human immunodeficiency virus type 1.

XX PN WO200124810-A1.

XX PD 12-APR-2001.

XX PF 05-OCT-2000; 2000WO-US27766.

XX PR 05-OCT-1999; 99US-0412863.

XX PA (EPIM-) EPIMMUNE INC.

XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Celis E, Kubo RT, Grey HM;

XX DR WPI; 2001-354887/37.

XX PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1 -

XX PS Claim 32; Page 313; 448pp; English.

XX CC The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of

CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP11501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.

XX SQ Sequence 8 AA;

Query Match 22.2%; Score 4; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PKVK 12  
 Db 5 PKVK 8

RESULT 36  
 ABP23544

ID ABP23544 standard; Peptide; 8 AA.

XX AC ABP23544;

XX DT 15-JUL-2002 (first entry)

XX DE HIV A11 motif pol peptide #486.

XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.

XX OS Human immunodeficiency virus type 1.

XX PN WO200124810-A1.

XX PD 12-APR-2001.

XX PF 05-OCT-2000; 2000WO-US27766.

XX PR 05-OCT-1999; 99US-0412863.

XX PA (EPIM-) EPIMMUNE INC.

XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Celis E, Kubo RT, Grey HM;

XX DR WPI; 2001-354887/37.

XX PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1 -

XX PS Claim 32; Page 351; 448pp; English.

XX CC The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability



CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.

XX Sequence 8 AA;

Query Match 22.2%; Score 4; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12

Db |||||

RESULT 37

AAG62330

ID AAG62330 standard; peptide; 8 AA.

XX AC

XX AAG62330;

XX 24-AUG-2001 (first entry)

XX DE

XX Casein-related peptide SEQ ID 29.

XX KW

XX Tripeptide; casein; hypotensive; tranquiliser; blood pressure; stress.

XX OS

XX Synthetic.

XX PN

XX WO200134828-A1.

XX PD

XX 17-MAY-2001.

XX PF

XX 10-NOV-2000; 2000WO-JF07930.

XX PR

XX 11-NOV-1999; 99JP-0321084.

XX XX

XX (CALV ) CALPIS CO LTD.

XX PI

XX Yamamoto N, Ueno K, Ejiri M;

XX DR

XX WPI; 2001-343606/36.

XX PT

XX Production of tripeptides for treating hypertension and stress by  
 processing casein with proteinase and peptidase -

XX PS

XX Example 4; Page 13; 32pp; Japanese.

XX XX

CC This invention relates to a method for the production of tripeptides. The  
 method comprises treating material containing milk casein with a  
 CC proteinase to produce intermediate peptide containing ValProPro or  
 CC IleProPro with no proline residue any where else in the peptide. Use of  
 CC the peptides may result in hypotensive and tranquiliser activity. The  
 CC peptide can be used in treatments to lower blood pressure and in the  
 CC treatment of stress. The present sequence represents a peptide used in an  
 CC example illustrating the method of the invention.

SQ Sequence 8 AA;

Query Match 22.2%; Score 4; DB 22; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4

Db |||||

5 LOPE 8

RESULT 38

AAR10635

ID AAR10635 standard; Protein; 9 AA.

XX AC

XX AAR10635;

XX DT

XX 25-MAR-2003 (updated)

XX DT

XX 18-APR-1991 (first entry)

XX DE

XX Human Papilloma Virus-16 "[Gln26]-E7-(20-28)-AMIDE" peptide.

XX KW

XX papilloma virus; retinoblastoma gene-binding protein; genital warts;

XX KW

XX cervical cancer.

XX OS

XX Synthetic.

XX PN

XX EP412762-A.

XX PD

XX 13-FEB-1991.

XX PF

XX 06-AUG-1990; 90EP-0308652.

XX PR

XX 09-APR-1990; 90US-0506981.

XX PR

XX 07-AUG-1989; 89US-0390569.

XX XX

XX (MERI ) MERCK & CO INC.

XX PA

XX (OLIF/) OLIFF A I.

XX PI

XX Oliff AI, Riemen MW;

XX DR

XX WPI; 1991-045887/07.

XX XX

XX Claim 12; Page 11; lpp; English.

XX CC

XX The peptide carries an amide group at the C-terminus. The sequence  
 CC comprises residues 20 to 28 of the deduced HPV-16 E7 protein  
 CC sequence (N.Salzman and P.Howley, "The Papovaviridae", Vol 2, p.379,  
 CC Plenum Press, N.Y. 1987) but with Gln replacing Thr at position 26.  
 CC The peptides are used as screening tools and in the prevention,  
 CC therapy, prophylaxis and treatment of HPV-induced diseases. They  
 CC can also be used to raise antibodies either as vaccines or to  
 CC heighten the immune response to an HPV infection all ready present.  
 CC See also AAR10628-R10634, AAR10636-7.  
 CC (Updated on 25-MAR-2003 to correct PA field.)

XX SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 12; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4

Db |||||

2 LOPE 5

RESULT 39

AAR33157

ID AAR33157 standard; peptide; 9 AA.

XX AC

XX AAR33157;

XX DT

XX 25-MAR-2003 (updated)

XX DT

XX 25-JUN-1993 (first entry)

XX XX

XX HPV E7 protein - RBG protein binding inhibitor peptide.

XX DE

XX XX

XX KW

XX Human papilloma virus; retinoblastoma gene; genital warts;

XX KW

XX cervical cancer; treatment.

```

OS Synthetic.
PN EP531080-A2.
XX
XX 10-MAR-1993.
XX
XX 01-SEP-1992; 92EP-0307905.
XX
XX 04-SEP-1991; 91US-0754829.
XX
XX (MERI ) MERCK & CO INC.
XX
XX Oliff AI, Riemen MW;
XX
XX WPI; 1993-078581/10.
DR
XX
XX New polypeptide(s) which inhibit human papilloma virus binding to
PT RBG protein - useful for treating genital warts and cervical cancer
XX
XX Claim 7; Page 15; 15pp; English.
XX
XX The sequence is that of a peptide which inhibits binding of human
CC papilloma virus (HPV) E7 protein to the retinoblastoma gene (RBG)
CC protein. It can be used in the treatment of conditions caused by HPV,
CC esp. genital warts and cervical cancer.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX PA (MERI ) MERCK & CO INC.
XX
XX PI Oliff AI, Riemen MW;
XX
XX WPI; 1993-078581/10.
DR
XX
XX Query Match 22.2%; Score 4; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LOPE 4
DB 2 LOPE 5
XX
XX RESULT 40
AAR33163
ID AAR33163 standard; peptide; 9 AA.
XX
XX AC AAR33163;
XX
XX 25-MAR-2003 (updated)
DT 25-JUN-1993 (first entry)
XX
XX HPV E7 protein - RBG protein binding inhibitor peptide.
XX
XX Human papilloma virus; retinoblastoma gene; genital warts;
KW cervical cancer; treatment.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT Modified-site 1
FT FT /label= OTHER
FT FT /note= "N-acetyl-Leu"
XX
XX EP531080-A2.
XX
XX 10-MAR-1993.
XX
XX 01-SEP-1992; 92EP-0307905.
XX
XX 04-SEP-1991; 91US-0754829.
XX
XX (MERI ) MERCK & CO INC.
XX
XX Oliff AI, Riemen MW;
XX
XX WPI; 1993-078581/10.
XX

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```

PT New polypeptide(s) which inhibit human papilloma virus binding to
PT RBG protein - useful for treating genital warts and cervical cancer
XX
XX Claim 7; Page 15; 15pp; English.
XX
XX The sequence is that of a peptide which inhibits binding of human
CC papilloma virus (HPV) E7 protein to the retinoblastoma gene (RBG)
CC protein. It can be used in the treatment of conditions caused by HPV,
CC esp. genital warts and cervical cancer.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX SQ Sequence 9 AA;
XX
XX Query Match 22.2%; Score 4; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LOPE 4
DB 1 LOPE 4
XX
XX RESULT 41
AAR33170
ID AAR33170 standard; peptide; 9 AA.
XX
XX AC AAR33170;
XX
XX 25-MAR-2003 (updated)
DT 25-JUN-1993 (first entry)
XX
XX HPV E7 protein - RBG protein binding inhibitor peptide.
XX
XX Human papilloma virus; retinoblastoma gene; genital warts;
KW cervical cancer; treatment.
XX
XX Synthetic.
XX
XX EP531080-A2.
XX
XX 10-MAR-1993.
XX
XX 01-SEP-1992; 92EP-0307905.
XX
XX 04-SEP-1991; 91US-0754829.
XX
XX (MERI ) MERCK & CO INC.
XX
XX Oliff AI, Riemen MW;
XX
XX WPI; 1993-078581/10.
XX
XX New polypeptide(s) which inhibit human papilloma virus binding to
PT RBG protein - useful for treating genital warts and cervical cancer
XX
XX Claim 7; Page 15; 15pp; English.
XX
XX The sequence is that of a peptide which inhibits binding of human
CC papilloma virus (HPV) E7 protein to the retinoblastoma gene (RBG)
CC protein. It can be used in the treatment of conditions caused by HPV,
CC esp. genital warts and cervical cancer.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX SQ Sequence 9 AA;
XX
XX Query Match 22.2%; Score 4; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LOPE 4
DB 2 LOPE 5
XX

```

XW	Human papilloma virus; major histocompatibility complex; prevention;
KW	treatment; virus-related diseases; T cell response; cervical; human;
KW	carcinoma; adenoma; screening tools; diagnostics; diagnosis.
OS	Synthetic.
XX	WO9322338-A1.
XX	11-NOV-1993.
XX	04-MAY-1993; 93WO-NL00093.
XX	05-MAY-1992; 92EP-0201252.
PR	10-DEC-1992; 92EP-0203870.
PR	01-FEB-1993; 93EP-0200243.
PR	05-MAR-1993; 93EP-0200621.
XX	(UPLS-) RIJKSUNIV LEIDEN.
PA	
XX	Kast WM, Melief CJM, Sette AD, Sidney JC;
XX	WPI; 1993-368718/46.
XX	Peptide(s) derived from human papilloma virus - which bind to a
PT	human major histocompatibility complex Class I molecule, used for
PT	prevention and treatment of virus-related diseases
XX	Claim 5; Page 51; 64pp; English.
PS	The sequence is that of a peptide, derived from the E7 protein of
CC	human papilloma virus (HPV) (residues 12-20), which is able to bind
CC	to human MHC Class I allele HLA-A2.1. It is able to induce a T cell
CC	response effective against HPV, in partic. a HLA class I-restricted
CC	Cp8+ cytotoxic T cell response. It can be used for prevention and
CC	treatment of cervical carcinoma and/or adenoma and other HPV-related
CC	diseases. It can also be used as a screening tool and in diagnostic
CC	applications.
CC	(Updated on 25-MAR-2003 to correct PN field.)
XX	
XX	Sequence 9 AA;
SQ	
Query Match	22.2%; Score 4; DB 14; Length 9;
Best Local Similarity	100.0%; Pred. No. 9.3e+05;
Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps
QY	1 LOPE 4
Db	4 LOPE 7
RESULT 44	
AAR59257	
ID	AAR59257 standard; peptide; 9 AA.
XX	AAR59257;
XX	25-MAR-2003 (updated)
DT	10-MAY-1995 (first entry)
XX	Peptide fragment (1.0229) of HPV binds HLA-A2.1.
DE	
XX	antigen; epitope; immunogenic target protein; PSA; HBVC; HBVs; EBV;
KW	HLV1; core antigen; surface antigen; pharmaceutical composition;
KW	in vivo; ex vivo; therapeutic; diagnostic; MHC class I molecule;
KW	major histocompatibility complex; HLA-A2.1; 9mer; 10mer; anchor;
KW	human leukocyte antigen.
XX	
OS	Human papilloma virus.
XX	
PN	WO9420127-A1.
XX	15-SEP-1994.
XX	

```

PF 04-MAR-1994; 94WO-US02353.
XX
XX
PR 05-MAR-1993; 93US-0027146.
PR 04-JUN-1993; 93US-0073205.
PR 29-NOV-1993; 93US-0159184.
XX
XX
PA (CYTE-) CYTEL CORP.
XX
XX
PI Grey HM, Kast WM, Sette A, Sidney J;
XX
XX
DR WPI; 1994-302678/37.
XX
XX
PT Immunogenic peptide(s) having an HLA-A2.1 binding motif - used
PT for treatment or prophylaxis of cancer, virus infection or
PT autoimmune diseases.
XX
XX
PS Example 5; Page 106; 138pp; English.
XX
XX
CC AAR59104-264 are immunogenic 9mer peptides that contain a HLA-A2.1
CC binding motif. These peptides bind HLA-A2.1 and have a binding affinity
CC of at least 1% as compared to a reference peptide (AAR71293). AAR59257
CC has an IC50 of <0.0003 and the sequence occurs at position 14 in the HPV
CC E7 protein. The peptides of the invention can induce cytotoxic T
CC lymphocytes which can react with target cells. They can be used for the
CC treatment or prophylaxis of cancer, eg. prostate cancer or lymphoma,
CC etc.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX
SQ Sequence 9 AA;
XX
XX
Query Match 22.2%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
QY 1 LOPE 4
Db ||||
2 LOPE 5
XX
XX
RESULT 46
AAR73799
ID AAR73799 standard; peptide; 9 AA.
XX
XX
AC AAR73799;
XX
XX
DT 25-MAR-2003 (updated)
DT 19-JUN-1995 (first entry)
XX
XX
DE Antigen fragment 115, from HPV(a) has binding affinity for HLA-2.1.
XX
XX
KW antigen; epitope; immunogenic target protein; PSA; HBVc; HBVs; EBV;
KW HIV1; plasma specific antigen; hepatitis B virus; Epstein Barr;
KW human immunodeficiency virus; human papilloma virus; p53; c-ERB2;
KW MAGE-1; melanoma antigen-1; core antigen; surface antigen;
KW pharmaceutical composition; in vivo; ex vivo; therapeutic;
KW diagnostic; MHC class I molecule; major histocompatibility complex;
KW HLA-A2.1; 9mer; 10mer; anchor; human leukocyte antigen; PLP; 8mer;
KW algorithm prediction; MBP; CMV; cytomegalovirus; HSV;
KW herpes simplex virus; influenza A; M1.
XX
XX
OS Human papilloma virus strain 16(a).
XX
XX
PN WO9420127-A1.
XX
XX
PD 15-SEP-1994.
XX
XX
PF 04-MAR-1994; 94WO-US02353.
XX
XX
PR 05-MAR-1993; 93US-0027146.
PR 04-JUN-1993; 93US-0073205.
PR 29-NOV-1993; 93US-0159184.
XX
XX
PA (CYTE-) CYTEL CORP.
XX
XX
PI Grey HM, Kast WM, Sette A, Sidney J;
XX
XX
DR WPI; 1994-302678/37.
XX
XX
PT Immunogenic peptide(s) having an HLA-A2.1 binding motif - used
PT for treatment or prophylaxis of cancer, virus infection or
PT autoimmune diseases.
XX
XX
PS Disclosure; Page 84; 138pp; English.
XX
XX

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PF 04-MAR-1994; 94WO-US02353.
XX
XX
PR 05-MAR-1993; 93US-0027146.
PR 04-JUN-1993; 93US-0073205.
PR 29-NOV-1993; 93US-0159184.
XX
XX
PA (CYTE-) CYTEL CORP.
XX
XX
PI Grey HM, Kast WM, Sette A, Sidney J;
XX
XX
DR WPI; 1994-302678/37.
XX
XX
PT Immunogenic peptide(s) having an HLA-A2.1 binding motif - used
PT for treatment or prophylaxis of cancer, virus infection or
PT autoimmune diseases.
XX
XX
PS Example 5; Page 106; 138pp; English.
XX
XX
CC AAR59104-264 are immunogenic 9mer peptides that contain a HLA-A2.1
CC binding motif. These peptides bind HLA-A2.1 and have a binding affinity
CC of at least 1% as compared to a reference peptide (AAR71293). AAR59257
CC has an IC50 of <0.0003 and the sequence occurs at position 14 in the HPV
CC E7 protein. The peptides of the invention can induce cytotoxic T
CC lymphocytes which can react with target cells. They can be used for the
CC treatment or prophylaxis of cancer, eg. prostate cancer or lymphoma,
CC etc.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX
SQ Sequence 9 AA;
XX
XX
Query Match 22.2%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
QY 1 LOPE 4
Db ||||
2 LOPE 5
XX
XX
RESULT 45
AAR59246
ID AAR59246 standard; peptide; 9 AA.
XX
XX
AC AAR59246;
XX
XX
DT 25-MAR-2003 (updated)
DT 04-MAY-1995 (first entry)
XX
XX
DE Peptide fragment (1.0316) of c-ERB2 binds HLA-A2.1.
XX
XX
KW antigen; epitope; immunogenic target protein; PSA; HBVc; HBVs; EBV;
KW HIV1; core antigen; surface antigen; pharmaceutical composition;
KW in vivo; ex vivo; therapeutic; diagnostic; MHC class I molecule;
KW major histocompatibility complex; HLA-A2.1; 9mer; 10mer; anchor;
KW human leukocyte antigen.
XX
XX
OS Homo sapiens.
XX
XX
PN WO9420127-A1.
XX
XX
PD 15-SEP-1994.
XX
XX
PF 04-MAR-1994; 94WO-US02353.
XX
XX
PR 05-MAR-1993; 93US-0027146.
PR 04-JUN-1993; 93US-0073205.
PR 29-NOV-1993; 93US-0159184.
XX
XX
PA (CYTE-) CYTEL CORP.
XX
XX
PI Grey HM, Kast WM, Sette A, Sidney J;
XX
XX
DR WPI; 1994-302678/37.
XX
XX

```

CC AAR73685-876 are potential peptide binders of HLA-A2.1 motif. Using  
 CC motifs disclosed in the invention, these peptides were screened for  
 CC further motifs. Only peptides with binding affinity of at least 1%  
 CC (binding affinity is expressed as an IC50 value) as compared to the  
 CC standard peptide (AAR71293) in assays. This peptide from HPV(a) E7(a)  
 CC antigen has a binding value of 1.9000. The peptides of the invention can  
 CC induce cytotoxic T lymphocytes which can react with target cells. They  
 CC can be used for the treatment or prophylaxis of cancer, eg. prostate  
 CC cancer or lymphoma, etc.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 15; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4  
 Db |||||  
 5 LOPE 8

RESULT 47  
 AAR73800  
 ID AAR73800 standard; peptide; 9 AA.  
 XX  
 AC AAR73800;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 19-JUN-1995 (first entry)  
 XX  
 DE Antigen fragment 116, from HPV has binding affinity for HLA-A2.1.  
 XX  
 KW antigen; epitope; immunogenic target protein; PSA; HBVc; HBVs; EBV;  
 KW HIV1; plasma specific antigen; hepatitis B virus; Epstein Barr;  
 KW human immunodeficiency virus; human papilloma virus; p53; c-ERB2;  
 KW MAGE-1; melanoma antigen-1; core antigen; surface antigen;  
 KW pharmaceutical composition; in vivo; ex vivo; therapeutic;  
 KW diagnostic; MHC class I molecule; major histocompatibility complex;  
 KW HLA-A2.1; 9mer; 10mer; anchor; human leukocyte antigen; PLP; 8mer;  
 KW algorithm prediction; MBP; CMV; cytomegalovirus; HSV;  
 KW herpes simplex virus; influenza A; M1.  
 XX  
 OS Human papilloma virus strain 16.  
 XX  
 PN WO9420127-A1.  
 XX  
 PD 15-SEP-1994.  
 XX  
 PF 04-MAR-1994; 94WO-US02353.  
 XX  
 PR 05-MAR-1993; 93US-0027146.  
 PR 04-JUN-1993; 93US-0073205.  
 PR 29-NOV-1993; 93US-0159184.  
 XX  
 FA (CYTE-) CYTEL CORP.  
 XX  
 PI Grey HM, Kast WM, Sette A, Sidney J;  
 XX  
 DR WPI; 1994-302678/37.  
 XX  
 PT Immunogenic peptide(s) having an HLA-A2.1 binding motif - used  
 PT for treatment or prophylaxis of cancer, virus infection or  
 PT autoimmune diseases.  
 XX  
 PS Disclosure; Page 84; 138pp; English.  
 XX  
 CC AAR73685-876 are potential peptide binders of HLA-A2.1 motif. Using  
 CC motifs disclosed in the invention, these peptides were screened for  
 CC further motifs. Only peptides with binding affinity of at least 1%  
 CC (binding affinity is expressed as an IC50 value) as compared to the  
 CC standard peptide (AAR71293) in assays. This peptide from HPV E7  
 CC antigen has a binding value of 0.0130. The peptides of the invention can

CC induce cytotoxic T lymphocytes which can react with target cells. They  
 CC can be used for the treatment or prophylaxis of cancer, eg. prostate  
 CC cancer or lymphoma, etc.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 15; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4  
 Db |||||  
 4 LOPE 7

RESULT 48  
 AAR73796  
 ID AAR73796 standard; peptide; 9 AA.  
 XX  
 AC AAR73796;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 19-JUN-1995 (first entry)  
 XX  
 DE Antigen fragment 112, from HPV has binding affinity for HLA-A2.1.  
 XX  
 KW antigen; epitope; immunogenic target protein; PSA; HBVc; HBVs; EBV;  
 KW HIV1; plasma specific antigen; hepatitis B virus; Epstein Barr;  
 KW human immunodeficiency virus; human papilloma virus; p53; c-ERB2;  
 KW MAGE-1; melanoma antigen-1; core antigen; surface antigen;  
 KW pharmaceutical composition; in vivo; ex vivo; therapeutic;  
 KW diagnostic; MHC class I molecule; major histocompatibility complex;  
 KW HLA-A2.1; 9mer; 10mer; anchor; human leukocyte antigen; PLP; 8mer;  
 KW algorithm prediction; MBP; CMV; cytomegalovirus; HSV;  
 KW herpes simplex virus; influenza A; M1.  
 XX  
 OS Human papilloma virus strain 16.  
 XX  
 PN WO9420127-A1.  
 XX  
 PD 15-SEP-1994.  
 XX  
 PF 04-MAR-1994; 94WO-US02353.  
 XX  
 PR 05-MAR-1993; 93US-0027146.  
 PR 04-JUN-1993; 93US-0073205.  
 PR 29-NOV-1993; 93US-0159184.  
 XX  
 FA (CYTE-) CYTEL CORP.  
 XX  
 PI Grey HM, Kast WM, Sette A, Sidney J;  
 XX  
 DR WPI; 1994-302678/37.  
 XX  
 PT Immunogenic peptide(s) having an HLA-A2.1 binding motif - used  
 PT for treatment or prophylaxis of cancer, virus infection or  
 PT autoimmune diseases.  
 XX  
 PS Disclosure; Page 84; 138pp; English.  
 XX  
 CC AAR73685-876 are potential peptide binders of HLA-A2.1 motif. Using  
 CC motifs disclosed in the invention, these peptides were screened for  
 CC further motifs. Only peptides with binding affinity of at least 1%  
 CC (binding affinity is expressed as an IC50 value) as compared to the  
 CC standard peptide (AAR71293) in assays. This peptide from HPV E7  
 CC antigen has a binding value of 1.4000. The peptides of the invention can  
 CC induce cytotoxic T lymphocytes which can react with target cells. They  
 CC can be used for the treatment or prophylaxis of cancer, eg. prostate  
 CC cancer or lymphoma, etc.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 9 AA;

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Query Match      22.2%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4
Db 5 LQPE 8

RESULT 49
AAR80939
ID AAR80939 standard; peptide; 9 AA.
XX
AC AAR80939;
XX
DT 03-MAY-1996 (first entry)
XX
XX Peptide for increasing HLA-A2.1 cell expression.
XX
XX Human melanoma-associated protein; MAGE-2; tumour rejection antigen;
XX precursor; major histocompatibility complex; MHC; class I; HLA-A2.1;
XX binding motif; cytolytic T cell; CTL; induction; peptide loading;
XX primary immune response.
XX
XX Synthetic.
XX
XX WO9525530-A1.
XX
XX 28-SEP-1995.
XX
XX 21-MAR-1995; 95WO-US03535.
XX
XX 24-MAR-1994; 94US-0217188.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX (UYLE-) RIJKSUNIV LEIDEN.
XX
XX Boon-Falleur T, Kast WM, Melief CJM, Van Der Bruggen P;
XX Visseren MW;
XX WPI; 1995-344456/44.
XX
XX New peptide(s) based on tumour rejection antigen precursor MAGE-2 -
XX which bind HLA-A2 molecules to provoke cytolytic T cell prodn., used
XX partic. for treating cancers
XX
XX Example 3; Page 37; 44pp; English.
XX
XX Expression of HLA-A2.1 (T2) cells is increased by incubating T2
XX cells in medium containing the present peptide. T2 cells will
XX present the peptide bound to HLA-A2.1 in high amount and are good
XX antigen presenting cells. The claimed MAGE-2 peptides (see AAR80878-
XX AAR80888) can induce a similar primary immune response.
XX
XX Sequence 9 AA;

Query Match      22.2%; Score 4; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4
Db 4 LQPE 7

RESULT 50
AAR78889
ID AAR78889 standard; peptide; 9 AA.
XX
AC AAR78889;
XX
DT 25-MAR-2003 (updated)
XX

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DT 27-MAR-1996 (first entry)
XX
DE HPV16 E7 11-19 cytotoxic T lymphocyte epitope.
XX
KW HPV16 E7 11-19; cytotoxic T; CTL; epitope; helper T; HTL; cell;
XX lymphocyte; antigens; treatment; disease prevention;
XX
OS Human papillomavirus.
XX
XX WO9522317-A1.
XX
XX 24-AUG-1995.
XX
XX 16-FEB-1995; 95WO-US02121.
XX
XX 16-FEB-1994; 94US-0197484.
XX
XX (CYTE-) CYTEL CORP.
XX
XX Vitello MA, Chesnut RW, Sette AD, Celis E, Grey H;
XX WPI; 1995-302545/39.
XX
XX Compn. inducing cytotoxic T lymphocyte response to pref. viral,
XX bacterial, parasitic or tumour antigens - useful in the treatment
XX and prevention of diseases associated with the antigen e.g.
XX hepatitis B
XX
XX Example 14; Page 72; 109pp; English.
XX
XX A compsn. which induces a cytotoxic T lymphocyte (CTL) response to
XX a human papillomavirus (HPV) antigen (Ag) in a mammal comprises, a
XX HPV CTL Ag response inducing peptide (i.e. AAR78888-R78895) and a
XX lipid conjugated helper T cell inducing peptide. The compsn. is
XX useful in the treatment and prevention of HPV associated diseases.
XX (Updated on 25-MAR-2003 to correct PI field.)
XX
XX Sequence 9 AA;

Query Match      22.2%; Score 4; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4
Db 5 LQPE 8

RESULT 51
AAR78894
ID AAR78894 standard; peptide; 9 AA.
XX
AC AAR78894;
XX
DT 25-MAR-2003 (updated)
XX
DT 27-MAR-1996 (first entry)
XX
DE HPV16 E7 12-20 cytotoxic T lymphocyte epitope.
XX
KW HPV16 E7 12-20; cytotoxic T; CTL; epitope; helper T; HTL; cell;
XX lymphocyte; antigens; treatment; disease prevention;
XX
OS Human papillomavirus.
XX
XX WO9522317-A1.
XX
XX 24-AUG-1995.
XX
XX 16-FEB-1995; 95WO-US02121.
XX
XX 16-FEB-1994; 94US-0197484.
XX
XX (CYTE-) CYTEL CORP.
XX

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XX Vitiello MA, Chesnut RW, Sette AD, Celis E, Grey H;  
 XX WPI; 1995-302545/39.  
 XX  
 XX Compn. inducing cytotoxic T lymphocyte response to pref. viral,  
 PT bacterial, parasitic or tumour antigens - useful in the treatment  
 PT and prevention of diseases associated with the antigen e.g.  
 PT hepatitis B  
 XX  
 XX Example 14; Page 72; 109pp; English.  
 XX  
 XX A compn. which induces a cytotoxic T lymphocyte (CTL) response to  
 CC a human papillomavirus (HPV) antigen (Ag) in a mammal comprises, a  
 CC HPV CTL Ag response inducing peptide (i.e. AAR7888-R78895) and a  
 CC lipid conjugated helper T cell inducing peptide. The compn. is  
 CC useful in the treatment and prevention of HPV associated diseases.  
 CC (Updated on 25-MAR-2003 to correct PI field.)  
 XX  
 XX Sequence 9 AA;  
 SQ  
 Query Match 22.2%; Score 4; DB 16; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LQPE 4  
 Db ||||  
 4 LQPE 7  
 RESULT 52  
 AAR78851  
 ID AAR78851 standard; peptide; 9 AA.  
 XX  
 XX AAR78851;  
 XX  
 XX 25-MAR-2003 (updated)  
 DT 27-MAR-1996 (first entry)  
 XX  
 XX HIV pol 185-193 cytotoxic T lymphocyte epitope.  
 XX  
 XX HIV pol 185-193; cytotoxic T; CTL; epitope; helper T; HTL; cell;  
 KW lymphocyte; viruses; parasites; tumours; antigens; treatment;  
 KW disease prevention.  
 XX  
 XX Human immunodeficiency virus.  
 OS  
 XX WO9522317-A1.  
 XX  
 XX 24-AUG-1995.  
 PD  
 XX 16-FEB-1995; 95WO-US02121.  
 PF  
 XX 16-FEB-1994; 94US-0197484.  
 PR  
 XX (CYTE-) CYTEL CORP.  
 PA  
 XX Vitiello MA, Chesnut RW, Sette AD, Celis E, Grey H;  
 PI  
 XX WPI; 1995-302545/39.  
 XX  
 XX Compn. inducing cytotoxic T lymphocyte response to pref. viral,  
 PT bacterial, parasitic or tumour antigens - useful in the treatment  
 PT and prevention of diseases associated with the antigen e.g.  
 PT hepatitis B  
 XX  
 XX Disclosure; Page 17; 109pp; English.  
 XX  
 XX A compn. which induces a cytotoxic T lymphocyte (CTL) response to  
 CC an antigen (Ag) in a mammal comprises, a CTL Ag response inducing  
 CC peptide (i.e. AAR78824-R78853) and a lipid conjugated helper T cell  
 CC inducing peptide. The compn. induces a CTL response to bacterial,  
 CC viral or tumour Ags, and is therefore useful in the treatment and

CC prevention of diseases associated with the Ag.  
 CC (Updated on 25-MAR-2003 to correct PI field.)  
 XX  
 XX Sequence 9 AA;  
 SQ  
 Query Match 22.2%; Score 4; DB 16; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 9 PKVK 12  
 Db ||||  
 2 PKVK 5  
 RESULT 53  
 AAR70601  
 ID AAR70601 standard; Peptide; 9 AA.  
 XX  
 XX AAR70601;  
 XX  
 XX 14-FEB-1996 (first entry)  
 DT  
 XX HIV(B35)POL-9, human immunodeficiency virus epitope.  
 DE  
 XX HLA; human lymphocyte antigen; HIV; human immunodeficiency virus;  
 KW binding peptide; induce killer cell; prevention; treatment; AIDS;  
 KW autoimmune disease syndrome; vaccine.  
 XX  
 XX Human immunodeficiency virus.  
 OS  
 XX WO9511255-A1.  
 XX  
 XX 27-APR-1995.  
 PD  
 XX 19-OCT-1994; 94WO-JP01756.  
 PF  
 XX 19-OCT-1993; 93JP-0261302.  
 PR  
 XX (AJIN ) AJINOMOTO CO INC.  
 PA (AJIN ) AJINOMOTO KK.  
 XX  
 XX Miwa K, Takiguchi M;  
 PI  
 XX WPI; 1995-170188/22.  
 DR  
 XX HLA-binding peptide fragments from HIV proteins - induce killer  
 PT cells which target HIV-infected cells and can be incorporated into  
 PT anti-HIV vaccines  
 PT  
 XX Example 1; Page 10; 61pp; Japanese.  
 PS  
 XX AAR70601 is a peptide fragment derived from an HIV (Human  
 CC Immunodeficiency Virus) protein and is capable of binding to a human  
 CC lymphocyte antigen. The peptide can induce killer cells which target  
 CC HIV-infected cells. It is also useful in the prevention and treatment of  
 CC HIV and AIDS. Anti-HIV vaccines may incorporate the peptides, or may  
 CC incorporate a vector (such as vaccinia or BCG) contg. DNA encoding the  
 CC peptides.  
 XX  
 XX Sequence 9 AA;  
 SQ  
 Query Match 22.2%; Score 4; DB 16; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 9 PKVK 12  
 Db ||||  
 2 PKVK 5  
 RESULT 54  
 AAR84331  
 ID AAR84331 standard; peptide; 9 AA.

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XX AC AAR84331;
XX DT 25-JAN-1996 (first entry)
XX DE HPV derived peptide (h).
XX KW Human papilloma virus; HPV; cytotoxic T-cell; HLA-B35 antigen;
XX OS prevention; treatment; carcinoma; cervix; cervical cancer.
XX PN Synthetic.
XX PD JPO7136289-A.
XX PD 16-MAY-1995.
XX PF 02-NOV-1993; 93JP-0297378.
XX PR 02-NOV-1993; 93JP-0297378.
XX PA (KENB/) KENBARA K.
XX PA (TAKI/) TAKIGUCHI M.
XX DR WPI; 1995-212956/28.
XX PT Human papilloma virus derived peptide(s) of 9-11 amino acids in
XX length - which bind with HLA-B35 antigen and are useful in
XX prevention and treatment of cervical cancer
XX PS Claim 1; Page 2; 7pp; Japanese.
XX CC The sequences given in AAR84324-35 are synthetic peptides which are
XX derived from human papilloma virus. These peptides are represented
XX in cytotoxic T-cells by binding with HLA-B35 antigen. They are
XX prepared by standard methods of peptide synthesis and may be used
XX for the prevention and treatment of carcinoma of the cervix.
XX SQ Sequence 9 AA;
Query Match 22.2%; Score 4; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 VPXV 11
Db 1 VPXV 4
RESULT 55
AAR89363
ID AAR89363 standard; peptide; 9 AA.
XX AC AAR89363;
XX DT 18-SEP-1996 (first entry)
XX DE Immunogenic peptide, based on Y1 analog of 1054.05.
XX KW Immunogenic peptide; supermotif; HLA molecule; CTL response;
XX therapeutic; diagnostic; cancer; viral infection; hepatitis B;
XX hepatitis C.
XX OS Synthetic.
XX PN WO9603140-A1.
XX PD 08-FEB-1996.
XX PF 21-JUL-1995; 95WO-US09234.
XX PR 30-MAY-1995; 95US-0452843.
XX PR 21-JUL-1994; 94US-0278634.
XX PR 23-NOV-1994; 94US-0344824.

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XX PA (CYTE-) CYTEL CORP.
XX FI Sette A, Sidney J;
XX DR WPI; 1996-116784/12.
XX CC Compan. comprising immunogenic peptide with supermotif allowing more
XX than one HLA mol. to bind - used to induce CTL response in patient
XX and for in vivo and ex vivo therapeutic and diagnostic applications
XX PS Claim 2; Page 26; 32pp; English.
XX CC The sequences given in AAR89362-82 are immunogenic peptides which were
XX use in the composition of the invention. The composition comprises
XX an immunogenic peptide of 9-10 residues with a supermotif which
XX allows binding of more than one HLA molecule. It pref. comprises
XX two conserved residues, a first at the 2nd position from the N-
XX terminal is Pro, and a 2nd at the C-terminal is Met. These peptides
XX are used to induce a CTL response in a patient. They are also
XX useful in compositions for in vivo and ex vivo therapeutic and
XX diagnostic applications, e.g the treatment of cancer and viral
XX infections, e.g. hepatitis B and C.
XX SQ Sequence 9 AA;
Query Match 22.2%; Score 4; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 PKVK 12
Db 2 PKVK 5
RESULT 56
AAW39661
ID AAW39661 standard; peptide; 9 AA.
XX AC AAW39661;
XX DT 11-JUN-1998 (first entry)
XX DE HPV16/18 E7 peptide (pos. 11-19).
XX KW T cell epitope; immune response; human leukocyte antigen; HLA Class I;
XX vaccine; immunogenic; major histocompatibility complex; MHC; B cell;
XX disease; anti-tumour; anti-viral.
XX OS Human papillomavirus.
XX PN WO9741440-A1.
XX PD 06-NOV-1997.
XX PF 28-APR-1997; 97WO-NL00229.
XX PR 23-DEC-1996; 96EP-0203670.
XX PR 26-APR-1996; 96EP-0201145.
XX PA (UYLE-) RIJXSUNIV LEIDEN.
XX PA (SCIS-) SCI SEED CAPITAL INVESTMENTS BV.
XX PI Kast WM, Melief CJM, Offringa R, Toes REM, Van Der Burg SH;
XX DR WPI; 1997-549891/50.
XX PT Method of selecting T cell peptide epitope(s) - by measuring the
XX stability of HLA class I-peptide complexes on intact B cells
XX PS Example 3; Page 78; 109pp; English.
XX CC Peptides AAW39430-W39734 are used in a novel method for the selection of

```



CC immunogenic T-cell peptide epitopes present in polypeptide antigens. The  
 CC method involves the identification of peptide sequences capable of  
 CC binding to an HLA (human leukocyte antigen) class I molecule and  
 CC measuring the binding of this epitope peptide to the HLA class I  
 CC peptide. The stability of binding of the peptide and MHC (major  
 CC histocompatibility complex) class I molecule is measured on intact human  
 CC B cells carrying the MHC molecule at their cell surfaces. The method can  
 CC be used to select peptide epitopes for generating vaccines against a  
 CC disease associated with the polypeptide, e.g. cancers or AIDS. The  
 CC peptide epitopes are especially T-cell peptide epitopes with strong  
 CC anti-tumour and anti-viral immune responses. Peptide AAW39661 is derived  
 CC from the human papillomavirus E7 protein and is capable of binding to the  
 CC human MHC Class I allele HLA-A2.1.

XX  
 SQ Sequence 9 AA;  
 Query Match 22.2%; Score 4; DB 18; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4  
 ||||  
 Db 5 LQPE 8

## RESULT 57

AAW39662  
 ID AAW39662 standard; peptide; 9 AA.

AC AAW39662;

DT 11-JUN-1998 (first entry)

XX HPV16/18 E7 peptide (pos. 12-20).

DE T cell epitope; immune response; human leukocyte antigen; HLA Class I;  
 KW vaccine; immunogenic; major histocompatibility complex; MHC; B cell;  
 KW disease; anti-tumour; anti-viral.

XX Human papillomavirus.

XX WO9741440-A1.

PD 06-NOV-1997.

XX 28-APR-1997; 97WO-NL00229.

XX 23-DEC-1996; 96EP-0203670.

PR 26-APR-1996; 96EP-0201145.

XX (UYLE-) RIJKSUNIV LEIDEN.

PA (SCIS-) SCI SEED CAPITAL INVESTMENTS BV.

XX Kast WM, Melief CJM, Offringa R, Toes REM, Van Der Burg SH;

PI WPI; 1997-549891/50.

DR Method of selecting T cell peptide epitope(s) - by measuring the  
 PT stability of HLA class I-peptide complexes on intact B cells

XX Example 3; Page 78; 109pp; English.

XX Peptides AAW39430-W39734 are used in a novel method for the selection of  
 CC immunogenic T-cell peptide epitopes present in polypeptide antigens. The  
 CC method involves the identification of peptide sequences capable of  
 CC binding to an HLA (human leukocyte antigen) class I molecule and  
 CC measuring the binding of this epitope peptide to the HLA class I  
 CC peptide. The stability of binding of the peptide and MHC (major  
 CC histocompatibility complex) class I molecule is measured on intact human  
 CC B cells carrying the MHC molecule at their cell surfaces. The method can  
 CC be used to select peptide epitopes for generating vaccines against a  
 CC disease associated with the polypeptide, e.g. cancers or AIDS. The  
 CC peptide epitopes are especially T-cell peptide epitopes with strong

CC anti-tumour and anti-viral immune responses. Peptide AAW39662 is derived  
 CC from the human papillomavirus E7 protein and is capable of binding to the  
 CC human MHC Class I allele HLA-A2.1.

XX Sequence 9 AA;

Query Match 22.2%; Score 4; DB 18; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4  
 ||||  
 Db 4 LQPE 7

## RESULT 58

AAW36590

ID AAW36590 standard; peptide; 9 AA.

AC AAW36590;

XX 25-MAR-2003 (updated)

DT 09-MAR-1998 (first entry)

XX Hepatitis B virus bulk antigen.

DE Melanoma protein; MAGE-2; tumour rejection antigen precursor; HBV;  
 KW binding motif; human leukocyte antigen; HLA-A2.1; cytolytic T cell;  
 KW CTL; induce; production; Hepatitis B virus.

XX Hepatitis B virus.

XX US5686068-A.

PN 11-NOV-1997.

XX 25-JUL-1996; 96US-0687226.

PR 25-JUL-1996; 96US-0687226.

PR 24-MAR-1994; 94US-0217188.

XX (LUDW-) LUDWIG INST CANCER RES.

PA (UYLE-) RIJKSUNIV LEIDEN.

XX Boon-Falleur T, Melief CJM, Van Der Bruggen P, Van Der Burg S;

PI Visseren MW;

XX WPI; 1997-558084/51.

DR Induction of cytolytic T cell production in vivo - by administering  
 PT MAGE-2 peptide(s)

XX Example 3; Column 9; 24pp; English.

XX This peptide sequence represents a hepatitis B virus reference peptide  
 CC used in determining the primary induction of the immune response against  
 CC MAGE-2 (a tumour rejection antigen precursor) peptides. Only peptides  
 CC AAW36529-39 have the ability to bind to human leukocyte antigen (HLA)  
 CC A2.1 molecule with high affinity and are therefore the only candidates of  
 CC the MAGE-2 protein to be recognised by human cytolytic T cells (CTL),  
 CC because CTL recognise peptides only when bound to HLA molecules.  
 CC Production of CTL in a subject can be induced by administering a MAGE-2  
 CC peptide (particularly AAW36531, AAW36533 and AAW36537) to a subject who  
 CC presents HLA-A2 molecules on cells. The method can be used to treat  
 CC subjects in need of additional CTL.  
 CC (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 9 AA;

Query Match 22.2%; Score 4; DB 18; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4  
 Db 4 LQPE 7

RESULT 59  
 AAW28811  
 ID AAW28811 standard; peptide; 9 AA.  
 XX  
 AC AAW28811;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 20-NOV-1997 (first entry)  
 XX  
 DE HPV-16 derived peptide (h), recognised by HLA-B35 antigen.  
 XX  
 KW Human papilloma virus; HPV; cervical cancer; diagnosis; epitope;  
 KW human leukocyte antigen; HLA-B35; vaccine; prevention; therapy;  
 KW cytotoxic T lymphocyte.  
 XX  
 OS Human papilloma virus type 16.  
 XX  
 PN JP09188695-A.  
 XX  
 PD 22-JUL-1997.  
 XX  
 PF 02-NOV-1993; 96JP-0220327.  
 XX  
 PR 02-NOV-1993; 93JP-0297378.  
 PR 02-NOV-1993; 93JP-0220327.  
 XX  
 PA (NOKI/) NOKIHARA K.  
 PA (TAKI/) TAKIGUCHI M.  
 XX  
 DR WPI; 1997-420579/39.  
 XX  
 XX  
 PT Synthetic peptide derived from human papilloma virus - is able to  
 PT bind to HLA-B35 antigen and is useful in a vaccine for prevention or  
 PT treatment of cervical cancer  
 XX  
 PS Claim 6; Page 2; 7pp; Japanese.  
 CC  
 CC The present sequence corresponds to amino acids 88-96 of the L1  
 CC antigen of human papilloma virus HPV-16. A synthetic peptide having  
 CC this sequence is shown in cytotoxic T cells by combining with HLA-B35  
 CC antigen. The peptide can be used in a preventive vaccine and a  
 CC therapeutic agent for cervical cancer caused by human papilloma virus.  
 CC (Updated on 25-MAR-2003 to correct PF field.)  
 XX  
 SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 18; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VPKV 11  
 Db 1 VPKV 4

RESULT 60  
 AAW78893  
 ID AAW78893 standard; peptide; 9 AA.  
 XX  
 AC AAW78893;  
 XX  
 DT 17-NOV-1998 (first entry)  
 XX  
 DE Human papillomavirus 16 E7 protein fragment 11-19.  
 XX  
 KW Microparticle; delivery; polymeric matrix; autoantigen; tumour antigen;  
 KW Class II associated peptide; pathogen; gene therapy; genetic disease;  
 KW infection; downregulation; immune response.

XX  
 OS Human papillomavirus.  
 OS Synthetic.  
 XX  
 PN WO9831398-A1.  
 XX  
 PD 23-JUL-1998.  
 XX  
 PF 22-JAN-1998; 98WO-US01499.  
 XX  
 PR 06-JAN-1998; 98US-0003253.  
 PR 22-JAN-1997; 97US-0787547.  
 XX  
 PA (PANG-) PANGAEA PHARM INC.  
 XX  
 PI Curley JM, Hedley ML, Langer RS, Lunsford LB;  
 XX  
 DR WPI; 1998-427556/36.  
 XX  
 PT New preparations of microparticles - comprising a synthetic polymer  
 PT matrix and nucleic acid comprising an expression vector for use in  
 PT gene therapy  
 XX  
 PS Disclosure; Page 10; 101pp; English.  
 XX  
 CC A microparticle preparation (MP) has been developed, consisting of  
 CC microparticles having a diameter of less than 100 nm. The MP  
 CC comprises: (a) a polymeric matrix (PM) consisting of one or more  
 CC synthetic polymers having a solubility in water of less than 1 mg/l; and  
 CC (b) an expression vector selected from RNA molecules (at least 50% of  
 CC which are closed circles) or circular plasmid DNA (at least 50% of  
 CC which are supercoiled). Also described is a MP of at most 20 microns in  
 CC diameter, comprising: (a) a PM; and (b) a NAM comprising an expression  
 CC control sequence operatively linked to a coding sequence, where the  
 CC coding sequence encodes an expression product selected from: (i) a  
 CC polypeptide at least 7 amino acids in length, having a sequence identical  
 CC to the sequence of: (i) a fragment of a naturally-occurring mammalian  
 CC protein; or (ii) a fragment of a naturally-occurring protein from an  
 CC infectious agent which infects a mammal; (2) a peptide having a length  
 CC and sequence which permits it to bind to an MHC class I or II molecule;  
 CC and (3) the polypeptide or the peptide linked to a trafficking sequence.  
 CC AAW69763 to AAW69765, and AAW7893 to AAW7897 are peptide fragments for  
 CC use in the present invention. The MPs are highly effective vehicles for  
 CC the delivery of polynucleotides into phagocytic cells. They can be used  
 CC for gene therapy, e.g. for treating genetic diseases, infections or  
 CC tumours or for downregulating an immune response.  
 XX  
 SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 19; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4  
 Db 5 LQPE 8

RESULT 61  
 AAW54766  
 ID AAW54766 standard; peptide; 9 AA.  
 XX  
 AC AAW54766;  
 XX  
 DT 25-SEP-1998 (first entry)  
 XX  
 DE Peptide from HPV 16 E7 (11-19).  
 XX  
 KW Mannose; antigen; antigen-presenting cell; mannosylated peptide; T cell;  
 KW vaccine; treatment.  
 XX  
 OS Synthetic.  
 XX

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PN WO9813378-A1.
XX
PD 02-APR-1998.
XX
PF 25-SEP-1997; 97WO-NL00536.
XX
PR 26-SEP-1996; 96EP-0202701.
XX
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
PI Drijfhout JW, Koning F;
XX
DR WPI; 1998-230631/20.
XX
XX
PT Increasing uptake and presentation of antigen(s) - by adding mannose
PT residue(s) to antigen for increasing T cell response, useful in,
PT e.g. vaccines against viral infection(s)
XX
XX Disclosure; Page 37; 47pp; English.
XX
CC The peptides AAW54559-W54809 are examples of peptides to which at least
CC 1 (preferably 2) mannose can be attached to increase their uptake as
CC antigens by antigen-presenting cells. Uptake of agonist mannoseylated
CC peptides will increase the T cell response, whereas uptake of antagonist
CC peptides blocks the T cell response. Blocking binding of immunogenic
CC autoantigens can be used in treatment of type I diabetes, rheumatoid
CC arthritis, graft rejection etc.; also to induce T-cell non-
CC responsiveness. Vaccines containing mannoseylated antigen are used to
CC prevent or treat infections by, e.g. bacteria, viruses, fungi, helminths
CC and parasites.
XX
SQ Sequence 9 AA;
XX
XX Query Match 22.2%; Score 4; DB 19; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 LOPE 4
DB |||||
4 LOPE 7
|||

RESULT 63
AAW53466
ID AAW53466 standard; Protein; 9 AA.
XX
AC AAY53466;
XX
XX 18-JAN-2000 (first entry)
XX
XX HIV-1 RT protein (aa 185-193) binds HLA-B*8.
XX
KW Lipopeptide; epitope; cytotoxic T lymphocyte; CTL; lipid; spacer; p53;
KW electrical charge; hydrophilicity; vaccine; immune response; HIV; HBV;
KW human immunodeficiency virus; hepatitis B virus; papilloma virus;
KW melanoma; malaria; parasite.
XX
OS Synthetic.
OS Human immunodeficiency virus type 1.
XX
XX FR2776926-A1.
XX
XX 08-OCT-1999.
XX
XX 07-APR-1998; 98FR-0004323.
XX
XX 07-APR-1998; 98FR-0004323.
XX
XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX (CNRS ) CNRS CENT NAT RECH SCI.
XX (INSP ) INST PASTEUR LILLE.
XX
PI Le Gal FA, Guillet JG, Gahery SH, Gras MH, Melnyk O, Tartar A;
XX
XX WPI; 1999-583113/50.
XX
XX
XX New lipopeptide containing lipid regions and two epitopes, all
XX separated by peptide spacers that impart hydrophilicity, useful in
XX vaccines -
XX
XX Disclosure; Page 21; 35pp; French.
XX
XX The invention relates to the generation of a lipopeptide comprising at
XX least one auxiliary T epitope, at least one cytotoxic T lymphocyte (CTL)
XX epitope and at least one lipid residue with (i) the epitopes and lipid
XX portion and (ii) the epitopes, being separated independently by peptide
XX spacers. These spacers comprise sequences of amino acids which carry an
XX overall electrical charge in neutral media to ensure that the
XX lipopeptide is hydrophilic. The peptides AAY53301-Y53549 represents

```

CC examples of peptide epitopes used to generate the lipopeptides. These are  
 CC used in therapeutic or prophylactic compositions and vaccines to induce  
 CC specific immune responses against human immunodeficiency, hepatitis B or  
 CC papilloma viruses; p53 of melanoma or the malaria parasite.

XX Sequence 9 AA;  
 SQ Query Match 22.2%; Score 4; DB 20; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12  
 Db 2 PKVK 5

RESULT 64  
 AAY55432  
 ID AAY55432 standard; peptide; 9 AA.

XX AC AAY55432;  
 XX DT 17-JAN-2000 (first entry)  
 XX DE HLA binding plu-1 peptide.  
 XX Human; cancer-associated polypeptide; plu-1; ovarian cancer; vaccine;  
 KW breast cancer; immune response; cytotoxic T lymphocyte; imaging agent;  
 KW therapeutic; plu-1 antigen; breast tumor; tumor antigen; epitope.  
 XX Synthetic.  
 OS Homo sapiens.

XX WO9949034-A1.  
 XX 30-SEP-1999.

XX 19-MAR-1999; 99WO-GH00866.

XX 20-MAR-1998; 98GB-0005877.

XX (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.

XX Taylor-papadimitriou J;

XX WPI; 1999-591090/50.

XX New nucleic acid encoding the cancer-associated polypeptide plu-1, for  
 PT diagnosis, treatment and prevention of cancer, especially of breast and  
 PT ovary

XX Example 2; Fig 12; 173pp; English.

XX The invention relates to a human cancer-associated polypeptide plu-1.  
 CC The plu-1 polypeptide can be recombinantly expressed by standard  
 CC recombinant methodology. Detection of the plu-1 nucleic acid or the  
 CC polypeptide is used for the following: (i) diagnosis (including imaging)  
 CC and prognosis of, and determination of susceptibility to, cancer,  
 CC specifically ovarian or breast cancer; and (ii) treating cancer (by  
 CC inducing an immune response against cancer cells, e.g. as a vaccine, or  
 CC by antisense inhibition). Antigens derived from the polypeptide are used  
 CC to generate activated cytotoxic T lymphocytes, or dendritic cells, for  
 CC subsequent return to the patient for treatment of cancer. The polypeptide  
 CC may also be used to identify inhibitors of plu-1 activity. Fragments of  
 CC the polypeptide, and antibodies raised against plu-1, are useful as assay  
 CC and imaging agents, also therapeutically (to induce an anti-idiotype  
 CC response or where conjugated to cytotoxic agents). The plu-1 antigen is  
 CC expressed more commonly in breast tumors than some known tumor antigens.  
 CC Sequences AAY55320-629 represent predicted peptides from the plu-1  
 CC polypeptide which may bind to the human class I alleles B27, A2, A3 and  
 CC A11.

XX Sequence 9 AA;

Query Match 22.2%; Score 4; DB 20; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4  
 Db 2 LQPE 5

RESULT 65  
 AAY40315  
 ID AAY40315 standard; Peptide; 9 AA.

XX AC AAY40315;

XX 19-NOV-1999 (first entry)

XX Amino acid sequence of a HIV-1 epitope.

XX Cytotoxic T cell; T lymphocyte; CD8+ epitope; T helper cell;  
 KW CD4+ epitope; B epitope; lipopeptide; interferon gamma; adjuvant;  
 KW vaccine; tumor; infection; immune response; cytokine profile;  
 KW acquired immune deficiency syndrome; papilloma; cancer; hepatitis;  
 KW autoimmune disease.

XX Human immunodeficiency virus type 1.

XX FR2774687-A1.

XX 13-AUG-1999.

XX 06-FEB-1998; 98FR-0001439.

XX 06-FEB-1998; 98FR-0001439.

XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.

XX (INSP ) INST PASTEUR LILLE.

XX Thiam K, Guillet JG, Ver Waerde C, Auriault C, Gras MH, Loing E;

XX WPI; 1999-510734/43.

XX New lipopeptide comprising C-terminal interferon-gamma fragment with  
 PT attached lipophilic groups, used as interferon mimic, e.g. for treating  
 PT cancer or virus infection

XX Disclosure; Page 39; 53pp; French.

XX AAY40123-Y40379 represent epitopes that are able to activate cytotoxic  
 CC T lymphocytes (CD8+ epitopes), T helper cells (CD4+ epitopes), or  
 CC B epitopes recognized by corresponding antibodies. The epitopes may be  
 CC used in the composition of the invention. The specification describes a  
 CC lipopeptide that has a peptide part derived from mammalian interferon  
 CC gamma (IFNg) and one or more lipophilic parts comprising a linear or  
 CC branched, (unsaturated 4-20C hydrocarbyl chain or a steroid. The  
 CC lipopeptide mimics the activity of IFNg. Compositions comprising the  
 CC lipopeptide are used to treat or prevent any condition that responds  
 CC to IFNg, and as adjuvant for vaccines (particularly those directed  
 CC against tumors, viral or parasitic infections), to stimulate or  
 CC (re)orient the immune response between types 1 and 2 cytokine profiles.  
 CC Particular applications are treatment of infections (particularly  
 CC viral, e.g. acquired immune deficiency syndrome, papilloma (cancer) and  
 CC hepatitis, but also bacterial, fungal, parasitic or helminth); cancers  
 CC (particularly of kidney, cutaneous T cells or ovary, chronic  
 CC myelogenous leukemia or mesothelioma), allergy; and autoimmune  
 CC diseases.

XX Sequence 9 AA;

Query Match 22.2%; Score 4; DB 20; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12  
Db ||||  
2 PKVK 5

RESULT 66  
AAV26807  
ID AAV26807 standard; peptide; 9 AA.  
XX  
AC AAY26807;  
XX  
XX 14-SEP-1999 (first entry)  
XX  
DE HIV-derived lipopeptide epitope #77 for mixed micelles.  
XX  
KW Micelle; microaggregate; induction; immune response; lipopeptide; CTL;  
KW cytotoxic T-lymphocyte; epitope; lipid; helper T-lymphocyte; HTL; HBV;  
KW tetanus; toxin; vaccine; HIV; hepatitis B virus; papilloma virus; p53;  
KW melanoma; Plasmodium falciparum; malaria.  
XX  
XX Synthetic.  
OS Human immunodeficiency virus type 1.  
XX  
XX FR2771640-A1.  
XX  
XX 04-JUN-1999.  
XX  
XX 03-DEC-1997; 97FR-0015246.  
XX  
XX 03-DEC-1997; 97FR-0015246.  
XX  
XX (CNRS ) CNRS CENT NAT RECH SCI.  
PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
PA (INSP ) INST PASTEUR LILLE.  
XX  
XX Bossus M, Bourgault VI, Gras-Masse H, Guillet JG, Lippens G;  
PI Tartar A, Wieruszkeski JM;  
PI  
DR WPI; 1999-349509/30.  
XX  
XX Immunogenic lipopeptide micelles - comprising lipopeptides  
PT containing cytotoxic and helper T-lymphocyte epitopes  
PT  
XX  
XX Disclosure; Page 34; 60pp; French.  
XX  
XX The invention relates to the generation of mixed micelles or  
CC microaggregates for inducing an immune response comprise: (a) a first  
CC lipopeptide comprising at least one CTL (cytotoxic T-lymphocyte) epitope  
CC and at least one lipid unit; and (b) a second lipopeptide comprising at  
CC least one HTL (helper T-lymphocyte) epitope and at least one lipid unit  
CC different from that of the first lipopeptide. This peptide represents  
CC an example of a lipopeptide epitope used in the invention and is derived  
CC from a human immunodeficiency virus type 1 (HIV-1) protein. The  
CC immunogenic lipopeptide micelles are used in vaccines, especially  
CC against HIV, hepatitis B virus (HBV), papilloma viruses, p53, melanoma  
CC or Plasmodium falciparum malaria.  
XX  
SQ Sequence 9 AA;  
Query Match 22.2%; Score 4; DB 20; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12  
Db ||||  
2 PKVK 5

RESULT 67  
AAV10346  
ID AAV10346 standard; peptide; 9 AA.  
XX

AC AAY10346;  
XX  
XX 12-MAY-1999 (first entry)  
XX  
DE T cell epitope/MHC ligand SEQ ID NO:276.  
XX  
KW Cytotoxic T-lymphocyte response; CTL; antigen; lymphatic system;  
KW immunisation; tumour; infectious disease; immunotherapy; cancer;  
KW malignant melanoma; viral disease; hepatitis; AIDS.  
XX  
XX Synthetic.  
OS Human papillomavirus.  
XX  
XX WO9902183-A2.  
XX  
XX 21-JAN-1999.  
XX  
XX 10-JUL-1998; 98WO-US14289.  
XX  
XX 10-DEC-1997; 97US-0988320.  
XX  
XX 10-JUL-1997; 97CA-2209815.  
XX  
XX (CTLI-) CTL IMMUNOTHERAPIES CORP.  
XX  
XX Kuendig TM, Simard JUL;  
XX  
XX WPI; 1999-120514/10.  
XX  
XX Inducing a cytotoxic T lymphocyte response - by maintaining a level  
PT of antigen in the lymphatic system of a mammal so as to provide a  
PT sustained CTL response, used to treat, e.g. AIDS  
XX  
XX Disclosure; Page 34; 199pp; English.  
XX  
XX The present invention describes a method of inducing and/or sustaining  
CC an immunological cytotoxic T lymphocyte (CTL) response in a mammal. The  
CC method comprises: (a) delivering an antigen to the mammal at a level to  
CC induce an immunological CTL response in the mammal; and (b) maintaining  
CC the level of the antigen in the mammal's lymphatic system to maintain  
CC the immunologic CTL response. The method can be used for the delivery of  
CC e.g. a differentiation antigen, a tumour-specific multilineage antigen,  
CC an embryonic antigen, an oncogene antigen, a mutated tumour-suppressor  
CC gene antigen, or a viral antigen. They can be used for the treatment of  
CC disease such as cancer, e.g. malignant melanoma or infectious disease,  
CC e.g. viral disease such as hepatitis or AIDS. Sustained antigen delivery  
CC to the lymphatic system provides for potent CTL stimulation that takes  
CC place in the milieu of the lymphoid organ, and it sustains stimulation  
CC that is necessary to keep CTL active, cytotoxic and recirculating  
CC through the body. AAY10071 to AAY10639 represent examples of peptide  
CC antigens given in the present invention.  
XX  
SQ Sequence 9 AA;  
Query Match 22.2%; Score 4; DB 20; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4  
Db ||||  
4 LQPE 7

RESULT 68  
AAV10511  
ID AAY10511 standard; Peptide; 9 AA.  
XX  
XX AAY10511;  
XX  
XX 12-MAY-1999 (first entry)  
XX  
XX HLA Class I motif peptide SEQ ID NO:441.  
XX  
XX Cytotoxic T-lymphocyte response; CTL; antigen; lymphatic system;

KW immunisation; tumour; infectious disease; immunotherapy; cancer;  
 XX malignant melanoma; viral disease; hepatitis; AIDS.

OS Synthetic.  
 OS Human papillomavirus.

XX WO9902183-A2.

XX 21-JAN-1999.

XX 10-JUL-1998; 98WO-US14289.

XX 10-DEC-1997; 97US-0988320.

XX 10-JUL-1997; 97CA-2209815.

XX (CTL1-) CTL IMMUNOTHERAPIES CORP.

XX Kuendig TM, Simard JUL;

XX WPI; 1999-120514/10.

XX Inducing a cytotoxic T lymphocyte response - by maintaining a level  
 PT of antigen in the lymphatic system of a mammal so as to provide a  
 PT sustained CTL response, used to treat, e.g. AIDS

XX Disclosure; Page 44; 199pp; English.

CC The present invention describes a method of inducing and/or sustaining  
 CC an immunological cytotoxic T lymphocyte (CTL) response in a mammal. The  
 CC method comprises: (a) delivering an antigen to the mammal at a level to  
 CC induce an immunological CTL response in the mammal; and (b) maintaining  
 CC the level of the antigen in the mammal's lymphatic system to maintain  
 CC the immunologic CTL response. The method can be used for the delivery of  
 CC e.g. a differentiation antigen, a tumour-specific multineage antigen,  
 CC an embryonic antigen, an oncogene antigen, a mutated tumour-suppressor  
 CC gene antigen, or a viral antigen. They can be used for the treatment of  
 CC disease such as cancer, e.g. malignant melanoma or infectious disease,  
 CC e.g. viral disease such as hepatitis or AIDS. Sustained antigen delivery  
 CC to the lymphatic system provides for potent CTL stimulation that takes  
 CC place in the milieu of the lymphoid organ, and it sustains stimulation  
 CC that is necessary to keep CTL active, cytotoxic and recirculating  
 CC through the body. AAY10071 to AAY10639 represent examples of peptide  
 CC antigens given in the present invention.

XX Sequence 9 AA;

Query Match 22.2%; Score 4; DB 20; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4  
 ||||  
 Db 4 LQPE 7

RESULT 69

AAB33705

ID AAB33705 standard; Peptide; 9 AA.

XX AAB33705;

XX 26-JAN-2001 (first entry)

XX MHC class I associated immunogenic peptide SEQ ID 104.

XX Microparticle; nucleic acid delivery; immunogenic peptide; MHC I; MHC II;  
 KW major histocompatibility complex; vaginal tissue; mucosal tissue..

XX Unidentified.

XX WO200053161-A2.

XX 14-SEP-2000.

XX 10-MAR-2000; 2000WO-US06578.

XX 11-MAR-1999; 99US-0266463.

XX 27-MAY-1999; 99US-0321346.

XX (ZYCO-) ZYCO INC.

XX Lunsford LB, Putnam D, Hedley ML;

XX WPI; 2000-638130/61.

XX Microparticles useful for administering a nucleic acid into the mucosal  
 PT tissue preferably vaginal tissue of an animal, comprises a polymeric  
 PT matrix, a lipid and a nucleic acid molecule -

XX Disclosure; Page 16; 96pp; English.

CC The present invention relates to microparticles which are less than 20  
 CC microns in diameter, which comprise a polymeric matrix, a lipid and a  
 CC nucleic acid molecule. The microparticle is specifically not  
 CC encapsulated in a liposome and does not comprise a cell. The nucleotide  
 CC sequence encodes an expression product that binds to major  
 CC histocompatibility complex (MHC) type I or II molecules. Peptides  
 CC AAB33602-B33647 represent MHC class I associated immunogenic peptides,  
 CC and AAB33648-B33710 represent MHC class II associated immunogenic  
 CC peptides. The peptides are examples of the expression products of the  
 CC nucleotide sequences which can be included in the microparticles of the  
 CC invention. Sequences AAB33711-B33716 represent alternative expression  
 CC products and nuclear localisation signals also used in the invention. The  
 CC microparticles are useful for administering a nucleic acid into the  
 CC mucosal tissue preferably vaginal tissue of an animal.

XX Sequence 9 AA;

Query Match 22.2%; Score 4; DB 21; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4  
 ||||  
 Db 5 LQPE 8

RESULT 70

AAB18492

ID AAB18492 standard; peptide; 9 AA.

XX AAB18492;

XX 15-JAN-2001 (first entry)

XX Peptide substrate used to test prolyl-tripeptidyl peptidase activity.

XX Prolyl tripeptidyl-peptidase; amidolytic activity; periodontal disease;  
 KW gingivitis; periodontitis.

XX Synthetic.

XX Key Location/Qualifiers  
 FT Modified-site 1 /note= "hydrogen attached"

XX WO200052147-A2.

XX 08-SEP-2000.

XX 03-MAR-2000; 2000WO-US05551.

XX 05-MAR-1999; 99US-0123148.

XX (UYGE-) UNIV GEORGIA RES FOUND INC.  
 PA (TRAV/) TRAVIS J.

PA (POTE/) POTEIPA J.  
 XX (BANB/) BANBULA A.  
 PI Travis J, Potempa J, Banbula A;  
 XX WPI; 2000-594181/56.  
 DR  
 XX Prolyl tripeptidyl-peptidase, active analog, fragment or variant useful  
 PT for identifying its inhibitor which is useful for protecting an animal  
 PT from a periodontal disease such as gingivitis and periodontitis -  
 XX  
 PS Claim 3; Page 37; 58pp; English.  
 XX  
 CC The present sequence represents a substrate which was used to test  
 CC the activity of prolyl tripeptidyl-peptidases PTP-A and DPP IV. The  
 CC prolyl tripeptidyl-peptidase has an amidolytic activity, and cleaves  
 CC a peptide bond in a target polypeptide having at least 4 amino acids.  
 CC This bond is between a proline and an amino acid attached to the  
 CC alpha-carboxyl group end of the proline. The polypeptide is useful for  
 CC identifying inhibitors. These inhibitors are then useful for reducing  
 CC the growth of bacterium or for protecting an animal from a periodontal  
 CC disease such as gingivitis and periodontitis caused by Porphyromonas  
 CC gingivalis.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 22.2%; Score 4; DB 21; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 GVPK 10  
 Db |||||  
 1 GVPK 4  
 RESULT 71  
 AAY96941  
 ID AAY96941 standard; peptide; 9 AA.  
 XX  
 AC AAY96941;  
 XX  
 DT 31-OCT-2000 (first entry)  
 XX  
 DE Processed N-terminal peptide of human IL-1RAIL and IL-1RAIV.  
 KW hIL-1RAIL; human interleukin-1 receptor antagonist-1 long; IL-1lp;  
 KW osteopathic; interleukin-1-like polypeptide; anti-inflammatory;  
 KW anti-asthmatic; anti-arthritis; antimicrobial; respiratory; vaccine;  
 KW anti-ischemic; dermatological; immunomodulatory; gastrointestinal;  
 KW gene therapy; N-terminal.  
 XX  
 CS Homo sapiens.  
 XX  
 PN WO200039297-A2.  
 XX  
 PD 06-JUL-2000.  
 XX  
 PF 22-DEC-1999; 99WO-US0720.  
 XX  
 PR 23-DEC-1998; 98US-0113430.  
 PR 22-JAN-1999; 99US-0116943.  
 PR 13-APR-1999; 99US-0129122.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Goddard A, Pan J;  
 XX  
 DR WPI; 2000-452395/39.  
 XX  
 CC Nucleic acids encoding interleukin-1-like polypeptides, useful for  
 PT preventing and treating e.g. inflammation, asthma and psoriasis  
 XX  
 PS Example 14; Page 94; 143pp; English.

XX An isolated nucleic acid molecule encoding an interleukin-1-like  
 CC polypeptide (IL-1lp) that retains one or more activities of the peptide  
 CC from which it is derived, such as the IL-18R binding activity of a human  
 CC interleukin-1 receptor antagonist-1 (hIL-1RAI) polypeptide, is new. The  
 CC nucleic acids may be used in molecular engineering applications, e.g.  
 CC hybridization assays and chromosome and gene mapping studies, for  
 CC recombinantly producing the IL-1lp polypeptide or for producing gene  
 CC knock out animals to study the role of the protein in metabolism and  
 CC disease processes (conversely, gene therapy protocols may be used to  
 CC supplement a patient's production of the polypeptide or to rectify  
 CC mutations that lead to the production of in active peptides). The  
 CC peptides produced may be used to screen for and produce modulators (e.g.  
 CC antibodies) of IL-1lp protein expression and activity which may be use  
 CC to treat disorders associated with inappropriate IL-1lp expression and  
 CC activity, such as inflammatory disorders, asthma, arthritis,  
 CC osteoarthritis, sepsis, acute lung injury, adult respiratory distress  
 CC syndrome, idiopathic pulmonary fibrosis, ischemic reperfusion disease,  
 CC psoriasis, graft versus host disease and/or inflammatory bowel disease.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 22.2%; Score 4; DB 21; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 9 PKVK 12  
 Db |||||  
 5 PKVK 8  
 RESULT 72  
 AAY66364  
 ID AAY66364 standard; Peptide; 9 AA.  
 XX  
 AC AAY66364;  
 XX  
 DT 22-FEB-2000 (first entry)  
 XX  
 DE HLA-B7-binding HIV-1 Pol peptide #166.  
 XX  
 KW HIV-1; MHC; major histocompatibility complex; Class I; HLA;  
 KW human leukocyte antigen; allele; binding; conserved; genome;  
 KW peptide; targeting; toxic; drug; antibody; antigen; antiviral;  
 KW molecular conjugate therapeutic; diagnosis; treatment; pathogen;  
 KW localisation; quantification; detection; infection; drug resistance;  
 KW immune response.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 PN WO9949893-A1.  
 XX  
 PD 07-OCT-1999.  
 XX  
 PF 31-MAR-1999; 99WO-US07111.  
 XX  
 PR 31-MAR-1998; 98US-0052530.  
 XX  
 PA (UYBO-) UNIV BOSTON.  
 XX  
 PI Delisi C, Berzofsky J, Gulukota K, Vaccaro D, Weng Z, Zhang C;  
 XX  
 DR WPI; 2000-038361/03.  
 XX  
 PT Novel methods for designing molecular conjugate therapeutics which are  
 PT used for diagnosis, imaging and treatment against pathogens -  
 XX  
 PS Example 3; Page 45; 62pp; English.  
 XX  
 CC AAY66199-Y66413 are peptides derived from conserved portions of the  
 CC HIV-1 genome which bind to different HLA alleles of MHC (major  
 CC histocompatibility complex) Class I molecules. The peptides are used to  
 CC construct targetting antigens comprising one or more peptides bound to

the corresponding MHC Class I molecule, which can be used to raise antibodies. The antibody may then be used as a targeting vehicle to deliver a potentially toxic drug to its target site of action, rather than administering it systemically, which may result in adverse side effects. The invention relates to improved methods for the design of molecular conjugate therapeutics for the diagnosis and treatment of HIV-1. This method involves identifying conserved peptide-encoding regions among the genomes of multiple variants of a pathogen, identifying the Class I MHC molecules which occur with greatest frequency in a population of interest (e.g., human sub-populations), and determining which of the peptides bind to the Class I MHC molecules. The MHC-binding peptides and the corresponding Class I MHC molecules are selected and used to construct targeting antigens, which are in turn used to produce quantification and in situ detection of specific peptide-MHC Class I complexes and also to detect and treat viral infection. The methods of the invention mitigate against the development of viral resistance for drugs and to the immune response, as well as providing a solution for targeting toxic compounds to destroy viruses sequestered in sites not accessible to T cells. In addition, the methods eliminate the virus, whereas current therapies only arrest viral replication.

Sequence 9 AA;  
Query Match 22.2%; Score 4; DB 21; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12  
|||  
Db 2 PKVK 5

## RESULT 73

AAV66378  
ID AAY66378 standard; Peptide; 9 AA.

AC AAY66378;

DT 22-FEB-2000 (first entry)

XX HLA-B8-Binding HIV-1 Pol peptide #180.

XX HIV-1; MHC; major histocompatibility complex; Class I; HLA;  
KW human leukocyte antigen; allele; binding; conserved; genome;  
KW peptide; targeting; toxic; drug; antibody; antigen; antiviral;  
KW molecular conjugate therapeutic; diagnosis; treatment; pathogen;  
KW localisation; quantification; detection; infection; drug resistance;  
KW immune response.

XX Human immunodeficiency virus type 1.

XX WO9949893-A1.

XX 07-OCT-1999.

XX 31-MAR-1999; 99WO-US07111.

XX 31-MAR-1998; 98US-0052530.

XX (UYBO-) UNIV BOSTON.

XX Delisi C, Berzofsky J, Gulukota K, Vaccaro D, Wang Z, Zhang C;

XX WPI; 2000-038361/03.

XX Novel methods for designing molecular conjugate therapeutics which are used for diagnosis, imaging and treatment against pathogens

XX Example 3; Page 46; 62pp; English.

XX AAY66199-Y66413 are peptides derived from conserved portions of the

CC HIV-1 genome which bind to different HLA alleles of MHC (major  
CC histocompatibility complex) Class I molecules. The peptides are used to  
CC construct targeting antigens comprising one or more peptides bound to  
CC the corresponding MHC Class I molecule, which can be used to raise  
CC antibodies. The antibody may then be used as a targeting vehicle to  
CC deliver a potentially toxic drug to its target site of action, rather  
CC than administering it systemically, which may result in adverse side  
CC effects. The invention relates to improved methods for the design of  
CC molecular conjugate therapeutics for the diagnosis and treatment of  
CC infections caused by pathogens with a high mutation rate (such as  
CC HIV-1). This method involves identifying conserved peptide-encoding  
CC regions among the genomes of multiple variants of a pathogen, identifying  
CC the Class I MHC molecules which occur with greatest frequency in a  
CC population of interest (e.g., human sub-populations), and determining  
CC which of the peptides bind to the Class I MHC molecules. The MHC-binding  
CC peptides and the corresponding Class I MHC molecules are selected and  
CC used to construct targeting antigens, which are in turn used to produce  
CC quantification and in situ detection of specific peptide-MHC Class I  
CC targeting antibodies. The methods may be used in localisation,  
CC quantification and in situ detection of specific peptide-MHC Class I  
CC complexes and also to detect and treat viral infection. The methods of  
CC the invention mitigate against the development of viral resistance to  
CC drugs and to the immune response, as well as providing a solution for  
CC targeting toxic compounds to destroy viruses sequestered in sites not  
CC accessible to T cells. In addition, the methods eliminate the virus,  
CC whereas current therapies only arrest viral replication.

Sequence 9 AA;

Query Match 22.2%; Score 4; DB 21; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12  
|||  
Db 2 PKVK 5

## RESULT 74

ABP11796  
ID ABP11796 standard; Peptide; 9 AA.

XX AC ABP11796;

XX 15-JUL-2002 (first entry)

XX HIV A01 super motif pol peptide #68.

XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
KW vpr; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
KW antigen; vaccine; HIV infection; immunisation; virucide.

XX Human immunodeficiency virus type 1.

XX WO200124810-A1.

XX 12-APR-2001.

XX 05-OCT-2000; 2000WO-US27766.

XX 05-OCT-1999; 99US-0412863.

XX (EPIM-) EPIMMUNE INC.

XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

XX Baker DM, Celis E, Kubo RT, Grey HM;

XX WPI; 2001-354887/37.

XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)

XX peptide groups, useful for vaccinating against HIV-1

XX Claim 32; Page 110; 448pp; English.



CC The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.

XX SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12

Db 5 PKVK 8

RESULT 75

ABP16116

ID ABP16116 standard; Peptide; 9 AA.

XX AC ABP16116;

XX DT 15-JUL-2002 (first entry)

XX XX HIV A24 super motif pol peptide #296.

XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;

XX KW vpu; vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;

XX KW antigen; vaccine; HIV infection; immunisation; virucide.

XX OS Human immunodeficiency virus type 1.

XX PN WC200124810-A1.

XX XX 12-APR-2001.

XX PF 05-OCT-2000; 2000WO-US27766.

XX PR 05-OCT-1999; 99US-0412863.

XX PA (EPIM-) EPIMMUNE INC.

XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

XX PI Baker DM, Cellis E, Kubo RT, Grey HM;

XX DR WPI; 2001-354887/37.

XX XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)

PT peptide groups, useful for vaccinating against HIV-1 -

XX PS Claim 32; Page 198; 448pp; English.

XX .

CC The present invention describes a composition (I) comprising a prepared

CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid

CC sequence selected from 51 defined amino acid sequences (ABL25347 to

CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.

XX SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12

Db 5 PKVK 8

Search completed: November 25, 2003, 19:27:08

Job time : 46.9419 secs

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OM protein - protein search, using sw model  
  
Run on: November 25, 2003, 20:25:48 ; Search time 28.9837 Seconds  
(without alignments)  
114.943 Million cell updates/sec

89 4 22.2 16 12 US-10-387-645-6 Sequence 6, Appli  
90 4 22.2 16 12 US-10-387-645-7 Sequence 7, Appli  
91 4 22.2 16 12 US-10-161-791-344 Sequence 344, App  
92 4 22.2 16 12 US-10-350-405-114 Sequence 114, App  
93 4 22.2 16 12 US-10-350-405-227 Sequence 227, App  
94 4 22.2 17 15 US-10-218-743-10 Sequence 10, Appl  
95 4 22.2 17 15 US-10-225-567A-1531 Sequence 1531, Ap  
96 4 22.2 18 12 US-09-569-197-8 Sequence 8, Appli  
97 4 22.2 18 12 US-10-016-986-173 Sequence 173, App  
98 4 22.2 19 12 US-10-029-386-32381 Sequence 32381, A  
99 4 22.2 19 15 US-10-225-567A-1545 Sequence 1545, Ap  
100 4 22.2 19 15 US-10-163-198-88 Sequence 88, Appl

ALIGNMENTS

RESULT 1  
US-10-281-652-21  
; Sequence 21, Application US/10281652  
; Publication No. US20030091606A1  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/10/281,652  
; PRIOR FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US/09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-10-281-652-21

Query Match 100.0%; Score 18; DB 15; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.9e-12;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPEIMGVVKVKTMTVPK 18  
Db 1 LOPEIMGVVKVKTMTVPK 18

RESULT 2  
US-09-789-561-163  
; Sequence 163, Application US/09789561  
; Patent No. US20020064818A1  
; GENERAL INFORMATION:  
; APPLICANT: NI et al.  
; TITLE OF INVENTION: 52 Human secreted proteins  
; FILE REFERENCE: PZ043PI  
; CURRENT APPLICATION NUMBER: US/09/789,561  
; CURRENT FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: PCT/US00/24008  
; PRIOR FILING DATE: 2000-08-31  
; PRIOR APPLICATION NUMBER: 60/152,317  
; PRIOR FILING DATE: 1999-09-03  
; PRIOR APPLICATION NUMBER: 60/152,315  
; PRIOR FILING DATE: 1999-09-03  
; NUMBER OF SEQ ID NOS: 194  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 163

; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-789-561-163

Query Match 27.8%; Score 5; DB 9; Length 12;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GVPKV 11  
Db 1 GVPKV 5

RESULT 3  
US-08-908-884-22  
; Sequence 22, Application US/08908884  
; Publication No. US20020138872A1  
; GENERAL INFORMATION:  
; APPLICANT: Dong et al.  
; TITLE OF INVENTION: ACQUIRED RESISTANCE GENES AND USES THEREOF  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Clark & Elbing LLP  
; STREET: 176 Federal Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/908,884  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/023,851  
FILING DATE: August 9, 1996  
APPLICATION NUMBER: 60/035,166  
FILING DATE: January 10, 1997  
APPLICATION NUMBER: 60/046,769  
FILING DATE: May 16, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Elbing, Karen L  
REGISTRATION NUMBER: 35,238  
REFERENCE/DOCKET NUMBER: 00786/339004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-428-0200  
TELEFAX: 617-428-7045  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-908-884-22

Query Match 27.8%; Score 5; DB 8; Length 14;  
Best Local Similarity 100.0%; Pred. No. 65;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VPKVK 12  
Db 9 VPKVK 13

RESULT 4  
US-09-908-323-22  
; Sequence 22, Application US/09908323

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; Patent No. US20020073447A1
; GENERAL INFORMATION:
; APPLICANT: Dong et al.
; TITLE OF INVENTION: ACQUIRED RESISTANCE GENES AND USES THEREOF
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/908,323
; FILING DATE: 17-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/908,884
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 60/035,166
; FILING DATE: January 10, 1997
; APPLICATION NUMBER: 60/046,769
; FILING DATE: May 16, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Elbing, Karen L.
; REGISTRATION NUMBER: 35,238
; REFERENCE/DOCKET NUMBER: 00786/339004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-908-323-22

Query Match      27.8%; Score 5; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 VPKVK 12
Db      9 VPKVK 13
      |||||
      |||||

RESULT 5
US-10-225-567A-1251
; Sequence 1251, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1251
; LENGTH: 16
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1251

Query Match      27.8%; Score 5; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      9 PKVKE 13
Db      2 PKVKE 6
      |||||
      |||||

RESULT 6
US-10-225-567A-1282
; Sequence 1282, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPT
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1282
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1282

Query Match      27.8%; Score 5; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      9 PKVKE 13
Db      8 PKVKE 12
      |||||
      |||||

RESULT 7
US-10-280-066-315
; Sequence 315, Application US/10280066
; Publication No. US20030180718A1
; GENERAL INFORMATION:
; APPLICANT: Pillutla, Renuka C.
; APPLICANT: Brissette, Renee
; APPLICANT: Spruyt, Michael
; APPLICANT: Dedova, Olga
; APPLICANT: Blume, Arthur J.
; APPLICANT: Prendergast, John
; APPLICANT: Goldstein, Neil I.
; TITLE OF INVENTION: TARGET SPECIFIC SCREENING AND ITS USE FOR IDENTIFYING TARGET B
; FILE REFERENCE: 2598-4009US1
; CURRENT APPLICATION NUMBER: US/10/280,066
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 60/345,471
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 537
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 315
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Eschericia coli
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: DGIS-20M-4-A9
US-10-280-066-315
```

Query Match 27.8%; Score 5; DB 12; Length 20;  
Best Local Similarity 100.0%; Pred. No. 88;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 6 MGVPK 10  
|  
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|  
|  
|  
Db 14 MGVPK 18  
  
RESULT 8  
US-09-985-357A-12  
; Sequence 12, Application US/09985357A  
; Patent No. US20020110913A1  
; GENERAL INFORMATION:  
; APPLICANT: Anne STERN; Michael BRANDT; Konrad HONOLD; Johannes AUER; Hans KOLL  
; TITLE OF INVENTION: Preparation of erythropoietin by endogenous gene activation  
; FILE REFERENCE: HUBR 1151.1 CON PFF/MAS  
; CURRENT APPLICATION NUMBER: US/09/985,357A  
; CURRENT FILING DATE: 2001-11-02  
; PRIOR APPLICATION NUMBER: US 09/463,380  
; PRIOR FILING DATE: 2000-01-21  
; PRIOR APPLICATION NUMBER: PCT/EP98/04590  
; PRIOR FILING DATE: 1998-07-22  
; PRIOR APPLICATION NUMBER: US 09/113,692  
; PRIOR FILING DATE: 1998-07-10  
; PRIOR APPLICATION NUMBER: DE 19753681.1  
; PRIOR FILING DATE: 1997-12-03  
; PRIOR APPLICATION NUMBER: EP 97112640  
; PRIOR FILING DATE: 1997-07-23  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Wordperfect  
; SEQ ID NO 12  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Amino acid sequence of the modified signal peptide start coded by  
; OTHER INFORMATION: EX5  
US-09-985-357A-12

Query Match 22.2%; Score 4; DB 10; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 6 MGVP 9  
|  
|  
|  
|  
|  
Db 1 MGVP 4

RESULT 9  
US-10-353-767-12  
; Sequence 12, Application US/10353767  
; Publication No. US20030166275A1  
; GENERAL INFORMATION:  
; APPLICANT: KOLL  
; APPLICANT: Anne STERN; Michael BRANDT; Konrad HONOLD; Johannes AUER; Hans  
; TITLE OF INVENTION: Preparation of erythropoietin by endogenous gene  
; FILE REFERENCE: HUBR 1151.1 CON PFF/MAS  
; CURRENT APPLICATION NUMBER: US/10/353,767  
; CURRENT FILING DATE: 2003-01-29  
; PRIOR APPLICATION NUMBER: US/09/985,357A  
; PRIOR FILING DATE: 2001-11-12  
; PRIOR APPLICATION NUMBER: US 09/463,380  
; PRIOR FILING DATE: 2000-01-21  
; PRIOR APPLICATION NUMBER: PCT/EP98/04590  
; PRIOR FILING DATE: 1998-07-22  
; PRIOR APPLICATION NUMBER: US 09/113,692  
; PRIOR FILING DATE: 1998-07-10  
; PRIOR APPLICATION NUMBER: DE 19753681.1  
; PRIOR FILING DATE: 1997-12-03  
; PRIOR APPLICATION NUMBER: EP 97112640

; PRIOR FILING DATE: 1997-07-23  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Wordperfect  
; SEQ ID NO 12  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Amino acid sequence of the modified signal peptide  
; OTHER INFORMATION: start coded by primer  
; OTHER INFORMATION: EX5  
US-10-353-767-12

Query Match 22.2%; Score 4; DB 12; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 MGVP 9  
|  
|  
|  
|  
|  
Db 1 MGVP 4

RESULT 10  
US-10-302-817A-46  
; Sequence 46, Application US/10302817A  
; Publication No. US20030198978A1  
; GENERAL INFORMATION:  
; APPLICANT: ROZZELLE, James  
; APPLICANT: BOLCHAKOVA, Elena  
; TITLE OF INVENTION: THERMUS BROCKIANUS NUCLEIC ACID POLYMERASES  
; FILE REFERENCE: 4768US  
; CURRENT APPLICATION NUMBER: US/10/302,817A  
; CURRENT FILING DATE: 2002-11-22  
; PRIOR APPLICATION NUMBER: 60/334,434  
; PRIOR FILING DATE: 2001-11-30  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 46  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Thermus brockianus  
US-10-302-817A-46

Query Match 22.2%; Score 4; DB 12; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12  
|  
|  
|  
|  
|  
Db 2 PKVK 5

RESULT 11  
US-09-045-020-14  
; Sequence 14, Application US/09045020  
; Patent No. US20020025942A1  
; GENERAL INFORMATION:  
; APPLICANT: Ingram, Vernon M., Roder, Hanno M.  
; TITLE OF INVENTION: No. US20020025942A1e1 Tau/Neurofilament Protein  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Massachusetts Institute of Technology  
; STREET: 28 Carleton Street  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: United States of America  
; ZIP: 02142  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch  
; COMPUTER: IBM-compatible  
; OPERATING SYSTEM: MS-DOS Version 3.3  
; SOFTWARE: WordPerfect 5.1

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/045,020
; FILING DATE: 20-Mar-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/480,793
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: 07/912,293
; FILING DATE: July 10, 1992
; APPLICATION NUMBER: 07/742,880
; FILING DATE: 9-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Gates, Edward R.
; REGISTRATION NUMBER: 31,616
; REFERENCES/DOCKET NUMBER: M0656/7008
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 14
US-09-045-020-14
Query Match 22.2%; Score 4; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PEIM 6
Db 2 PEIM 5

RESULT 12
US-10-281-652-16
; Sequence 16, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265, 002201.01
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 7
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-16
Query Match 22.2%; Score 4; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQPE 4
Db 4 LQPE 7

RESULT 13
US-08-344-824-33
; Sequence 33, Application US/08344824
```

```
; Publication No. US20030152580A1
; GENERAL INFORMATION:
; APPLICANT: SETTE, Alessandro
; APPLICANT: SIDNEY, John
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
; NUMBER OF SEQUENCES: 399
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Street Tower, 20th
; STREET: Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,824
; FILING DATE: 23-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,634
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-80-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-344-824-33
Query Match 22.2%; Score 4; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PKVK 12
Db 2 PKVK 5

RESULT 14
US-08-344-824-118
; Sequence 118, Application US/08344824
; Publication No. US20030152580A1
; GENERAL INFORMATION:
; APPLICANT: SETTE, Alessandro
; APPLICANT: SIDNEY, John
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
; NUMBER OF SEQUENCES: 399
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Street Tower, 20th
; STREET: Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
```

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,824
; FILING DATE: 23-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,634
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-80-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 118:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-344-824-118

Query Match      22.2%; Score 4; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
Db 2 PKVK 5

RESULT 15
US-08-452-843A-2
; Sequence 2, Application US/08452843A
; Publication No. US20020098197A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; TITLE OF INVENTION: HLA Binding Peptides and Their Uses
; FILE REFERENCE: 399632001321
; CURRENT APPLICATION NUMBER: US/08/452,843A
; CURRENT FILING DATE: 1995-05-03
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Y1 analog of 1054.05
; US-08-452-843A-2

Query Match      22.2%; Score 4; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
Db 2 PKVK 5

RESULT 16
US-09-759-960-17
; Sequence 17, Application US/09759960
; Patent No. US20010006639A1
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.

```

```

; APPLICANT: Collins, Edward J.
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/759,960
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/169,425
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/004002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-543-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-759-960-17

Query Match      22.2%; Score 4; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4
Db 5 LQPE 8

RESULT 17
US-09-909-460-104
; Sequence 104, Application US/09909460
; Publication No. US20020182258A1
; GENERAL INFORMATION:
; APPLICANT: Lunsford, Lynn B.
; APPLICANT: Putnam, David
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY OF NUCLEIC
; TITLE OF INVENTION: ACID
; FILE REFERENCE: 08191/014001
; CURRENT APPLICATION NUMBER: US/09/909,460
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/321,346
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 104
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus
; US-09-909-460-104

Query Match      22.2%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;

```

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4  
|||||  
Db 5 LOPE 8

## RESULT 18

US-09-942-052-33  
; Sequence 33, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Faris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85PIB3  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 33  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-33

Query Match 22.2%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4  
|||||  
Db 2 LOPE 5

## RESULT 19

US-09-942-052-39  
; Sequence 39, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Faris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85PIB3  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn ver. 2.1  
; SEQ ID NO 39  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-39

Query Match 22.2%; Score 4; DB 12; Length 9;

Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4  
|||||  
Db 5 LOPE 8

## RESULT 20

US-09-942-052-104  
; Sequence 104, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Faris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85PIB3  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 104  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-104

Query Match 22.2%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4  
|||||  
Db 2 LOPE 5

## RESULT 21

US-09-942-052-218  
; Sequence 218, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Faris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85PIB3  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 218  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-218



```
Query Match          22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
Db 2 LOPE 5

RESULT 22
US-09-942-052-235
; Sequence 235, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 235
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-235

Query Match          22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
Db 1 LOPE 4

RESULT 23
US-09-942-052-236
; Sequence 236, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 236
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-236
```

```
Query Match          22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
Db 6 LOPE 9

RESULT 24
US-09-942-052-312
; Sequence 312, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 312
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-312

Query Match          22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
Db 5 LOPE 8

RESULT 25
US-09-942-052-339
; Sequence 339, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 339
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-339
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## US-09-942-052-339

Query Match 22.2%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQPE 4  
|  
|  
|  
|  
Db 1 LQPE 4

## RESULT 26

US-09-942-052-424  
; Sequence 424, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Faris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Bid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR FILING DATE: 2000-08-28  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 424  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-424

Query Match 22.2%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQPE 4  
|  
|  
|  
|  
Db 1 LQPE 4

## RESULT 27

US-09-942-052-548  
; Sequence 548, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Faris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Bid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR FILING DATE: 2000-08-28  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 548  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-548

Query Match 22.2%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQPE 4  
|  
|  
|  
|  
Db 2 LQPE 5

## RESULT 28

US-09-942-052-619  
; Sequence 619, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Faris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Bid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR FILING DATE: 2000-08-28  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 619  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-619

Query Match 22.2%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQPE 4  
|  
|  
|  
|  
Db 1 LQPE 4

## RESULT 29

US-10-365-908-3  
; Sequence 3, Application US/10365908  
; Publication No. US20030170269A1  
; GENERAL INFORMATION:  
; APPLICANT: Neefe, John R.  
; APPLICANT: Boux, Leslie J.  
; APPLICANT: Winmett, Mark T.  
; APPLICANT: Goldstone, Stephen E.  
; APPLICANT: Siegel, Marvin  
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT  
; FILE REFERENCE: 12071-003001  
; CURRENT APPLICATION NUMBER: US/10/365,908  
; CURRENT FILING DATE: 2003-02-13  
; PRIOR FILING DATE: 2003-02-13  
; PRIOR FILING DATE: 2001-10-19  
; PRIOR FILING DATE: 2001-10-19  
; PRIOR FILING DATE: 2000-06-26  
; NUMBER OF SEQ ID NOS: 140  
; SOFTWARE: Fast-SEQ for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Human papilloma virus

## US-10-365-908-3

Query Match 22.2%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4  
Db 5 LOPE 8

## RESULT 30

US-10-365-908-26  
; Sequence 26, Application US/10355908  
; Publication No. US20030170268A1  
; GENERAL INFORMATION:  
; APPLICANT: Neefe, John R.  
; APPLICANT: Boux, Leslie J.  
; APPLICANT: Winnett, Mark T.  
; APPLICANT: Goldstone, Stephen E.  
; APPLICANT: Siegel, Marvin  
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT  
; FILE REFERENCE: 12071-003001  
; CURRENT APPLICATION NUMBER: US/10/365,908  
; PRIOR FILING DATE: 2003-02-13  
; PRIOR APPLICATION NUMBER: US/09/891,823  
; PRIOR FILING DATE: 2001-10-19  
; PRIOR APPLICATION NUMBER: US 60/214,202  
; PRIOR FILING DATE: 2000-06-26  
; NUMBER OF SEQ ID NOS: 140  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 26  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Human papilloma virus  
US-10-365-908-26

Query Match 22.2%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4  
Db 1 LOPE 4

## RESULT 31

US-10-200-708-634  
; Sequence 634, Application US/10200708  
; Publication No. US20030180314A1  
; GENERAL INFORMATION:  
; APPLICANT: Degroot, Anne S.  
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES  
; FILE REFERENCE: 17999-001  
; CURRENT APPLICATION NUMBER: US/10/200,708  
; PRIOR FILING DATE: 2002-07-22  
; PRIOR APPLICATION NUMBER: US/09/351,036  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: 60/092,346  
; PRIOR FILING DATE: 1998-07-10  
; PRIOR APPLICATION NUMBER: 60/115,145  
; PRIOR FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: 60/130,677  
; PRIOR FILING DATE: 1999-04-23  
; NUMBER OF SEQ ID NOS: 672  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 634  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus  
US-10-200-708-634

Query Match 22.2%; Score 4; DB 12; Length 9;

Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12  
Db 2 PKVK 5

## RESULT 32

US-10-200-708-648  
; Sequence 648, Application US/10200708  
; Publication No. US20030180314A1  
; GENERAL INFORMATION:  
; APPLICANT: Degroot, Anne S.  
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES  
; FILE REFERENCE: 17999-001  
; CURRENT APPLICATION NUMBER: US/10/200,708  
; PRIOR FILING DATE: 2002-07-22  
; PRIOR APPLICATION NUMBER: US/09/351,036  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: 60/092,346  
; PRIOR FILING DATE: 1998-07-10  
; PRIOR APPLICATION NUMBER: 60/115,145  
; PRIOR FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: 60/130,677  
; PRIOR FILING DATE: 1999-04-23  
; NUMBER OF SEQ ID NOS: 672  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 648  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus  
US-10-200-708-648

Query Match 22.2%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12  
Db 2 PKVK 5

## RESULT 33

US-10-200-708-669  
; Sequence 669, Application US/10200708  
; Publication No. US20030180314A1  
; GENERAL INFORMATION:  
; APPLICANT: Degroot, Anne S.  
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES  
; FILE REFERENCE: 17999-001  
; CURRENT APPLICATION NUMBER: US/10/200,708  
; PRIOR FILING DATE: 2002-07-22  
; PRIOR APPLICATION NUMBER: US/09/351,036  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: 60/092,346  
; PRIOR FILING DATE: 1998-07-10  
; PRIOR APPLICATION NUMBER: 60/115,145  
; PRIOR FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: 60/130,677  
; PRIOR FILING DATE: 1999-04-23  
; NUMBER OF SEQ ID NOS: 672  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 669  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus  
US-10-200-708-669

Query Match 22.2%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12  
Db 6 PKVK 9

RESULT 34  
US-10-001-546-12  
; Sequence 12, Application US/10001546  
; Publication No. US20030027766A1  
; GENERAL INFORMATION:  
; APPLICANT: IOANNIDES, CONSTANTIN G.  
; APPLICANT: FISK, BRYAN A.  
; APPLICANT: IOANNIDES, MARIA G.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING  
; FILE REFERENCE: T-LYMPHOCYTES  
; CURRENT APPLICATION NUMBER: US/10/001,546  
; PRIOR FILING DATE: 2001-10-31  
; PRIOR APPLICATION NUMBER: 08/403,459  
; NUMBER OF SEQ ID NOS: 68  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-10-001-546-12

Query Match 22.2%; Score 4; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4  
Db 2 LOPE 5

RESULT 35  
US-10-128-711-28  
; Sequence 28, Application US/10128711  
; Publication No. US20030099634A1  
; GENERAL INFORMATION:  
; APPLICANT: VITIELLO, MARIA A.  
; CHESTNUT, ROBERT W.  
; SETTE, ALESSANDRO D.  
; CELIS, ESTEBAN  
; GRAY, HOWARD  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING  
; CTL IMMUNITY  
; NUMBER OF SEQUENCES: 153  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Hourie and Crew  
; STREET: Steuart Street Tower, One Market Plaza  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: US  
; ZIP: 94105-1493  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/128,711  
; FILING DATE: 22-Apr-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/197,484  
; FILING DATE: 16-FEB-1994  
; APPLICATION NUMBER: US 07/935,811

; FILING DATE: 26-AUG-1992  
; APPLICATION NUMBER: US 07/874,491  
; FILING DATE: 27-APR-1992  
; APPLICATION NUMBER: US 07/827,682  
; FILING DATE: 29-JAN-1992  
; APPLICATION NUMBER: US 07/749,568  
; FILING DATE: 26-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parmelee, Steven W.  
; REGISTRATION NUMBER: 31,990  
; REFERENCE/DOCKET NUMBER: 14137-26-4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 467-9600  
; TELEFAX: (206) 623-6793  
; INFORMATION FOR SEQ ID NO: 28:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 28:  
US-10-128-711-28

Query Match 22.2%; Score 4; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12  
Db 2 PKVK 5

RESULT 36  
US-10-128-711-66  
; Sequence 66, Application US/10128711  
; Publication No. US20030099634A1  
; GENERAL INFORMATION:  
; APPLICANT: VITIELLO, MARIA A.  
; CHESTNUT, ROBERT W.  
; SETTE, ALESSANDRO D.  
; CELIS, ESTEBAN  
; GRAY, HOWARD  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING  
; CTL IMMUNITY  
; NUMBER OF SEQUENCES: 153  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Hourie and Crew  
; STREET: Steuart Street Tower, One Market Plaza  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: US  
; ZIP: 94105-1493  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/128,711  
; FILING DATE: 22-Apr-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/197,484  
; FILING DATE: 16-FEB-1994  
; APPLICATION NUMBER: US 07/935,811  
; FILING DATE: 26-AUG-1992  
; APPLICATION NUMBER: US 07/874,491  
; FILING DATE: 27-APR-1992  
; APPLICATION NUMBER: US 07/827,682  
; FILING DATE: 29-JAN-1992  
; APPLICATION NUMBER: US 07/749,568  
; FILING DATE: 26-AUG-1991

```

;
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-10-128-711-66

Query Match      22.2%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LQPE 4
DB      5 LQPE 8

RESULT 37
US-10-128-711-71
; Sequence 71, Application US/10128711
; Publication No. US20030099634A1
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; CHESTNUT, Robert W.
; SETTE, Alessandro D.
; CELIS, Esteban
; GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Hourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/128,711
; FILING DATE: 22-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
;
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 71:
US-10-128-711-71

Query Match      22.2%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LQPE 4
DB      4 LQPE 7

RESULT 38
US-10-133-210-146
; Sequence 146, Application US/10133210
; Publication No. US20030103964A1
; GENERAL INFORMATION:
; APPLICANT: Delisi, Charles
; APPLICANT: Berzofsky, Jay
; APPLICANT: Gulukota, Kamalakara
; APPLICANT: Vaccaro, Dennis
; APPLICANT: Weng, Zhiping
; APPLICANT: Zhang, Chao
; TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
; FILE REFERENCE: BU-035AX
; CURRENT APPLICATION NUMBER: US/10/133,210
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 146
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-146

Query Match      22.2%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PKVK 12
DB      2 PKVK 5

RESULT 39
US-10-133-210-167
; Sequence 167, Application US/10133210
; Publication No. US20030103964A1
; GENERAL INFORMATION:
; APPLICANT: Delisi, Charles
; APPLICANT: Berzofsky, Jay
; APPLICANT: Gulukota, Kamalakara
; APPLICANT: Vaccaro, Dennis
; APPLICANT: Weng, Zhiping
; APPLICANT: Zhang, Chao
; TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
; FILE REFERENCE: BU-035AX
; CURRENT APPLICATION NUMBER: US/10/133,210
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 167
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LENGTH: 9  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 US-10-133-210-167

Query Match 22.2%; Score 4; DB 15; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12  
 ||||  
 DB 2 PKVK 5

## RESULT 40

US-09-847-185-19  
 ; Sequence 19, Application US/09847185  
 ; Patent No. US20020076392A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Soo Hoo, William  
 ; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS  
 ; COMBINING GM-CSF AND METHODS OF MODULATING AN IMMUNE  
 ; RESPONSE USING SAME

NUMBER OF SEQUENCES: 50  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: CAMPBELL & FLORES, LLP  
 STREET: 4370 La Jolla Village Drive, Suite 700  
 CITY: San Diego  
 STATE: California  
 COUNTRY: United States  
 ZIP: 92121

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/847,185  
 FILING DATE: 01-May-2001  
 CLASSIFICATION: <Unknown>

## PRIORITY INFORMATION DATA:

APPLICATION NUMBER: 09/201,931  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Campbell, Cathryn A.  
 REGISTRATION NUMBER: 31,815  
 REFERENCE/DOCKET NUMBER: P-IM 2442  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619)535-5001  
 TELEFAX: (619)535-8949

## INFORMATION FOR SEQ ID NO: 19:

## SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 19:

US-09-847-185-19

Query Match 22.2%; Score 4; DB 9; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4  
 ||||  
 DB 5 LQPE 8

## RESULT 41

US-09-922-261-283  
 ; Sequence 283, Application US/09922261

Patent No. US20020111471A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: COGENT NEUROSCIENCE, Inc.  
 ; APPLICANT: Lo, Donald C.  
 ; APPLICANT: Barney, Shawn  
 ; APPLICANT: Thomas, Mary Beth  
 ; APPLICANT: Portbury, Stuart D.  
 ; APPLICANT: Puranam, Kasturi  
 ; APPLICANT: Katz, Lawrence C.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING  
 ; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING  
 ; TITLE OF INVENTION: CELL DEATH  
 ; FILE REFERENCE: 10001-005-999  
 ; CURRENT APPLICATION NUMBER: US/09/922,261  
 ; CURRENT FILING DATE: 2001-08-03  
 ; PRIOR APPLICATION NUMBER: US/09/461,697  
 ; PRIOR FILING DATE: 1999-12-14  
 ; NUMBER OF SEQ ID NOS: 466  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 283  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-922-261-283

Query Match 22.2%; Score 4; DB 10; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 MVPK 18  
 ||||  
 DB 1 MVPK 4

## RESULT 42

US-09-833-328-10  
 ; Sequence 10, Application US/09833328  
 ; Patent No. US20020136713A1  
 ; GENERAL INFORMATION:

APPLICANT: Laemmle, Bernhard  
 APPLICANT: Schwarz, Hans-Peter  
 APPLICANT: Scheiflinger, Friedrich  
 APPLICANT: Antoine, Gerhard  
 APPLICANT: Kerschbaumer, Rndolf  
 APPLICANT: Tagliavacca, Luigina  
 APPLICANT: Zimmermann, Klaus  
 APPLICANT: Furlan, Miha  
 APPLICANT: Turecek, Peter  
 APPLICANT: Geritsen, Helena E.

TITLE OF INVENTION: Composition Exhibiting a von Willebrand Factor (vWF) Protease /  
 TITLE OF INVENTION: Comprising a Polypeptide Chain with the Amino Acid Sequence A/  
 FILE REFERENCE: 247.00CIP  
 CURRENT APPLICATION NUMBER: US/09/833,328  
 CURRENT FILING DATE: 2001-04-12  
 PRIOR APPLICATION NUMBER: 09/721,254  
 PRIOR FILING DATE: 2000-11-22  
 NUMBER OF SEQ ID NOS: 15  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 10  
 LENGTH: 10  
 TYPE: PRT  
 ORGANISM: human  
 US-09-833-328-10

Query Match 22.2%; Score 4; DB 10; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TMVP 17  
 ||||  
 DB 5 TMVP 8

RESULT 43  
US-09-835-853-22  
; Sequence 22, Application US/09835853  
; Patent No. US20020165136A1  
; GENERAL INFORMATION:  
; APPLICANT: BASERGA, Renato L.  
; APPLICANT: RESNICOFF, Mariana  
; APPLICANT: HUANG, Ziwei  
; TITLE OF INVENTION: MHC PEPTIDES AND METHODS OF USE  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HALE and DORR LLP  
; STREET: 1455 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/835,853  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/704,344  
; FILING DATE: 28-AUG-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WIXON, Henry N.  
; REGISTRATION NUMBER: 32,073  
; REFERENCE/DOCKET NUMBER: 104322.196  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 942-8459  
; TELEFAX: (202) 942-8484  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-09-835-853-22

Query Match 22.2%; Score 4; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred.No. 5.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LQPE 4  
Db 5 LQPE 8  
RESULT 44  
US-09-876-904A-388  
; Sequence 388, Application US/09876904A  
; Publication No. US20030072794A1  
; GENERAL INFORMATION:  
; APPLICANT: BOULIKAS, TENI  
; TITLE OF INVENTION: ENCAPSULATION OF PLASMTD DNA (LIPOGENES TM) AND THERAPEUTIC  
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE  
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES  
; FILE REFERENCE: TB-2002.00  
; CURRENT APPLICATION NUMBER: US/09/876,904A  
; CURRENT FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: US 60/210,925  
; PRIOR FILING DATE: 2000-06-09  
; NUMBER OF SEQ ID NOS: 629  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 388

; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Caenorhabditis elegans  
; FEATURE:  
; OTHER INFORMATION: C. elegans Sdc-3 protein.  
US-09-876-904A-388  
Query Match 22.2%; Score 4; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred.No. 5.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 10 KVKE 13  
Db 7 KVKE 10  
RESULT 45  
US-09-572-404B-1436  
; Sequence 1436, Application US/09572404B  
; Publication No. US20030078374A1  
; GENERAL INFORMATION:  
; APPLICANT: Proteom Ltd  
; TITLE OF INVENTION: Complementary peptide ligands from the human genome  
; FILE REFERENCE: Human patent  
; CURRENT APPLICATION NUMBER: US/09/572,404B  
; CURRENT FILING DATE: 2000-05-17  
; NUMBER OF SEQ ID NOS: 4203  
; SOFTWARE: ProtPatent version 1.0  
; SEQ ID NO 1436  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; OTHER INFORMATION: sequence located in SLC12A2 OR NKCC1 at 281-290 and may intera  
; OTHER INFORMATION: Sequence 1435 in this patent.  
US-09-572-404B-1436

Query Match 22.2%; Score 4; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred.No. 5.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 9 PKVK 12  
Db 4 PKVK 7

RESULT 46  
US-10-177-390-33  
; Sequence 33, Application US/10177390  
; Publication No. US20030143743A1  
; GENERAL INFORMATION:  
; APPLICANT: Schuler, Gerold  
; APPLICANT: N.V. Antwerps Innovatiecentrum  
; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear  
; TITLE OF INVENTION: Polynucleotides by Electroporation  
; FILE REFERENCE: 021505wo/JH/ml  
; CURRENT APPLICATION NUMBER: US/10/177,390  
; CURRENT FILING DATE: 2002-06-20  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 33  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Influenza virus  
US-10-177-390-33

Query Match 22.2%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred.No. 5.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LQPE 4  
Db 5 LQPE 8

RESULT 47  
US-09-942-052-54  
; Sequence 54, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 54  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-54

Query Match 22.2%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4  
|||  
Db 2 LQPE 5

RESULT 48  
US-09-942-052-74  
; Sequence 74, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 74  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-74

Query Match 22.2%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4  
|||

Db 6 LQPE 9

RESULT 49  
US-09-942-052-256  
; Sequence 256, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 256  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-256

Query Match 22.2%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4  
|||  
Db 6 LQPE 9

RESULT 50  
US-09-942-052-257  
; Sequence 257, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 257  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-257

Query Match 22.2%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4



```
Db          1 LOPE 4
           ||||
           2 LOPE 5

RESULT 51
US-09-942-052-360
; Sequence 360, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 360
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-360

Query Match      22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 LOPE 4
           ||||
           6 LOPE 9

RESULT 52
US-09-942-052-476
; Sequence 476, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 476
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-476

Query Match      22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 LOPE 4
           ||||
           6 LOPE 9

RESULT 53
US-09-942-052-573
; Sequence 573, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 573
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-573

Query Match      22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 LOPE 4
           ||||
           5 LOPE 8

RESULT 54
US-09-942-052-669
; Sequence 669, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 669
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-669

Query Match      22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 LOPE 4
      ||||
Db      5 LOPE 8

RESULT 55
US-09-942-052-688
; Sequence 688, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20028-00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 688
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-688

Query Match      22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LOPE 4
      ||||
Db      2 LOPE 5

RESULT 56
US-10-200-708-122
; Sequence 122, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 122
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-122

Query Match      22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PKVK 12
      ||||
Db      6 PKVK 9

RESULT 57
US-10-200-708-223
; Sequence 223, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 223
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-223

Query Match      22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PKVK 12
      ||||
Db      2 PKVK 5

RESULT 58
US-10-200-708-248
; Sequence 248, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 248
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-248

Query Match      22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PKVK 12
      ||||
Db      2 PKVK 5
```

RESULT 59  
US-10-200-708-338  
; Sequence 338, Application US/10200708  
; Publication No. US20030180314A1  
; GENERAL INFORMATION:  
; APPLICANT: DeGroot, Anne S.  
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES  
; FILE REFERENCE: 17999-001  
; CURRENT APPLICATION NUMBER: US/10/200,708  
; CURRENT FILING DATE: 2002-07-22  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: 60/092,346  
; PRIOR FILING DATE: 1998-07-10  
; PRIOR APPLICATION NUMBER: 60/115,145  
; PRIOR FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: 60/130,677  
; PRIOR FILING DATE: 1999-04-23  
; NUMBER OF SEQ ID NOS: 672  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 338  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus  
US-10-200-708-338

Query Match 22.2%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12  
|||  
Db 2 PKVK 5

RESULT 60  
US-10-200-708-345  
; Sequence 345, Application US/10200708  
; Publication No. US20030180314A1  
; GENERAL INFORMATION:  
; APPLICANT: DeGroot, Anne S.  
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES  
; FILE REFERENCE: 17999-001  
; CURRENT APPLICATION NUMBER: US/10/200,708  
; CURRENT FILING DATE: 2002-07-22  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: 60/092,346  
; PRIOR FILING DATE: 1998-07-10  
; PRIOR APPLICATION NUMBER: 60/115,145  
; PRIOR FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: 60/130,677  
; PRIOR FILING DATE: 1999-04-23  
; NUMBER OF SEQ ID NOS: 672  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 345  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus  
US-10-200-708-345

Query Match 22.2%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12  
|||  
Db 7 PKVK 10

RESULT 61

US-10-200-708-520  
; Sequence 520, Application US/10200708  
; Publication No. US20030180314A1  
; GENERAL INFORMATION:  
; APPLICANT: DeGroot, Anne S.  
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES  
; FILE REFERENCE: 17999-001  
; CURRENT APPLICATION NUMBER: US/10/200,708  
; CURRENT FILING DATE: 2002-07-22  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: 60/092,346  
; PRIOR FILING DATE: 1998-07-10  
; PRIOR APPLICATION NUMBER: 60/115,145  
; PRIOR FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: 60/130,677  
; PRIOR FILING DATE: 1999-04-23  
; NUMBER OF SEQ ID NOS: 672  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 520  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus  
US-10-200-708-520

Query Match 22.2%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12  
|||  
Db 2 PKVK 5

RESULT 62  
US-10-200-708-542  
; Sequence 542, Application US/10200708  
; Publication No. US20030180314A1  
; GENERAL INFORMATION:  
; APPLICANT: DeGroot, Anne S.  
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES  
; FILE REFERENCE: 17999-001  
; CURRENT APPLICATION NUMBER: US/10/200,708  
; CURRENT FILING DATE: 2002-07-22  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: 60/092,346  
; PRIOR FILING DATE: 1998-07-10  
; PRIOR APPLICATION NUMBER: 60/115,145  
; PRIOR FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: 60/130,677  
; PRIOR FILING DATE: 1999-04-23  
; NUMBER OF SEQ ID NOS: 672  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 542  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus  
US-10-200-708-542

Query Match 22.2%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12  
|||  
Db 7 PKVK 10

RESULT 63  
US-10-200-708-635  
; Sequence 635, Application US/10200708  
; Publication No. US20030180314A1

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; GENERAL INFORMATION:
; APPLICANT: Degroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; PRIOR FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 635
; TYPE: PRT
; LENGTH: 10
; ORGANISM: Human immunodeficiency virus
US-10-200-708-635

Query Match      22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PKVK 12
        ||||
Db      2 PKVK 5

RESULT 64
US-10-200-708-649
; Sequence 649, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: Degroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 649
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-649

Query Match      22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PKVK 12
        ||||
Db      2 PKVK 5

RESULT 65
US-10-200-708-670
; Sequence 670, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: Degroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; PRIOR FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 670
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-670

Query Match      22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PKVK 12
        ||||
Db      2 PKVK 5

RESULT 66
US-10-062-710-228
; Sequence 228, Application US/10062710
; Publication No. US20030049253A1
; GENERAL INFORMATION:
; APPLICANT: Li, Frank Q.
; APPLICANT: Chu, Yong-Liang
; APPLICANT: Qiu, Jian-Tai
; TITLE OF INVENTION: Polymeric Conjugates for Delivery of
; TITLE OF INVENTION: MHC-Recognized Epitopes
; TITLE OF INVENTION: Via Peptide Vaccines
; FILE REFERENCE: 3781-001-27
; CURRENT APPLICATION NUMBER: US/10/062,710
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 60/310,498
; PRIOR FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 228
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Epstein-Barr Virus
US-10-062-710-228

Query Match      22.2%; Score 4; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LQPE 4
        ||||
Db      5 LQPE 8

RESULT 67
US-10-133-210-271
; Sequence 271, Application US/10133210
; Publication No. US20030103964A1
; GENERAL INFORMATION:
; APPLICANT: Delisi, Charles
; APPLICANT: Berzofsky, Jay
; APPLICANT: Gulukota, Kamalakara
; APPLICANT: Vaccaro, Dennis
; APPLICANT: Weng, Zhiping
; APPLICANT: Zhang, Chao
; TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND

```

;; TITLE OF INVENTION: COMPOSITIONS THEREOF  
;; FILE REFERENCE: BU-035AX  
;; CURRENT APPLICATION NUMBER: US/10/133,210  
;; CURRENT FILING DATE: 2002-04-26  
;; NUMBER OF SEQ ID NOS: 281  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 271  
;; LENGTH: 10  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-133-210-271

Query Match 22.2%; Score 4; DB 15; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQPE 4  
Db 5 LQPE 8

RESULT 68  
US-10-224-286-19  
;; Sequence 19, Application US/10224286  
;; Publication No. US20030108517A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Seo Hoo, William  
;; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS  
;; COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE  
;; RESPONSE USING SAME  
;; NUMBER OF SEQUENCES: 50  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: CAMPBELL & FLORES, LLP  
;; STREET: 4370 La Jolla Village Drive, Suite 700  
;; CITY: San Diego  
;; STATE: California  
;; COUNTRY: United States  
;; ZIP: 92121  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/10/224,286  
;; FILING DATE: 19-Aug-2002  
;; CLASSIFICATION: <Unknown>  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/902,516  
;; FILING DATE: 29-JUL-1997  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Campbell, Cathryn A.  
;; REGISTRATION NUMBER: 31,815  
;; REFERENCE/DOCKET NUMBER: P-IM 2442  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (619)535-9001  
;; TELEFAX: (619)535-8949  
;; INFORMATION FOR SEQ ID NO: 19:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 10 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 19:

US-10-224-286-19

Query Match 22.2%; Score 4; DB 15; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQPE 4

Db 5 LQPE 8

RESULT 69  
US-10-054-968-13  
;; Sequence 13, Application US/10054968  
;; Publication No. US20030119101A1  
;; GENERAL INFORMATION:  
;; APPLICANT: NEUTEC PHARMA PLC  
;; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF INFECTIONS OF GRAM  
;; TITLE OF INVENTION: POSITIVE  
;; TITLE OF INVENTION: COCCI  
;; FILE REFERENCE: PM 259204  
;; CURRENT APPLICATION NUMBER: US/10/054,968  
;; CURRENT FILING DATE: 2002-01-25  
;; PRIOR APPLICATION NUMBER: US/09/214,307  
;; PRIOR FILING DATE: 1999-01-04  
;; PRIOR APPLICATION NUMBER: PCT/GB97/01830  
;; PRIOR FILING DATE: 1997-07-07  
;; PRIOR APPLICATION NUMBER: GB9614274.0  
;; PRIOR FILING DATE: 1996-07-06  
;; NUMBER OF SEQ ID NOS: 15  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 13  
;; LENGTH: 10  
;; TYPE: PRT  
;; ORGANISM: Staphylococcus aureus  
US-10-054-968-13

Query Match 22.2%; Score 4; DB 15; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GVPK 10  
Db 7 GVPK 10

RESULT 70  
US-09-852-910-264  
;; Sequence 264, Application US/09852910  
;; Publication No. US20030096297A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Hamm, Heidi  
;; APPLICANT: Gilchrist, Annette  
;; TITLE OF INVENTION: Method For Identifying Inhibitors of G Protein Coupled Recepto  
;; FILE REFERENCE: 2661-101  
;; CURRENT APPLICATION NUMBER: US/09/852,910  
;; CURRENT FILING DATE: 2001-09-18  
;; PRIOR APPLICATION NUMBER: US 60/275,472  
;; PRIOR FILING DATE: 2001-03-14  
;; NUMBER OF SEQ ID NOS: 271  
;; SOFTWARE: PatentIn version 3.0  
;; SEQ ID NO 264  
;; LENGTH: 11  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; NAME/KEY: misc\_feature  
;; LOCATION: (1)..(11)  
;; OTHER INFORMATION: G11 library peptide  
US-09-852-910-264

Query Match 22.2%; Score 4; DB 11; Length 11;  
Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KVXE 13  
Db 4 KVXE 7

## RESULT 71

US-10-062-710-206  
; Sequence 206, Application US/10062710  
; Publication No. US20030049253A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Frank Q.  
; APPLICANT: Chu, Yong-Liang  
; APPLICANT: Qiu, Jian-Tai  
; TITLE OF INVENTION: Polymetric Conjugates for Delivery of  
; TITLE OF INVENTION: MHC-Recognized Epitopes  
; TITLE OF INVENTION: Via Peptide Vaccines  
; FILE REFERENCE: 3781-001-27  
; CURRENT FILING DATE: 2002-02-05  
; PRIOR APPLICATION NUMBER: US/10/062,710  
; PRIOR FILING DATE: 2002-02-05  
; PRIOR APPLICATION NUMBER: US 60/310,498  
; PRIOR FILING DATE: 2001-08-08  
; NUMBER OF SEQ ID NOS: 232  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 206  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: T Cell epitopes  
US-10-062-710-206

Query Match 22.2%; Score 4; DB 15; Length 11;  
Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4  
|||  
Db 6 LQPE 9

## RESULT 72

US-09-832-723-42  
; Sequence 42, Application US/09832723  
; Patent No. US20020098524A1  
; GENERAL INFORMATION:  
; APPLICANT: Estell, David A.  
; APPLICANT: Chen, Yiyou  
; APPLICANT: Murray, Christopher J.  
; APPLICANT: Tijerina, Pilar  
; TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING  
; FILE REFERENCE: GC617-2  
; CURRENT APPLICATION NUMBER: US/09/832,723  
; CURRENT FILING DATE: 2001-04-11  
; PRIOR APPLICATION NUMBER: US 60/197,259  
; PRIOR FILING DATE: 2000-04-14  
; NUMBER OF SEQ ID NOS: 117  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 42  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: peptides screened from a phage display random  
; OTHER INFORMATION: peptide library  
US-09-832-723-42

Query Match 22.2%; Score 4; DB 9; Length 12;  
Best Local Similarity 100.0%; Pred. No. 6.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TMVP 17  
|||  
Db 7 TMVP 10

## RESULT 73

US-10-303-331-42  
; Sequence 42, Application US/10303331

; Publication No. US20030152976A1  
; GENERAL INFORMATION:  
; APPLICANT: Janssen, Giselle G.  
; APPLICANT: Murray, Christopher J.  
; APPLICANT: Winetzky, Deborah S.  
; TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING  
; FILE REFERENCE: GC617-3  
; CURRENT APPLICATION NUMBER: US/10/303,331  
; CURRENT FILING DATE: 2002-11-25  
; PRIOR APPLICATION NUMBER: US 09/832,723  
; PRIOR FILING DATE: 2001-04-11  
; PRIOR APPLICATION NUMBER: US 60/197,259  
; PRIOR FILING DATE: 2000-04-14  
; NUMBER OF SEQ ID NOS: 125  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 42  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: peptides screened from a phage display random  
; OTHER INFORMATION: peptide library  
US-10-303-331-42

Query Match 22.2%; Score 4; DB 12; Length 12;  
Best Local Similarity 100.0%; Pred. No. 6.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TMVP 17  
|||  
Db 7 TMVP 10

## RESULT 74

US-10-116-275-72  
; Sequence 72, Application US/10116275  
; Publication No. US20030211476A1  
; GENERAL INFORMATION:  
; APPLICANT: Elan Pharmaceutical Technology  
; APPLICANT: O'Mahony, Daniel J.  
; APPLICANT: Brayden, David  
; APPLICANT: Byrne, Daragh  
; APPLICANT: Lambkin, Imelda  
; APPLICANT: Higgins, Lisa  
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and  
; TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors  
; FILE REFERENCE: E1067/20087  
; CURRENT APPLICATION NUMBER: US/10/116,275  
; CURRENT FILING DATE: 2002-10-04  
; NUMBER OF SEQ ID NOS: 349  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 72  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Listed in Table titled "Peptides that Target to and/or Enhance  
; OTHER INFORMATION: take Across the GIT"  
US-10-116-275-72

Query Match 22.2%; Score 4; DB 12; Length 12;  
Best Local Similarity 100.0%; Pred. No. 6.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TMVP 17  
|||  
Db 7 TMVP 10

## RESULT 75

US-10-185-815-26  
; Sequence 26, Application US/10185815  
; Publication No. US20030096354A1

; GENERAL INFORMATION:  
; APPLICANT: Elan Corporation, plc  
; APPLICANT: O'Mahony, Daniel  
; APPLICANT: Lambkin, Imelda  
; APPLICANT: Higgins, Lisa  
; TITLE OF INVENTION: Pever's Patch And/Or M-cell Targeting Ligands  
; FILE REFERENCE: E1067-20093  
; CURRENT APPLICATION NUMBER: US/10/185,815  
; CURRENT FILING DATE: 2002-10-09  
; PRIOR APPLICATION NUMBER: 60/302,591  
; PRIOR FILING DATE: 2001-07-02  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 26  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: polypeptide ligand  
US-10-185-815-26

Query Match 22.2%; Score 4; DB 15; Length 12;  
Best Local Similarity 100.0%; Pred.No. 6.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 TMVP 17  
|||  
Db 7 TMVP 10

Search completed: November 25, 2003, 20:36:59  
Job time : 29.8837 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:16:22 ; Search time 14.5465 Seconds  
(without alignments)  
52.356 Million cell updates/sec

Title: US-09-641-801-21

Perfect score: 18

Sequence: 1 LQPEIMGVPKVKETWVPK 18

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5A COMB pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B COMB pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A COMB pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B COMB pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	4	US-09-641-803-21
2	4	22.2	4	4	US-09-385-357A-12
3	4	22.2	4	4	US-09-113-692B-9
4	4	22.2	4	4	US-09-607-277A-9
5	4	22.2	5	2	US-08-760-075A-29
6	4	22.2	5	3	US-09-338-546-29
7	4	22.2	5	4	US-09-659-084-29
8	4	22.2	6	2	US-08-480-793-14
9	4	22.2	6	5	PCT-US92-05825A-14
10	4	22.2	7	3	US-09-458-754-383
11	4	22.2	7	3	US-09-042-107-383
12	4	22.2	7	4	US-09-641-803-16
13	4	22.2	8	3	US-09-296-284-14
14	4	22.2	9	1	US-08-217-188A-62
15	4	22.2	9	1	US-08-687-226-62
16	4	22.2	9	1	US-08-467-083-2
17	4	22.2	9	1	US-08-615-181-79
18	4	22.2	9	1	US-08-414-417B-2
19	4	22.2	9	1	US-08-787-547-104
20	4	22.2	9	2	US-08-486-348A-2
21	4	22.2	9	2	US-08-468-545B-2
22	4	22.2	9	3	US-08-948-378A-17
23	4	22.2	9	3	US-08-667-725B-62
24	4	22.2	9	3	US-08-466-680B-2
25	4	22.2	9	3	US-09-007-748-62
26	4	22.2	9	3	US-09-169-425C-17
27	4	22.2	9	4	US-08-197-484-28
28	4	22.2	9	4	US-08-197-484-66
29	4	22.2	9	4	US-08-197-484-71
30	4	22.2	9	4	US-08-403-459-12
31	4	22.2	9	4	US-09-759-960-17
32	4	22.2	9	5	PCT-US95-02131-28
33	4	22.2	9	5	PCT-US95-02131-66
34	4	22.2	9	5	PCT-US95-02131-71
35	4	22.2	10	2	US-08-302-516-19
36	4	22.2	10	2	US-08-760-075A-34
37	4	22.2	10	3	US-08-704-344-22
38	4	22.2	10	3	US-09-338-546-34
39	4	22.2	10	3	US-09-461-697-283
40	4	22.2	10	4	US-09-659-084-34
41	4	22.2	10	4	US-09-847-185-19
42	4	22.2	10	4	US-09-214-307A-13
43	4	22.2	11	3	US-08-760-075A-1
44	4	22.2	11	3	US-09-101-886B-57
45	4	22.2	11	3	US-09-338-546-1
46	4	22.2	11	4	US-09-659-084-1
47	4	22.2	12	4	US-08-949-059A-29
48	4	22.2	12	4	US-08-949-059A-31
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50	4	22.2	13	1	US-07-610-525-5
51	4	22.2	13	4	US-08-403-459-36
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54	4	22.2	14	4	US-08-949-059A-28
55	4	22.2	15	1	US-07-610-525-4
56	4	22.2	15	1	US-08-097-997A-2
57	4	22.2	15	1	US-08-259-672-11
58	4	22.2	15	1	US-08-459-351-11
59	4	22.2	15	1	US-08-460-533-11
60	4	22.2	15	1	US-08-787-547-44
61	4	22.2	15	2	US-08-553-257A-62
62	4	22.2	15	3	US-08-660-347-3
63	4	22.2	15	3	US-09-041-889-16
64	4	22.2	15	3	US-08-837-058-16
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67	4	22.2	15	4	US-09-417-264-16
68	4	22.2	15	4	US-09-441-992-62
69	4	22.2	15	5	PCT-US94-06654-11
70	4	22.2	16	2	US-08-591-438-13
71	4	22.2	16	2	US-08-760-075A-2
72	4	22.2	16	3	US-09-011-525-1
73	4	22.2	16	3	US-08-405-647B-11
74	4	22.2	16	3	US-08-602-999A-344
75	4	22.2	16	3	US-08-985-499-11
76	4	22.2	16	3	US-09-204-335-1
77	4	22.2	16	3	US-09-204-335-2
78	4	22.2	16	3	US-09-338-546-2
79	4	22.2	16	4	US-09-659-084-2
80	4	22.2	16	4	US-09-500-124-344
81	4	22.2	16	5	PCT-US96-03180-11
82	4	22.2	16	6	5200320-32
83	4	22.2	17	1	US-07-610-525-3
84	4	22.2	17	1	US-08-445-909A-14
85	4	22.2	17	2	US-08-733-982A-12
86	4	22.2	17	4	US-09-352-078-5
87	4	22.2	17	4	US-09-292-225-10
88	4	22.2	18	1	US-08-259-672-10
89	4	22.2	18	1	US-08-459-351-10
90	4	22.2	18	1	US-08-460-533-10
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92	4	22.2	18	1	US-08-451-472-48
93	4	22.2	18	1	US-08-451-472-68
94	4	22.2	18	3	US-08-075-541D-34
95	4	22.2	18	3	US-08-075-541D-35
96	4	22.2	18	3	PCT-US94-06654-10
97	4	22.2	19	1	US-07-610-525-2
98	4	22.2	20	1	US-07-678-974D-6
99	4	22.2	20	2	US-08-484-530-39
100	4	22.2	20	2	US-08-484-530-39

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Sequence 71, Appl  
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Sequence 19, Appl  
Sequence 13, Appl  
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Sequence 29, Appl  
Sequence 31, Appl  
Patent No. 5460961  
Sequence 5, Appl  
Sequence 36, Appl  
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Sequence 48, Appl  
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Sequence 2, Appl  
Sequence 6, Appl  
Sequence 39, Appl



ALIGNMENTS

RESULT 1  
US-09-641-803-21  
; Sequence 21, Application US/09641803  
; Patent No. 6500798  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDGOUGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUTENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/09/641,803  
; CURRENT FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-09-641-803-21  
Query Match 100.0%; Score 18; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 8.4e-13;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 LQPEIMGVVKVKTNPVK 18  
Db 1 LQPEIMGVVKVKTNPVK 18  
RESULT 2  
US-09-985-357A-12  
; Sequence 12, Application US/09985357A  
; Patent No. 6544748  
; GENERAL INFORMATION:  
; APPLICANT: Anne STERN; Michael BRANDT; Konrad HONOLD; Johannes AUER; Hans KOLL  
; TITLE OF INVENTION: Preparation of erythropoietin by endogenous gene activation  
; FILE REFERENCE: HUBR 1151.1 CON EPF/MAS  
; CURRENT APPLICATION NUMBER: US/09/985,357A  
; CURRENT FILING DATE: 2001-11-02  
; PRIOR APPLICATION NUMBER: US 09/463,380  
; PRIOR FILING DATE: 2000-01-21  
; PRIOR APPLICATION NUMBER: PCT/EP98/04590  
; PRIOR FILING DATE: 1998-07-22  
; PRIOR APPLICATION NUMBER: US 09/113,692  
; PRIOR FILING DATE: 1998-07-10  
; PRIOR APPLICATION NUMBER: DE 19753681.1  
; PRIOR FILING DATE: 1997-12-03  
; PRIOR APPLICATION NUMBER: EP 97112640  
; PRIOR FILING DATE: 1997-07-23  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Wordperfect  
; SEQ ID NO 12  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Amino acid sequence of the modified signal peptide start coded by  
; OTHER INFORMATION: EX5  
US-09-985-357A-12  
Query Match 22.2%; Score 4; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 6 MGVP 9  
Db 1 MGVP 4  
RESULT 3  
US-09-113-692B-9  
; Sequence 9, Application US/09113692B  
; Patent No. 6548296  
; GENERAL INFORMATION:  
; APPLICANT: Stern, Anne  
; APPLICANT: Brandt, Michael  
; APPLICANT: Honold, Konrad  
; APPLICANT: Auer, Johannes  
; APPLICANT: Koll, Hans  
; APPLICANT: Franze, Reinhard  
; APPLICANT: Pessara, Ulrich  
; TITLE OF INVENTION: Methods For Identifying Human Cell Lines Useful for  
; TITLE OF INVENTION: Endogenous Gene Activation, Isolated Human Cell Lines  
; TITLE OF INVENTION: Identified Thereby, And Uses Thereof  
; FILE REFERENCE: Hubr 1126  
; CURRENT APPLICATION NUMBER: US/09/113,692B  
; CURRENT FILING DATE: 1998-07-10  
; PRIOR APPLICATION NUMBER: EP/97 112 640  
; PRIOR FILING DATE: 1997-07-23  
; PRIOR APPLICATION NUMBER: EP/97 121 073  
; PRIOR FILING DATE: 1997-12-01  
; PRIOR APPLICATION NUMBER: EP/97 53 681  
; PRIOR FILING DATE: 1997-12-03  
; NUMBER OF SEQ ID NOS: 10  
; SEQ ID NO 9  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-09-113-692B-9  
Query Match 22.2%; Score 4; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 6 MGVP 9  
Db 1 MGVP 4  
RESULT 4  
US-09-607-277A-9  
; Sequence 9, Application US/09607277A  
; Patent No. 6555373  
; GENERAL INFORMATION:  
; APPLICANT: Stern, Anne  
; APPLICANT: Brandt, Michael  
; APPLICANT: Honold, Konrad  
; APPLICANT: Auer, Johannes  
; APPLICANT: Koll, Hans  
; APPLICANT: Franze, Reinhard  
; APPLICANT: Pessara, Ulrich  
; TITLE OF INVENTION: Methods For Identifying Human Cell Lines Useful for  
; TITLE OF INVENTION: Endogenous Gene Activation, Isolated Human Cell Lines  
; TITLE OF INVENTION: Identified Thereby, And Uses Thereof  
; FILE REFERENCE: Hubr 1126.1  
; CURRENT APPLICATION NUMBER: US/09/607,277A  
; CURRENT FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/113,692  
; PRIOR FILING DATE: 1998-07-10  
; PRIOR APPLICATION NUMBER: EP/97 112 640  
; PRIOR FILING DATE: 1997-07-23  
; PRIOR APPLICATION NUMBER: EP/97 121 073  
; PRIOR FILING DATE: 1997-12-01  
; PRIOR APPLICATION NUMBER: EP/97 53 681  
; PRIOR FILING DATE: 1997-12-03

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; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 9
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-607-277A-9
    Query Match      22.2%; Score 4; DB 4; Length 4;
    Best Local Similarity 100.0%; Pred. No. 2.5e+05;
    Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 MGVP 9
      ||||
Db      1 MGVP 4

RESULT 5
US-08-760-075A-29
; Sequence 29, Application US/08760075A
; Patent No. 5942429
; GENERAL INFORMATION:
; APPLICANT: KIRSCHBAUM, Bernd
; APPLICANT: MUELLNER, Stefan
; APPLICANT: BARTLETT, Robert
; TITLE OF INVENTION: NOVEL DEAH-BOX PROTEINS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 19545126.0
; FILING DATE: 04-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 18748/309
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-760-075A-29
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-760-075A-29

    Query Match      22.2%; Score 4; DB 2; Length 5;
    Best Local Similarity 100.0%; Pred. No. 2.5e+05;
    Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 IMGV 8
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Db      2 IMGV 5

RESULT 6
US-09-338-546-29
; Sequence 29, Application US/09338546
; Patent No. 6251645
; GENERAL INFORMATION:
; APPLICANT: KIRSCHBAUM, Bernd
; APPLICANT: MUELLNER, Stefan
; APPLICANT: BARTLETT, Robert
; TITLE OF INVENTION: NOVEL DEAH-BOX PROTEINS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 04-DEC-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08760,075
; FILING DATE: 04-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 18748/309
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-338-546-29
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-338-546-29

    Query Match      22.2%; Score 4; DB 3; Length 5;
    Best Local Similarity 100.0%; Pred. No. 2.5e+05;
    Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 IMGV 8
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Db      2 IMGV 5

RESULT 7
US-09-659-084-29
; Sequence 29, Application US/09659084
; Patent No. 6403299
; GENERAL INFORMATION:
; APPLICANT: KIRSCHBAUM, Bernd
; APPLICANT: MUELLNER, Stefan
; APPLICANT: BARTLETT, Robert
; TITLE OF INVENTION: NOVEL DEAH-BOX PROTEINS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/659,084
; FILING DATE: 11-Sep-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/338,546
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 18748/309
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-659-084-29
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; Query Match 22.2%; Score 4; DB 4; Length 5;
; Best Local Similarity 100.0%; Pred. No. 2.5e+05;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Qy 5 IMGV 8
; Db 2 IMGV 5
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; RESULT 8
; US-08-480-793-14
; Sequence 14, Application US/08480793
; Patent No. 5955444
; GENERAL INFORMATION:
; APPLICANT: Ingram, Vernon M., Roder, Hanno M.
; TITLE OF INVENTION: No. 5955444el Tau/Neurofilament Protein
; TITLE OF INVENTION: Kinases
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Massachusetts Institute of Technology
; STREET: 28 Carleton Street
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch
; COMPUTER: IBM-compatible
; OPERATING SYSTEM: MS-DOS Version 3.3
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,793
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/912,293
; FILING DATE: July 10, 1992
; APPLICATION NUMBER: 07/742,880
; FILING DATE: 9-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Gates, Edward R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: M0656/7008
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US92-05825A-14
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; Query Match 22.2%; Score 4; DB 5; Length 6;
; Best Local Similarity 100.0%; Pred. No. 2.5e+05;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Qy 3 PEIM 6
; Db 2 PEIM 5
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; RESULT 10
; US-09-258-754-383
; Sequence 383, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-480-793-14
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; Query Match 22.2%; Score 4; DB 2; Length 6;
; Best Local Similarity 100.0%; Pred. No. 2.5e+05;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Qy 3 PEIM 6
; Db 2 PEIM 5
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; RESULT 9
; PCT-US92-05825A-14
; Sequence 14, Application PC/TUS9205825A
; GENERAL INFORMATION:
; APPLICANT: Ingram, Vernon M., Roder, Hanno M.
; TITLE OF INVENTION: Novel Tau/Neurofilament Protein
; TITLE OF INVENTION: Kinases
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Massachusetts Institute of Technology
; STREET: 28 Carleton Street
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch
; COMPUTER: IBM-compatible
; OPERATING SYSTEM: MS-DOS Version 3.3
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05825A
; FILING DATE: 19920710
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/742,880
; FILING DATE: 9-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Gates, Edward R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: M0656/7008
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US92-05825A-14
;
; Query Match 22.2%; Score 4; DB 5; Length 6;
; Best Local Similarity 100.0%; Pred. No. 2.5e+05;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Qy 3 PEIM 6
; Db 2 PEIM 5
;
; RESULT 10
; US-09-258-754-383
; Sequence 383, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
```

```
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 383
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-383

Query Match      22.2%; Score 4; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PKVK 12
Db      1 PKVK 4

RESULT 11
US-09-042-107-383
; Sequence 383, Application US/09042107
; Patent No. 6232287
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 2892
; CURRENT APPLICATION NUMBER: US/09/042,107
; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 436
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 383
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-042-107-383

Query Match      22.2%; Score 4; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PKVK 12
Db      1 PKVK 4

RESULT 12
US-09-641-803-16
; Sequence 16, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 7
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-641-803-16

Query Match      22.2%; Score 4; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LQPE 4
Db      4 LQPE 7

RESULT 13
US-09-296-284-14
; Sequence 14, Application US/09296284A
; Patent No. 6204040
; GENERAL INFORMATION:
; APPLICANT: Choi, Bui-Sung
; APPLICANT: Rhee, Sang-Ki
; APPLICANT: Lee, Eun-Hae
; TITLE OF INVENTION: Gluconobacter Suboxydans Sorbitol Dehydrogenase, Genes
; TITLE OF INVENTION: and Methods of Use Thereof
; FILE REFERENCE: 1533.0870000
; CURRENT APPLICATION NUMBER: US/09/296,284A
; CURRENT FILING DATE: 1999-04-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Gluconobacter suboxydans
US-09-296-284-14

Query Match      22.2%; Score 4; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GVPK 10
Db      5 GVPK 8

RESULT 14
US-08-217-188A-62
; Sequence 62, Application US/08217188A
; Patent No. 5554724
; GENERAL INFORMATION:
; APPLICANT: Melief, Cornelis J. M.
; APPLICANT: Visseren, M. J. W.
; APPLICANT: Kast, W. M.
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Tumor Rejection Antigen
; TITLE OF INVENTION: Precursor MAG8-2 Derived Peptides, and Uses Thereof
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/217,188A
; FILING DATE: 24-MARCH-1994
```

```
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5554724man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5340
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-217-188A-62

Query Match 22.2%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4
Db 4 LQPE 7

RESULT 15
US-08-687-226-62
; Sequence 62, Application US/08687226
; Patent No. 5686068
; GENERAL INFORMATION:
; APPLICANT: Melief, Cornelis J. M.; Visseren, M. W.;
; APPLICANT: van der Burg, Sjoerd; van der Bruggen, Pierre;
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Peptides Derived From
; TITLE OF INVENTION: Mage-2, Cytolytic T Cells Specific To Complexes Of
; TITLE OF INVENTION: Peptides And HLA-A2 Molecules, And Uses Thereof
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,226
; FILING DATE: 25-JULY-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/217,188
; FILING DATE: 24-MARCH-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5686068man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5447
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-687-226-62

Query Match 22.2%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-09-641-801-21.oligo.ra1

; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5554724man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5340
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-217-188A-62

Query Match 22.2%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4
Db 4 LQPE 7

RESULT 16
US-08-467-083-2
; Sequence 2, Application US/08467083
; Patent No. 5726023
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,083
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/414,417
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; TELEX: 3723836 SEEDANBERRY
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-467-083-2

Query Match 22.2%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4
Db 2 LQPE 5

RESULT 17
US-08-615-181-79
; Sequence 79, Application US/08615181
; Patent No. 5756666
; GENERAL INFORMATION:
; APPLICANT: MASAFUML, TAKIGUCHI
; APPLICANT: MIWA, KIYOSHI
; TITLE OF INVENTION: PEPTIDES CAPABLE OF INDUCING IMMUNE
; TITLE OF INVENTION: RESPONSE TO HIV AND ANTI-AIDS AGENT FOR PREVENTING AND
; TITLE OF INVENTION: CURING AIDS
; NUMBER OF SEQUENCES: 115
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
ADDRESSEE: P.C.  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/615,181  
FILING DATE: 04-APR-1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP94/01756  
FILING DATE: 19-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 261302/1993  
FILING DATE: 19-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 10-796-0 PCT  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 79:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-08-615-181-79

Query Match 22.2%; Score 4; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12  
Db |||||  
2 PKVK 5

RESULT 18  
US-08-787-547-104  
Sequence 104, Application US/08787547  
Patent No. 5783567  
GENERAL INFORMATION:  
APPLICANT: Hedley, Mary Lynne  
APPLICANT: Curley, Joanne M.  
APPLICANT: Langer, Robert S.  
TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY  
TITLE OF INVENTION: OF NUCLEIC ACID  
NUMBER OF SEQUENCES: 107  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/787,547  
FILING DATE: 22-JAN-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 08191/003001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 104:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-787-547-104

Query Match 22.2%; Score 4; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4  
Db |||||  
5 LQPE 8

RESULT 19  
US-08-414-417B-2  
Sequence 2, Application US/08414417B  
Patent No. 5801005  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
APPLICANT: Disis, Mary L.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/414,417B  
FILING DATE: 31-MAR-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-414-417B-2

Query Match 22.2%; Score 4; DB 1; Length 9;

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Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQPE 4
Db 2 LQPE 5

RESULT 20
US-08-486-348A-2
; Sequence 2, Application US/08486348A
; Patent No. 5846538
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486.348A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-486-348A-2

Query Match 22.2%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQPE 4
Db 2 LQPE 5

RESULT 21
US-08-468-545B-2
; Sequence 2, Application US/08468545B
; Patent No. 5876712
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
```

```
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468.545B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-468-545B-2

Query Match 22.2%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQPE 4
Db 2 LQPE 5

RESULT 22
US-08-948-378A-17
; Sequence 17, Application US/08948378A
; Patent No. 6013258
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; APPLICANT: Collins, Edward J.
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM
; TITLE OF INVENTION: THE HPV E7 PROTEIN
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/948.378A
; FILING DATE: 09-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-543-8906
; TELEX: 200154
```

```

; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 9 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-08-948-378A-17

Query Match      22.2%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LOPE 4
Db      5 LQPE 8

RESULT 23
US-08-667-725B-62
; Sequence 62, Application US/08667725B
; GENERAL INFORMATION:
; APPLICANT: Melief, Cornelis J. M.
; APPLICANT: Visseren, M. J. W.
; APPLICANT: Kast, W. M.
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Tumor Rejection Antigen
; TITLE OF INVENTION: Precursor MAGE-2 Derived Peptides, and Uses Thereof
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,725B
; FILING DATE: 21 June 1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6063900man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LJD 5340.1 DIV (081585)
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 9 amino acid residues
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-667-725B-62

Query Match      22.2%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LOPE 4
Db      4 LQPE 7

RESULT 24
US-08-466-680B-2
; Sequence 2, Application US/08466680B
; Patent No. 6075122
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; MOLECULE TYPE: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,680B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 9 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
US-08-466-680B-2

Query Match      22.2%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LOPE 4
Db      2 LQPE 5

RESULT 25
US-09-007-748-62
; Sequence 62, Application US/09007748
; Patent No. 6147187
; GENERAL INFORMATION:
; APPLICANT: Melief, Cornelis J. M.
; APPLICANT: Visseren, M. J. W.
; APPLICANT: Kast, W. M.
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Tumor Rejection Antigen
; TITLE OF INVENTION: Precursor MAGE-2 Derived Peptides, and Uses Thereof
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:

```



APPLICATION NUMBER: US/09/007,748  
FILING DATE: 15 January 1998  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 6147187man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LUD 5340.2 DIV (081572)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 318-3000  
TELEFAX: (212) 752-5958  
INFORMATION FOR SEQ ID NO: 62:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acid residues  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-007-748-62

Query Match 22.2%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 1 LOPE 4  
Db 4 LOPE 7

RESULT 26  
US-09-169-425C-17  
Sequence 17, Application US/09169425C  
Patent No. 6183746  
GENERAL INFORMATION:  
APPLICANT: Urban, Robert G.  
APPLICANT: Chiciz, Roman M.  
APPLICANT: Collins, Edward J.  
APPLICANT: Hedley, Mary Lynn  
TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7  
TITLE OF INVENTION: PROTEIN  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/169,425C  
FILING DATE: 09-OCT-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/061,657  
FILING DATE: 09-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 08191/004002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-543-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-169-425C-17

Query Match 22.2%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 1 LOPE 4  
Db 5 LOPE 8

RESULT 27  
US-08-197-484-28  
Sequence 28, Application US/08197484  
Patent No. 641931  
GENERAL INFORMATION:  
APPLICANT: VITIELLO, Maria A.  
APPLICANT: CHESTNUT, Robert W.  
APPLICANT: SETTE, Alessandro D.  
APPLICANT: CELIS, Esteban  
APPLICANT: GRAY, Howard  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING  
TITLE OF INVENTION: CTL IMMUNITY  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: Steuart Street Tower, One Market Plaza  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94105-1493  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/197,484  
FILING DATE: 16-FEB-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/935,811  
FILING DATE: 26-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/874,491  
FILING DATE: 27-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/827,682  
FILING DATE: 29-JAN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/749,568  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 14137-26-4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 467-9600  
TELEFAX: (206) 623-6793  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-197-484-28

Query Match 22.2%; Score 4; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 9 PKVK 12  
Db 2 PKVK 5

RESULT 28  
US-08-197-484-66  
; Sequence 66, Application US/08197484  
; Patent No. 6419931  
; GENERAL INFORMATION:  
; APPLICANT: VITIELLO, Maria A.  
; APPLICANT: CHESTNUT, Robert W.  
; APPLICANT: SETTE, Alessandro D.  
; APPLICANT: CELIS, Esteban  
; APPLICANT: GRAY, Howard  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING  
; TITLE OF INVENTION: CTL IMMUNITY  
; NUMBER OF SEQUENCES: 153  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Khourie and Crew  
; STREET: Steuart Street Tower, One Market Plaza  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: US  
; ZIP: 94105-1493  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/197,484  
; FILING DATE: 16-FEB-1994  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/935,811  
; FILING DATE: 26-AUG-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/874,491  
; FILING DATE: 27-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/827,682  
; FILING DATE: 29-JAN-1992  
; APPLICATION NUMBER: US 07/749,568  
; FILING DATE: 26-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parmelee, Steven W.  
; REGISTRATION NUMBER: 31,990  
; REFERENCE/DOCKET NUMBER: 14137-26-4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 467-9600  
; TELEFAX: (206) 623-6793  
; INFORMATION FOR SEQ ID NO: 66:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-197-484-66

Query Match 22.2%; Score 4; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4  
Db 5 LQPE 8

RESULT 29  
US-08-197-484-71  
; Sequence 71, Application US/08197484  
; Patent No. 6419931  
; GENERAL INFORMATION:

; APPLICANT: VITIELLO, Maria A.  
; APPLICANT: CHESTNUT, Robert W.  
; APPLICANT: SETTE, Alessandro D.  
; APPLICANT: CELIS, Esteban  
; APPLICANT: GRAY, Howard  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING  
; TITLE OF INVENTION: CTL IMMUNITY  
; NUMBER OF SEQUENCES: 153  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Khourie and Crew  
; STREET: Steuart Street Tower, One Market Plaza  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: US  
; ZIP: 94105-1493  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/197,484  
; FILING DATE: 16-FEB-1994  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/935,811  
; FILING DATE: 26-AUG-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/874,491  
; FILING DATE: 27-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/827,682  
; FILING DATE: 29-JAN-1992  
; APPLICATION NUMBER: US 07/749,568  
; FILING DATE: 26-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parmelee, Steven W.  
; REGISTRATION NUMBER: 31,990  
; REFERENCE/DOCKET NUMBER: 14137-26-4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 467-9600  
; TELEFAX: (206) 623-6793  
; INFORMATION FOR SEQ ID NO: 71:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-197-484-71

Query Match 22.2%; Score 4; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4  
Db 4 LQPE 7

RESULT 30  
US-08-403-459-12  
; Sequence 12, Application US/08403459  
; Patent No. 6514942  
; GENERAL INFORMATION:

; APPLICANT: Ioannides, Constantine G.  
; APPLICANT: Fisk, Bryan A.  
; APPLICANT: Ioannides, Maria G.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING  
; TITLE OF INVENTION: T-LYMPHOCYTES  
; NUMBER OF SEQUENCES: 68  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: United States of America  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/403,459  
FILING DATE: Concurrently Herewith  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Kitchell, Barbara S.  
REGISTRATION NUMBER: 33,928  
REFERENCE/DOCKET NUMBER: UTSC:390/KIT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (713) 789-2679  
TELEX: 79-0924  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-403-459-12

Query Match 22.2%; Score 4; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOPE 4  
Db 2 LOPE 5

RESULT 31  
US-09-759-960-17  
Sequence 17, Application US/09759960  
Patent No. 6582704  
GENERAL INFORMATION:  
APPLICANT: Urban, Robert G.  
APPLICANT: Chiciz, Roman M.  
APPLICANT: Collins, Edward J.  
APPLICANT: Hedley, Mary Lynn  
TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7  
TITLE OF INVENTION: PROTEIN  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/759,960  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/169,425  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K.

REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 08191/004002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-543-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-759-960-17

Query Match 22.2%; Score 4; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOPE 4  
Db 5 LOPE 8

RESULT 32  
PCT-US95-02121-28  
Sequence 28, Application PC/TUS9502121  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING  
TITLE OF INVENTION: CTL IMMUNITY  
NUMBER OF SEQUENCES: 153  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/02121  
FILING DATE: 16-FEB-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/197,484  
FILING DATE: 16-FEB-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/935,811  
FILING DATE: 26-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/874,491  
FILING DATE: 27-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/827,682  
FILING DATE: 29-JAN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/749,568  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 14137-26-4PC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 467-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
PCT-US95-02121-28

Query Match 22.2%; Score 4; DB 5; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PKVK 12  
|||||  
Db 2 PKVK 5

## RESULT 33

PCT-US95-02121-66  
; Sequence 66, Application PC/TUS9502121  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING  
; TITLE OF INVENTION: CTL IMMUNITY  
; NUMBER OF SEQUENCES: 153  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/02121  
; FILING DATE: 16-FEB-1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/197,484  
; FILING DATE: 16-FEB-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/935,811  
; FILING DATE: 26-AUG-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/874,491  
; FILING DATE: 27-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/827,682  
; FILING DATE: 29-JAN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/749,568  
; FILING DATE: 26-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parmelee, Steven W.  
; REGISTRATION NUMBER: 31,990  
; REFERENCE/DOCKET NUMBER: 14137-26-4PC  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 467-9600  
; TELEFAX: (415) 543-5043  
; INFORMATION FOR SEQ ID NO: 66:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
PCT-US95-02121-66

Query Match 22.2%; Score 4; DB 5; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQPE 4  
|||||  
Db 5 LQPE 8

## RESULT 34

PCT-US95-02121-71  
; Sequence 71, Application PC/TUS9502121  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING  
; TITLE OF INVENTION: CTL IMMUNITY  
; NUMBER OF SEQUENCES: 153  
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/02121  
; FILING DATE: 16-FEB-1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/197,484  
; FILING DATE: 16-FEB-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/935,811  
; FILING DATE: 26-AUG-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/874,491  
; FILING DATE: 27-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/827,682  
; FILING DATE: 29-JAN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/749,568  
; FILING DATE: 26-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parmelee, Steven W.  
; REGISTRATION NUMBER: 31,990  
; REFERENCE/DOCKET NUMBER: 14137-26-4PC  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 467-9600  
; TELEFAX: (415) 543-5043  
; INFORMATION FOR SEQ ID NO: 71:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
PCT-US95-02121-71

Query Match 22.2%; Score 4; DB 5; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQPE 4  
|||||  
Db 4 LQPE 7

## RESULT 35

US-08-902-516-19  
; Sequence 19, Application US/08902516  
; Patent No. 5891432  
; GENERAL INFORMATION:  
; APPLICANT: Soo Hoo, William  
; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS  
; TITLE OF INVENTION: COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE  
; TITLE OF INVENTION: RESPONSE USING SAME  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CAMPBELL & FLORES, LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92121  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/902,516  
; FILING DATE: 29-JUL-1997

CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-IM 2442  
TELEPHONE: (619)535-9001  
TELEFAX: (619)535-8949  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-902-516-19

Query Match 22.2%; Score 4; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 1 LQPE 4  
Db 5 LQPE 8

RESULT 36  
US-08-760-075A-34  
Sequence 34, Application US/08760075A  
Patent No. 5942429  
GENERAL INFORMATION:  
APPLICANT: KIRSCHBAUM, Bernd  
APPLICANT: MUELLNER, Stefan  
APPLICANT: BARTLETT, Robert  
TITLE OF INVENTION: NOVEL DEAH-BOX PROTEINS  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: 04-DEC-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION NUMBER: DE 19545126.0  
FILING DATE: 04-DEC-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: GRANADOS, Patricia D.  
REGISTRATION NUMBER: 33,683  
REFERENCE/DOCKET NUMBER: 18748/309  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-760-075A-34

Query Match 22.2%; Score 4; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 5 IMGV 8  
Db 5 IMGV 8

RESULT 37  
US-08-704-344-22  
Sequence 22, Application US/08704344  
Patent No. 6218363  
GENERAL INFORMATION:  
APPLICANT: BASERGA, Renato L.  
APPLICANT: RESNICOFF, Mariana  
APPLICANT: HUANG, Ziwei  
TITLE OF INVENTION: MHC PEPTIDES AND METHODS OF USE  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HALE and DORR LLP  
STREET: 1455 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: 28-AUG-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: WIXON, Henry N.  
REGISTRATION NUMBER: 32,073  
REFERENCE/DOCKET NUMBER: 104322.196  
TELEPHONE: (202) 942-8459  
TELEFAX: (202) 942-8484  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-704-344-22

Query Match 22.2%; Score 4; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 1 LQPE 4  
Db 5 LQPE 8

RESULT 38  
US-09-338-546-34  
Sequence 34, Application US/09338546  
Patent No. 6251645  
GENERAL INFORMATION:  
APPLICANT: KIRSCHBAUM, Bernd  
APPLICANT: MUELLNER, Stefan  
APPLICANT: BARTLETT, Robert  
TITLE OF INVENTION: NOVEL DEAH-BOX PROTEINS  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington

STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/338,546  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/760,075  
FILING DATE: 04-DEC-1996  
APPLICATION NUMBER: DE 19545126.0  
FILING DATE: 04-DEC-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: GRANADOS, Patricia D.  
REGISTRATION NUMBER: 33,683  
REFERENCE/DOCKET NUMBER: 18748/309  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-338-546-34

Query Match 22.2%; Score 4; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IMGV 8  
Db 5 IMGV 8

RESULT 39  
US-09-461-697-283  
Sequence 283, Application US/09461697  
Patent No. 6277974  
GENERAL INFORMATION:  
APPLICANT: COGENT NEUROSCIENCE, Inc.  
APPLICANT: Lo, Donald C.  
APPLICANT: Barney, Shawn  
APPLICANT: Thomas, Mary Beth  
APPLICANT: Portbury, Stuart D.  
APPLICANT: Purnam, Kasturi  
APPLICANT: Katz, Lawrence C.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING  
TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING  
FILE REFERENCE: 10001-005-999  
CURRENT FILING DATE: 1999-12-14  
NUMBER OF SEQ ID NOS: 466  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 283  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-461-697-283

Query Match 22.2%; Score 4; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 MVPK 18

Db 1 MVPK 4  
RESULT 40  
US-09-659-084-34  
Sequence 34, Application US/09659084  
Patent No. 6403299  
GENERAL INFORMATION:  
APPLICANT: KIRSCHBAUM, Bernd  
MUELLNER, Stefan  
BARTLETT, Robert  
TITLE OF INVENTION: NOVEL DEAH-BOX PROTEINS  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/659,084  
FILING DATE: 11-Sep-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/338,546  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: GRANADOS, Patricia D.  
REGISTRATION NUMBER: 33,683  
REFERENCE/DOCKET NUMBER: 18748/309  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 34:  
US-09-659-084-34

Query Match 22.2%; Score 4; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IMGV 8  
Db 5 IMGV 8

RESULT 41  
US-09-847-185-19  
Sequence 19, Application US/09847185  
Patent No. 6482407  
GENERAL INFORMATION:  
APPLICANT: SOO HOO, William  
TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS  
COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE  
RESPONSE USING SAME  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CAMPBELL & FLORES, LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego

```

; STATE: California
; COUNTRY: United States
; ZIP: 92121
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/847,185
; FILING DATE: 01-May-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/201,931
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IM 2442
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)535-9001
; TELEFAX: (619)535-8949
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-847-185-19

Query Match 22.2%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 1 LOPE 4
Db 5 LOPE 8

RESULT 42
US-09-214-307A-13
; Sequence 13, Application US/09214307A
; Patent No. 6544516
; GENERAL INFORMATION:
; APPLICANT: NEUTEC PHARMA PLC
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF INFECTIONS OF GRAM POSITIVE
; FILE REFERENCE: PM 259204
; CURRENT APPLICATION NUMBER: US/09/214,307A
; CURRENT FILING DATE: 1999-01-04
; PRIOR APPLICATION NUMBER: PCT/GB97/01830
; PRIOR FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: GB9614274.0
; PRIOR FILING DATE: 1996-07-06
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-214-307A-13

Query Match 22.2%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GVPK 10
Db 7 GVPK 10

RESULT 43
; Sequence 1, Application US/08760075A
; Patent No. 5942429
; GENERAL INFORMATION:
; APPLICANT: KIRSCHBAUM, Bernd
; APPLICANT: MUELLNER, Stefan
; APPLICANT: BARTLETT, Robert
; TITLE OF INVENTION: NOVEL DEAH-BOX PROTEINS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/760,075A
; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 19545126.0
; FILING DATE: 04-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 18748/309
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-760-075A-1

Query Match 22.2%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 IMGV 8
Db 5 IMGV 8

RESULT 44
US-09-101-886B-57
; Sequence 57, Application US/09101886B
; Patent No. 6197507
; GENERAL INFORMATION:
; APPLICANT: BERG, THOMAS
; APPLICANT: TOLLERSRUD, OLE K
; APPLICANT: NILSEN, OIVIND
; TITLE OF INVENTION: GENETIC TEST FOR ALPHA-MANNOSIDOSIS
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BARBARA G. ERNST
; STREET: 555 13TH STREET, NW SUITE 701E
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/101,886B  
; FILING DATE: 29-JANUARY-1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB97/00109  
; FILING DATE: 12-JAN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ERNST, BARBARA G  
; REGISTRATION NUMBER: 30,377  
; REFERENCE/DOCKET NUMBER: 1181-240  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-783-6040  
; TELEFAX: 202-783-6031  
; INFORMATION FOR SEQ ID NO: 57:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: not relevant  
; ANTI-SENSE: not relevant  
; FRAGMENT TYPE: internal  
; US-09-101-886B-57

Query Match 22.2%; Score 4; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 IMGV 12  
Db 7 PKVK 10

RESULT 45  
US-09-338-546-1  
; Sequence 1, Application US/09338546  
; Patent No. 6251645  
; GENERAL INFORMATION:  
; APPLICANT: KIRSCHBAUM, Bernd  
; APPLICANT: MUELLNER, Stefan  
; APPLICANT: BARTLETT, Robert  
; TITLE OF INVENTION: NOVEL DEAH-BOX PROTEINS  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/338,546  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/760,075  
; FILING DATE: 04-DEC-1996  
; APPLICATION NUMBER: DE 19545126.0  
; FILING DATE: 04-DEC-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: GRANADOS, Patricia D.  
; REGISTRATION NUMBER: 33,683  
; REFERENCE/DOCKET NUMBER: 18748/309  
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-09-338-546-1

Query Match 22.2%; Score 4; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IMGV 8  
Db 5 IMGV 8

RESULT 46  
US-09-659-084-1  
; Sequence 1, Application US/09659084  
; Patent No. 6403299  
; GENERAL INFORMATION:  
; APPLICANT: KIRSCHBAUM, Bernd  
; APPLICANT: MUELLNER, Stefan  
; APPLICANT: BARTLETT, Robert  
; TITLE OF INVENTION: NOVEL DEAH-BOX PROTEINS  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/659,084  
; FILING DATE: 11-Sep-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/338,546  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: GRANADOS, Patricia D.  
; REGISTRATION NUMBER: 33,683  
; REFERENCE/DOCKET NUMBER: 18748/309  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
; US-09-659-084-1

Query Match 22.2%; Score 4; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IMGV 8  
Db 5 IMGV 8



```
RESULT 47
US-08-949-059A-29
; Sequence 29, Application US/08949059A
; Patent No. 6358921
; GENERAL INFORMATION:
; APPLICANT: Kondejewski, Leslie H.
; APPLICANT: Hodges, Robert S.
; APPLICANT: Wishart, David S.
; APPLICANT: Hancock, Robert E.W.
; APPLICANT: McElhaney, Ronald N.
; APPLICANT: Prenner, Elmar J.
; APPLICANT: Lewis, Ruthven N.A.H.
; APPLICANT: SEED and BERRY LLP
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE COMPOSITIONS AND
; TITLE OF INVENTION: METHOD
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/949,059A
; FILING DATE: 10-OCT-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 660081.412
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: cyclic
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
US-08-949-059A-29
Query Match 22.2%; Score 4; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 PKVK 12
Db 8 PKVK 11
RESULT 48
US-08-949-059A-31
; Sequence 31, Application US/08949059A
; Patent No. 6358921
; GENERAL INFORMATION:
```

```
; APPLICANT: Kondejewski, Leslie H.
; APPLICANT: Hodges, Robert S.
; APPLICANT: Wishart, David S.
; APPLICANT: Hancock, Robert E.W.
; APPLICANT: McElhaney, Ronald N.
; APPLICANT: Prenner, Elmar J.
; APPLICANT: Lewis, Ruthven N.A.H.
; APPLICANT: SEED and BERRY LLP
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE COMPOSITIONS AND
; TITLE OF INVENTION: METHOD
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/949,059A
; FILING DATE: 10-OCT-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 660081.412
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: cyclic
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "Residue is a D-Phenylalanine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: /note= "Residue is a D-Phenylalanine"
US-08-949-059A-31
Query Match 22.2%; Score 4; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 PKVK 12
Db 8 PKVK 11
RESULT 49
US-08-949-059A-31
; Patent No. 5460961
; APPLICANT: DEBY, CAROL/PINCMAIL, JOEL/BOLLEN, ALEX
; TITLE OF INVENTION: HUMAN MYELOPEROXIDASE AND ITS
; THERAPEUTIC APPLICATION
; NUMBER OF SEQUENCES: 13
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/641,678
; FILING DATE: 16-JAN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 460,931
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; FILING DATE: 14-FEB-1990

; SEQ ID NO:8;

; LENGTH: 12

5460961-8

Query Match 22.2%; Score 4; DB 6; Length 12;

Best Local Similarity 100.0%; Pred. No. 2.2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 MGVP 9

Db 1 MGVP 4

RESULT 50

US-07-610-525-5

; Sequence 5, Application US/07610525

; Patent No. 5196512

; GENERAL INFORMATION:

; APPLICANT: BIANCHI Elisabetta

; APPLICANT: PESSI Antonello

; APPLICANT: CORRADIN Giampietro

; TITLE OF INVENTION: SYNTHETIC PEPTIDES USEFUL AS

; UNIVERSAL CARRIERS FOR THE PREPARATION OF IMMUNOGENIC CONJUGATES

; AND THEIR USE IN THE DEVELOPMENT OF SYNTHETIC VACCINES.

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SHEA & GOULD

; STREET: 1251 AVENUE OF THE AMERICAS

; CITY: NEW YORK

; STATE: NEW YORK

; COUNTRY: UNITED STATES

; ZIP: 10020-1193

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.24

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/610,525

; FILING DATE: 19901108

; CLASSIFICATION: 424

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-827-3000

; TELEFAX: 212-840-6702

; TELEX: 423973

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 13 amino acid residues

; TYPE: AMINO ACID

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: no

; FRAGMENT TYPE: internal fragment

US-07-610-525-5

Query Match

Best Local Similarity 22.2%; Score 4; DB 1; Length 13;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VPKV 11

Db 4 VPKV 7

RESULT 51

US-08-403-459-36

; Sequence 36, Application US/08403459

; Patent No. 6514942

; GENERAL INFORMATION:

; APPLICANT: Ioannides, Constantine G.

; APPLICANT: Fisk, Bryan A.

; APPLICANT: Ioannides, Maria G.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING

; T-LYMPHOCYTES

; NUMBER OF SEQUENCES: 68

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

; STREET: P.O. Box 4433

; CITY: Houston

; STATE: Texas

; COUNTRY: United States of America

; ZIP: 77210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/403,459

; FILING DATE: Concurrently Herewith

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Kitchell, Barbara S.

; REGISTRATION NUMBER: 33,928

; REFERENCE/DOCKET NUMBER: UTSC:390/KIT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (512) 418-3000

; TELEFAX: (713) 789-2679

; TELEX: 79-0924

; INFORMATION FOR SEQ ID NO: 36:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 13 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-403-459-36

Query Match

Best Local Similarity 22.2%; Score 4; DB 4; Length 13;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQPE 4

Db 1 LQPE 4

RESULT 52

US-08-949-059A-26

; Sequence 26, Application US/08949059A

; Patent No. 6358921

; GENERAL INFORMATION:

; APPLICANT: Kondejewski, Leslie H.

; APPLICANT: Hodges, Robert S.

; APPLICANT: Wishart, David S.

; APPLICANT: Hancock, Robert E.W.

; APPLICANT: McElhaney, Ronald N.

; APPLICANT: Prenner, Elmar J.

; APPLICANT: Lewis, Ruthven N.A.H.

; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE COMPOSITIONS AND

; METHOD

; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SEED and BERRY LLP

; STREET: 6300 Columbia Center, 701 Fifth Avenue

; CITY: Seattle

; STATE: Washington

; COUNTRY: USA

; ZIP: 98104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/949,059A  
;; FILING DATE: 10-OCT-1997  
;; CLASSIFICATION: 514  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: McMasters, David D.  
;; REGISTRATION NUMBER: 33,963  
;; REFERENCE/DOCKET NUMBER: 660081.412  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (206) 622-4900  
;; TELEFAX: (206) 682-6031  
;; INFORMATION FOR SEQ ID NO: 26:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 14 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: cyclic  
;; MOLECULE TYPE: peptide  
;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
;; FEATURE:  
;; NAME/KEY: Modified-site  
;; LOCATION: 6  
;; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"  
;; FEATURE:  
;; NAME/KEY: Modified-site  
;; LOCATION: 13  
;; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"  
;; US-08-949-059A-26

Query Match 22.2%; Score 4; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12  
DB 7 PKVK 10

RESULT 53  
US-08-949-059A-27  
; Sequence 27, Application US/08949059A  
; Patent No. 6358921  
; GENERAL INFORMATION:  
; APPLICANT: Kondejewski, Leslie H.  
; APPLICANT: Hodges, Robert S.  
; APPLICANT: Wishart, David S.  
; APPLICANT: Hancock, Robert E.W.  
; APPLICANT: McElhaney, Ronald N.  
; APPLICANT: Prenner, Elmar J.  
; APPLICANT: Lewis, Ruthven N.A.H  
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE COMPOSITIONS AND  
; TITLE OF INVENTION: METHOD  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED AND BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/949,059A  
; FILING DATE: 10-OCT-1997  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMasters, David D.  
; REGISTRATION NUMBER: 33,963

;; REFERENCE/DOCKET NUMBER: 660081.412  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (206) 622-4900  
;; TELEFAX: (206) 682-6031  
;; INFORMATION FOR SEQ ID NO: 27:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 14 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: cyclic  
;; MOLECULE TYPE: peptide  
;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
;; FEATURE:  
;; NAME/KEY: Modified-site  
;; LOCATION: 1  
;; OTHER INFORMATION: /note= "Residue is a D-Lysine"  
;; FEATURE:  
;; NAME/KEY: Modified-site  
;; LOCATION: 6  
;; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"  
;; FEATURE:  
;; NAME/KEY: Modified-site  
;; LOCATION: 13  
;; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"  
;; US-08-949-059A-27

Query Match 22.2%; Score 4; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12  
DB 7 PKVK 10

RESULT 54  
US-08-949-059A-28  
; Sequence 28, Application US/08949059A  
; Patent No. 6358921  
; GENERAL INFORMATION:  
; APPLICANT: Kondejewski, Leslie H.  
; APPLICANT: Hodges, Robert S.  
; APPLICANT: Wishart, David S.  
; APPLICANT: Hancock, Robert E.W.  
; APPLICANT: McElhaney, Ronald N.  
; APPLICANT: Prenner, Elmar J.  
; APPLICANT: Lewis, Ruthven N.A.H  
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE COMPOSITIONS AND  
; TITLE OF INVENTION: METHOD  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED AND BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/949,059A  
; FILING DATE: 10-OCT-1997  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 660081.412  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900

; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 28:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: cyclic  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 2  
; OTHER INFORMATION: /note= "Residue is a D-Valine"  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 6  
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 13  
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"  
; US-08-949-059A-28  
Query Match 22.2%; Score 4; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 9 PKVK 12  
DB 7 PKVK 10  
RESULT 55  
US-07-610-525-4  
; Sequence 4, Application US/07610525  
; Patent No. 5196512  
; GENERAL INFORMATION:  
; APPLICANT: BIANCHI Elisabetta  
; APPLICANT: PESSI Antonello  
; APPLICANT: CORRADIN Giampaolo  
; TITLE OF INVENTION: SYNTHETIC PEPTIDES USEFUL AS  
; TITLE OF INVENTION: UNIVERSAL CARRIERS FOR THE PREPARATION OF IMMUNOGENIC CONJUGATES  
; TITLE OF INVENTION: AND THEIR USE IN THE DEVELOPMENT OF SYNTHETIC VACCINES.  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SHEA & GOULD  
; STREET: 1251 AVENUE OF THE AMERICAS  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: UNITED STATES  
; ZIP: 10020-1193  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/610,525  
; FILING DATE: 19901108  
; CLASSIFICATION: 424  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-827-3000  
; TELEFAX: 212-840-6702  
; TELEX: 423973  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acid residues  
; TYPE: AMINO ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: no

; FRAGMENT TYPE: internal fragment  
; US-07-610-525-4  
Query Match 22.2%; Score 4; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 VPKV 11  
DB 6 VPKV 9  
RESULT 56  
US-08-097-997A-2  
; Sequence 2, Application US/08097997A  
; Patent No. 5728536  
; GENERAL INFORMATION:  
; APPLICANT: Ihle, James N.  
; APPLICANT: Silvennoinen, Ollie  
; APPLICANT: Witthuhn, Bruce A.  
; APPLICANT: Quelle, Frederick W.  
; TITLE OF INVENTION: Jak Kinases and Regulation of Cytokine Signal  
; TITLE OF INVENTION: Transduction  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/097,997A  
; FILING DATE: 29-JULY-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fox, Samuel L.  
; REGISTRATION NUMBER: 30,353  
; REFERENCE/DOCKET NUMBER: 0656.0370000/SLF/GKT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; US-08-097-997A-2  
Query Match 22.2%; Score 4; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 10 KVKE 13  
DB 10 KVKE 13  
RESULT 57  
US-08-259-672-11  
; Sequence 11, Application US/08259672  
; Patent No. 5736337  
; GENERAL INFORMATION:  
; APPLICANT: Joseph Avruch  
; APPLICANT: Xian-feng Zhang  
; APPLICANT: Mark S. Marshall  
; TITLE OF INVENTION: INHIBITING PROTEIN  
; TITLE OF INVENTION: INTERACTIONS

```
;
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/259,672
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,256
; FILING DATE: June 11, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark, Esq.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/234001
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-259-672-11

Query Match 22.2%; Score 4; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
DB 1 LOPE 4

RESULT 59
US-08-459-351-11
; Sequence 11, Application US/08459351
; Patent No. 5763571
; GENERAL INFORMATION:
; APPLICANT: Joseph Avruch
; APPLICANT: Xian-Feng Zhang
; APPLICANT: Mark S. Marshall
; TITLE OF INVENTION: INHIBITING PROTEIN INTERACTIONS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,533
; FILING DATE: June 2, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/259,672
; FILING DATE: June 10, 1994
; APPLICATION NUMBER: 08/077,256
; FILING DATE: June 11, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark, Esq.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/234002
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-459-351-11

;
; FILING DATE: June 10, 1994
; APPLICATION NUMBER: 08/077,256
; FILING DATE: June 11, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark, Esq.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/234003
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-459-351-11

Query Match 22.2%; Score 4; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOPE 4
DB 1 LOPE 4

RESULT 59
US-08-460-533-11
; Sequence 11, Application US/08460533
; Patent No. 5767075
; GENERAL INFORMATION:
; APPLICANT: Joseph Avruch
; APPLICANT: Xian-Feng Zhang
; APPLICANT: Mark S. Marshall
; TITLE OF INVENTION: INHIBITING PROTEIN INTERACTIONS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,533
; FILING DATE: June 2, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/259,672
; FILING DATE: June 10, 1994
; APPLICATION NUMBER: 08/077,256
; FILING DATE: June 11, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark, Esq.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/234002
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-459-351-11
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US-08-460-533-11

Query Match 22.2%; Score 4; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOPE 4  
| | | |  
Db 1 LOPE 4

RESULT 60

US-08-787-547-44  
; Sequence 44, Application US/08787547  
; Patent No. 5783567  
; GENERAL INFORMATION:  
; APPLICANT: Hedley, Mary Lynne  
; APPLICANT: Curley, Joanne M.  
; APPLICANT: Langer, Robert S.  
; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY  
; TITLE OF INVENTION: OF NUCLEIC ACID  
; NUMBER OF SEQUENCES: 107  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson, P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: US  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/787,547  
; FILING DATE: 22-JAN-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fraser, Janis K.  
; REGISTRATION NUMBER: 34,819  
; REFERENCE/DOCKET NUMBER: 08191/003001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-542-5070  
; TELEFAX: 617-542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 44:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-787-547-44

Query Match 22.2%; Score 4; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VPKV 11  
| | | |  
Db 6 VPKV 9

RESULT 61

US-08-553-257A-62  
; Sequence 62, Application US/08553257A  
; Patent No. 5994083  
; GENERAL INFORMATION:  
; APPLICANT: ISTITUTO DI RICERCHE DI BIOLOGIA  
; APPLICANT: MOLECOLARE P. ANGELETTI S.p.A.

; APPLICANT: FELICI, Franco  
; APPLICANT: LUZZAGO, Alessandra  
; APPLICANT: NICOSIA, Alfredo  
; APPLICANT: MONACI, Paolo  
; APPLICANT: CORTESE, Riccardo  
; TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF IMMUNOGENS  
; TITLE OF INVENTION: OR DIAGNOSTIC REAGENTS, AND IMMUNOGENS OR  
; TITLE OF INVENTION: DIAGNOSTIC REAGENTS THEREBY OBTAINABLE  
; NUMBER OF SEQUENCES: 68  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Browdy and Neimark  
; STREET: 419 Seventh Street N.W. Ste. 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/553,257A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA: PCT/IT94/00054  
; APPLICATION NUMBER: 05-MAY-1994  
; FILING DATE: 05-MAY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: RM93A000301  
; FILING DATE: 11-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Browdy, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: FELICI=1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 628-5197  
; TELEFAX: (202) 737-3528  
; INFORMATION FOR SEQ ID NO: 62:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-553-257A-62

Query Match 22.2%; Score 4; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PKVK 12  
| | | |  
Db 7 PKVK 10

RESULT 62  
US-08-660-347-3  
; Sequence 3, Application US/08660347  
; Patent No. 6027935  
; GENERAL INFORMATION:  
; APPLICANT: Purchio, Anthony F.  
; APPLICANT: New, Liguio  
; APPLICANT: Liu, Kang  
; APPLICANT: Kamali, Vafa  
; APPLICANT: Naughton, Brian  
; TITLE OF INVENTION: No. 6027935el Gene Up-Regulated in  
; TITLE OF INVENTION: Regenerating Liver  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS  
; STREET: 1155 Avenue of the Americas  
; CITY: New York

```

; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,347
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6261-0151-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)7909090
; TELEFAX: (212)8699741
; TELEX: 66141 PENNTE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6027935e
; US-08-660-347-3

Query Match 22.2%; Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKET 14
DB 4 VKET 7

RESULT 63
US-09-041-889-16
; Sequence 16, Application US/09041889
; Patent No. 6033864
; GENERAL INFORMATION:
; APPLICANT: Braun, Jonathan
; APPLICANT: Cohavy, Offer
; TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
; TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
; TITLE OF INVENTION: Microbial UC PANCA antigens
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/041,889
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/837,058
; FILING DATE: 11-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.

```

```

; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-PM 3006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-09-041-889-16

Query Match 22.2%; Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
DB 4 PKVK 7

RESULT 64
US-08-837-058-16
; Sequence 16, Application US/08837058
; Patent No. 6074835
; GENERAL INFORMATION:
; APPLICANT: Braun, Jonathan
; APPLICANT: Targan, Stephan R.
; APPLICANT: Eggena, Mark
; TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
; TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
; TITLE OF INVENTION: Histone H1
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/837,058
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-PM 2438
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-837-058-16

Query Match 22.2%; Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PKVK 12
DB 4 PKVK 7

RESULT 65

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US-08-665-574C-2
; Sequence 2, Application US/08665574C
; Patent No. 6136595
; GENERAL INFORMATION:
; APPLICANT: Ihle, James N.
; APPLICANT: Silvennoinen, Ollie
; APPLICANT: Witthuhn, Bruce A.
; TITLE OF INVENTION: Jak Kinases and Regulation of Cytokine
; TITLE OF INVENTION: Signal Transduction
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,574C
; FILING DATE: 18-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/282,012
; FILING DATE: 29-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/097,997
; FILING DATE: 29-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/118,968
; FILING DATE: 09-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bugalsky, Lawrence B.
; REGISTRATION NUMBER: 35,086
; REFERENCE/DOCKET NUMBER: 0656.0370002/SLF/LBB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-665-574C-2

Query Match 22.2%; Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KVKE 13
Db 10 KVKE 13

RESULT 66
US-08-946-994-2
; Sequence 2, Application US/08946994
; Patent No. 6210654
; GENERAL INFORMATION:
; APPLICANT: Ihle, James N.
; APPLICANT: Silvennoinen, Ollie
; APPLICANT: Witthuhn, Bruce A.
; APPLICANT: Quelle, Frederick W.
; TITLE OF INVENTION: Jak Kinases and Regulation of Cytokine Signal
; TITLE OF INVENTION: Transduction
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
```

```
US-08-946-994-2
; Sequence 2, Application US/08665574C
; Patent No. 6136595
; GENERAL INFORMATION:
; APPLICANT: Ihle, James N.
; APPLICANT: Silvennoinen, Ollie
; APPLICANT: Witthuhn, Bruce A.
; TITLE OF INVENTION: Jak Kinases and Regulation of Cytokine
; TITLE OF INVENTION: Signal Transduction
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,574
; FILING DATE: 18-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/282,012
; FILING DATE: 29-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/097,997
; FILING DATE: 29-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/118,968
; FILING DATE: 09-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fox, Samuel L.
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 0656.0370002/SLF/GKT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-946-994-2

Query Match 22.2%; Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KVKE 13
Db 10 KVKE 13

RESULT 67
US-09-417-264-16
; Sequence 16, Application US/09417264
; Patent No. 6537768
; GENERAL INFORMATION:
; APPLICANT: Braun, Jonathan
; APPLICANT: Cohavy, Offer
; TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
; TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
; TITLE OF INVENTION: Microbial UC PANCA antigens
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/417,264
; FILING DATE:
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```
;
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/041,889
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-PM 3006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-09-417-264-16

Query Match 22.2%; Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PKVK 12
Db 4 PKVK 7

RESULT 68
US-09-441-992-62
; Sequence 62, Application US/09441992
; Patent No. 6541210
; GENERAL INFORMATION:
; APPLICANT: ISTITUTO DI RICERCHE DI BIOLOGIA
; MOLECOLARE P. ANGELETTI S.p.A.
; FELICI, Franco
; LUZZAGO, Alessandra
; NICOSIA, Alfredo
; MONACI, Paolo
; CORTESE, Riccardo
; TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF IMMUNOGENS
; OR DIAGNOSTIC REAGENTS AND IMMUNOGENS OR
; DIAGNOSTIC REAGENTS THEREBY OBTAINABLE
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brody and Neimark
; STREET: 419 Seventh Street N.W. Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/441,992
; FILING DATE: 18-Nov-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/553,257
; FILING DATE: <Unknown>
; APPLICATION NUMBER: RM93A000301
; FILING DATE: 11-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Brody, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: FELICI=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
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;
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 62:
US-09-441-992-62

Query Match 22.2%; Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PKVK 12
Db 7 PKVK 10

RESULT 69
PCT-US94-06654-11
; Sequence 11, Application PC/TUS9406654
; GENERAL INFORMATION:
; APPLICANT: Joseph Avruch
; APPLICANT: Xian-feng Zhang
; APPLICANT: Mark S. Marshall
; TITLE OF INVENTION: INHIBITING PROTEIN INTERACTIONS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06654
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark, Esq.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/234001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; PCT-US94-06654-11

Query Match 22.2%; Score 4; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOPE 4
Db 1 LOPE 4

RESULT 70
US-08-591-438-13
; Sequence 13, Application US/08591438
```

```
; Patent No. 5939063
; GENERAL INFORMATION:
; APPLICANT: Vadas, Mathew A.
; APPLICANT: Lopez, Angel F.
; APPLICANT: Shannon, Mary F.
; TITLE OF INVENTION: HAEMOPOIETIC GROWTH FACTOR ANTAGONISTS
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,438
; FILING DATE: 08-APR-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio Esq., Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9972
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
US-08-591-438-13

Query Match 22.2%; Score 4; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VKET 14
DB 3 VKET 6

RESULT 71
US-08-760-075A-2
; Sequence 2, Application US/08760075A
; Patent No. 5942429
; GENERAL INFORMATION:
; APPLICANT: KIRSCHBAUM, Bernd
; APPLICANT: MUELLNER, Stefan
; APPLICANT: BARTLETT, Robert
; TITLE OF INVENTION: NOVEL DEAH-BOX PROTEINS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/760,075A
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; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 19545126.0
; FILING DATE: 04-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 18748/309
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-760-075A-2

Query Match 22.2%; Score 4; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IMGV 8
DB 5 IMGV 8

RESULT 72
US-09-011-525-1
; Sequence 1, Application US/09011525
; Patent No. 6020172
; GENERAL INFORMATION:
; APPLICANT: BOTH, GERALD W.
; TITLE OF INVENTION: GENE THERAPY USING OVINE ADENOVIRAL VECTORS
; FILE REFERENCE: Gene Therapy Using Ovine Adenoviral Ve
; CURRENT APPLICATION NUMBER: US/09/011,525
; CURRENT FILING DATE: 1998-04-20
; EARLIER APPLICATION NUMBER: PCT/AU96/00518
; EARLIER FILING DATE: 1996-08-14
; EARLIER APPLICATION NUMBER: AU PN4776
; EARLIER FILING DATE: 1995-08-14
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Ovine adenovirus
US-09-011-525-1

Query Match 22.2%; Score 4; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 MVPK 18
DB 4 MVPK 7

RESULT 73
US-08-405-647B-11
; Sequence 11, Application US/08405647B
; Patent No. 6124262
; GENERAL INFORMATION:
; APPLICANT: Sherman, Irwin W.
; APPLICANT: Crandall, Ian E.
; APPLICANT: Sholet, Stephen B.
; APPLICANT: Thevenin, Bernard Jean-Marie
; TITLE OF INVENTION: Compositions and Methods for Reducing
; TITLE OF INVENTION: Adhesiveness of Defective Red Blood Cells
; NUMBER OF SEQUENCES: 50
```

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Townsend and Townsend and Crew LLP  
;; STREET: Two Embarcadero Center, Eighth Floor  
;; CITY: San Francisco  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94111-3834  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/405,647B  
;; FILING DATE: 17-MAR-1995  
;; CLASSIFICATION: 514  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Weber, Kenneth A.  
;; REGISTRATION NUMBER: 31,677  
;; REFERENCE/DOCKET NUMBER: 02307E-068700US  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 576-0200  
;; TELEFAX: (415) 576-0300  
;; INFORMATION FOR SEQ ID NO: 11:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 16 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; US-08-405-647B-11

Query Match 22.2%; Score 4; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred.No. 2.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 15 MVPK 18  
Db 6 MVPK 9

RESULT 74  
US-08-602-999A-344  
; Sequence 344, Application US/08602999A  
; Patent No. 6184205  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999A  
; FILING DATE: 16-FEB-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:

;; NAME: Mierock, S. Leslie  
;; REGISTRATION NUMBER: 18,872  
;; REFERENCE/DOCKET NUMBER: 1101-202  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212) 790-9090  
;; TELEFAX: (212) 869-9741/8864  
;; TELEX: 66141 PENNIE  
;; INFORMATION FOR SEQ ID NO: 344:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 16 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: peptide  
;; US-08-602-999A-344  
Query Match 22.2%; Score 4; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred.No. 2.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;  
Qy 9 PKVK 12  
Db 11 PKVK 14  
RESULT 75  
US-08-985-499-11  
; Sequence 11, Application US/08985499  
; Patent No. 6191103  
; GENERAL INFORMATION:  
; APPLICANT: Shohet, Stephen B.  
; APPLICANT: Sherman, Irwin  
; APPLICANT: von Andrian, Ulrich  
; TITLE OF INVENTION: Methods for Enhancing Thrombolysis in a  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRES:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/985,499  
; FILING DATE: 05-DEC-1997  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hyman, Laurence J.  
; REGISTRATION NUMBER: 35,551  
; REFERENCE/DOCKET NUMBER: 02307E-084500US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-985-499-11  
Query Match 22.2%; Score 4; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred.No. 2.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;  
Qy 15 MVPK 18  
Db 6 MVPK 9

Db 6 MVEK 9

Search completed: November 25, 2003, 20:29:58  
Job time : 15.5465 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:28:30 ; Search time 12.3488 Seconds  
(without alignments)  
140.178 Million cell updates/sec

Title: US-09-641-801-22

Perfect score: 18

Sequence: 1 HKMPFPKYPVEPFTESQ 18

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : PIR 76:\*\*

1: pir1:\*\*

2: pir2:\*\*

3: pir3:\*\*

4: pir4:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	22.2	14	H64008	hypothetical prote
2	4	22.2	16	PC4371	telomeric and tetr
3	3	16.7	5	PQ0009	angiotensin-conver
4	3	16.7	5	JT0520	Ig kappa chain V-I
5	3	16.7	6	A61049	halo-toxin - Pseud
6	3	16.7	7	I51317	bHLH transcription
7	3	16.7	7	XEYDGD	galactose oxidase
8	3	16.7	7	S33244	neuromodulatory pe
9	3	16.7	8	A32523	peptidyl-dipectida
10	3	16.7	8	S20162	leghemoglobin III
11	3	16.7	9	PD0443	3-oxoacid CoA-tran
12	3	16.7	10	A60410	beta-neoendorphin
13	3	16.7	10	S65728	hemoglobin, extrac
14	3	16.7	10	A37268	Ig heavy chain C r
15	3	16.7	11	F58501	43.5K bile stone p
16	3	16.7	11	PA0028	protein QA300042 -
17	3	16.7	11	PC4267	ribosomal protein
18	3	16.7	11	PQ0731	unidentified 5.7/3
19	3	16.7	11	I54193	Rhesus blood group
20	3	16.7	11	A54348	N-acetylglucosamin
21	3	16.7	13	PQ0491	self-incompatibili
22	3	16.7	13	A44818	extracellular lipa
23	3	16.7	13	A28953	alpha-conotoxin Si
24	3	16.7	13	S21152	tryptophyllin-rela
25	3	16.7	13	A60458	protocatechuate 3,
26	3	16.7	13	PC2371	probable endopepti
27	3	16.7	13	D56661	S-locus specific g
28	3	16.7	13	B61620	locustamyotropin I
29	3	16.7	13	D61458	Ig kappa chain V-I

30	3	16.7	13	E61458	Ig kappa chain V-I
31	3	16.7	13	PH1772	T cell receptor al
32	3	16.7	14	PT0026	calotropin DI - mu
33	3	16.7	14	E33098	214K exoantigen (v
34	3	16.7	15	PA0024	protein QA300050 -
35	3	16.7	15	P90452	32K protein 3306 -
36	3	16.7	15	PA0062	fumate hydratase
37	3	16.7	15	B61457	alpha-glucosidase
38	3	16.7	15	A36527	juvenile-hormone e
39	3	16.7	15	A49480	major immunophilin
40	3	16.7	15	PT0205	insulin-like growt
41	3	16.7	15	B45115	peptidylprolyl iso
42	3	16.7	16	B42324	casein kinase II (
43	3	16.7	16	C45133	cytochrome P450c27
44	3	16.7	16	I40065	shikimate 5-dehydr
45	3	16.7	16	C53113	Lys-gingipain form
46	3	16.7	17	S05671	hirudin Ia - medic
47	3	16.7	17	S05033	photosystem II pro
48	3	16.7	17	B31769	T-cell receptor de
49	3	16.7	17	G85956	hypothetical prote
50	3	16.7	18	S29264	ovohemerythrin - d
51	3	16.7	18	H64711	hypothetical prote
52	3	16.7	18	S58277	insulin-like growt
53	3	16.7	18	S71592	serine proteinase
54	3	16.7	18	I46653	T-cell receptor de
55	3	16.7	18	A59137	protein Pii - Gold
56	3	16.7	19	EW5MCN	cinnamycin - Strept
57	3	16.7	19	S59485	hyroxyproline-rich
58	3	16.7	19	S43641	carboxylesterase (
59	3	16.7	19	C56661	S-locus specific g
60	3	16.7	19	PQ0492	self-incompatibili
61	3	16.7	19	A61144	probable flagellar
62	3	16.7	19	C39305	neurotoxin Tx3 - s
63	3	16.7	19	I46654	T-cell receptor de
64	3	16.7	19	S69166	ferredoxin b - Jap
65	3	16.7	19	S11611	ribosomal protein
66	3	16.7	20	S06466	T-cell receptor al
67	3	16.7	20	JP0059	ribosomal protein
68	3	16.7	20	PL0145	carbon-monoxide de
69	3	16.7	20	PQ0046	citrate (si)-synth
70	3	16.7	20	S29635	jacalin beta chain
71	3	16.7	20	B30208	hypothetical prote
72	3	16.7	20	S83382	hypothetical prote
73	3	16.7	20	I46652	T-cell receptor de
74	3	16.7	20	A41439	acid ribonuclease
75	2	11.1	3	GKHU	growth-modulating
76	2	11.1	3	A33802	thyrotropin-releas
77	2	11.1	3	A43391	TRH-like tripeptid
78	2	11.1	3	I78890	tyrosine protein k
79	2	11.1	4	A32039	tyrosine-melanocyt
80	2	11.1	4	S53508	starvation-induced
81	2	11.1	4	PT0240	Ig heavy chain CRD
82	2	11.1	4	I54357	schwannomin - mous
83	2	11.1	5	JN0862	peptidyl-dipectida
84	2	11.1	5	C41225	copper resistance
85	2	11.1	5	E60274	major protein anti
86	2	11.1	5	T14908	hypothetical prote
87	2	11.1	5	PQ0689	photosystem I 10.4
88	2	11.1	5	B37988	acid proteinase li
89	2	11.1	5	JS0319	subesophageal gang
90	2	11.1	5	S53595	hypothetical prote
91	2	11.1	5	S11127	phosphoprotein, bo
92	2	11.1	5	PT0308	Ig heavy chain CRD
93	2	11.1	5	PT0610	T-cell receptor be
94	2	11.1	5	PT0644	T-cell receptor be
95	2	11.1	6	JN0861	peptidyl-dipectida
96	2	11.1	6	B34835	dnA protein - Pse
97	2	11.1	6	S11556	hydrogensulfite re
98	2	11.1	6	B60110	repetitive protein
99	2	11.1	6	A31263	dihydrofolate redu
100	2	11.1	6	B31263	dihydrofolate redu

Ig kappa chain V-I  
T cell receptor al  
calotropin DI - mu  
214K exoantigen (v  
protein QA300050 -  
32K protein 3306 -  
fumate hydratase  
alpha-glucosidase  
juvenile-hormone e  
major immunophilin  
insulin-like growt  
peptidylprolyl iso  
casein kinase II (  
cytochrome P450c27  
shikimate 5-dehydr  
Lys-gingipain form  
hirudin Ia - medic  
photosystem II pro  
T-cell receptor de  
hypothetical prote  
ovohemerythrin - d  
hypothetical prote  
insulin-like growt  
serine proteinase  
T-cell receptor de  
protein Pii - Gold  
cinnamycin - Strept  
hyroxyproline-rich  
carboxylesterase (  
S-locus specific g  
self-incompatibili  
probable flagellar  
neurotoxin Tx3 - s  
T-cell receptor de  
ferredoxin b - Jap  
ribosomal protein  
T-cell receptor al  
ribosomal protein  
carbon-monoxide de  
citrate (si)-synth  
jacalin beta chain  
hypothetical prote  
hypothetical prote  
T-cell receptor de  
acid ribonuclease  
growth-modulating  
thyrotropin-releas  
TRH-like tripeptid  
tyrosine protein k  
tyrosine-melanocyt  
starvation-induced  
Ig heavy chain CRD  
schwannomin - mous  
peptidyl-dipectida  
copper resistance  
major protein anti  
hypothetical prote  
photosystem I 10.4  
acid proteinase li  
subesophageal gang  
hypothetical prote  
phosphoprotein, bo  
Ig heavy chain CRD  
T-cell receptor be  
T-cell receptor be  
peptidyl-dipectida  
dnA protein - Pse  
hydrogensulfite re  
repetitive protein  
dihydrofolate redu  
dihydrofolate redu

## ALIGNMENTS

RESULT 1  
H64008  
hypothetical protein HI0492 - Haemophilus influenzae (strain Rd KW20)  
C:Species: Haemophilus influenzae  
C>Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 30-Jun-1998  
C:Accession: H64008  
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.  
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.  
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.  
Science 269, 496-512, 1995  
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,  
A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
A:Reference number: A64000; MUID:95350630; PMID:7542800  
A:Accession: H64008  
A>Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-14 <TIGR>  
A:Cross-references: GB:U32731; GB:L42023; NID:91573465; PID:91573478; TIGR:HI0492  
Query Match 22.2%; Score 4; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 PKYP 10  
DB 3 PKYP 6

RESULT 2  
PC4371  
telomeric and tetraplex DNA binding protein qTBP42 I - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 28-Oct-1997 #sequence\_revision 28-Oct-1997 #text\_change 07-May-1999  
C:Accession: PC4371  
R;Sarg, G.; Weisman-Shomer, P.; Fry, M.  
Biochem. Biophys. Res. Commun. 237, 617-623, 1997  
A:Title: Telomeric and tetraplex DNA binding properties of qTBP42: A homologue of the CA  
A:Reference number: PC4371; MUID:97445086; PMID:9299414  
A:Accession: PC4371  
A:Molecule type: protein  
A:Residues: 1-16 <SAR>  
C:Comment: This protein binds either strand of the telomeric DNA as well as unimolecular  
Query Match 22.2%; Score 4; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 10 PVEP 13  
DB 5 PVEP 8

RESULT 3  
PQ0009  
angiotensin-converting enzyme inhibitor (FLP-2) - common fig  
N:Alternate names: ficus latex peptide 2  
C:Species: Ficus carica (common fig)  
C>Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 08-Dec-1995  
C:Accession: PQ0009  
R;Maruyama, S.; Miyoshi, S.; Tanaka, H.  
Agric. Biol. Chem. 53, 2763-2767, 1989  
A:Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.  
A:Reference number: PQ0008  
A:Accession: PQ0009  
A:Molecule type: protein  
A:Residues: 1-5 <MAR>  
A:Experimental source: latex  
C:Keywords: angiotensin-converting enzyme inhibitor  
Query Match. 16.7%; Score 3; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 9 YPV 11  
DB 2 YPV 4

RESULT 4  
JT0520  
IG kappa chain V-III region (SD1) - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 23-Oct-1992 #sequence\_revision 23-Oct-1992 #text\_change 16-Aug-1996  
C:Accession: JT0520  
R;Anker, R.; Conley, M.E.; Pollok, B.A.  
J. Exp. Med. 169, 2109-2119, 1989  
A:Title: Clonal diversity in the B cell repertoire of patients with X-linked agammag  
A:Reference number: JT0511; MUID:89279157; PMID:2786547  
A:Accession: JT0520  
A:Molecule type: mRNA  
A:Residues: 1-5 <ANK>  
A>Note: the sequence shown here is one of eight productive V-D-J mu chain rearrangem  
A>Note: a stop codon terminates the sequence in the V region  
C:Keywords: heterotetramer; immunoglobulin  
F;1-5/Domain: V kappa region <VRE>  
Query Match 16.7%; Score 3; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 15 TES 17  
DB 1 TES 3

RESULT 5  
A61049  
halo-toxin - Pseudomonas syringae pv. mori  
C:Species: Pseudomonas syringae pv. mori  
A:Note: host mulberry tree  
C>Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 21-Jan-1997  
C:Accession: A61049  
R;Kajimoto, T.; Yokomizo, K.; Yahiro, K.; Umeda, T.; Shoji, S.; Kubota, Y.; Shibata,  
Chem. Lett. 00, 679-680, 1989  
A:Title: Structure of halo-toxin produced by phytopathogenic bacterium, Pseudomonas  
A:Reference number: A61049  
A:Accession: A61049  
A:Molecule type: protein  
A:Residues: 1-6 <KAJ>  
A:Note: sequence confirmed by synthesis  
C:Comment: This toxin is one of the etiological agents of halo bright disease in mul  
C:Keywords: toxin  
Query Match 16.7%; Score 3; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 PFP 7  
DB 1 PFP 3

RESULT 6  
I51317  
bHLH transcription factor inhibitor - African clawed frog (fragment)  
C:Species: Xenopus laevis (African clawed frog)  
C>Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jul-2000  
C:Accession: I51317  
R;Zhang, H.; Reynaud, S.; Kloc, M.; Etkin, L.D.; Spohr, G.  
Mech. Dev. 50, 119-130, 1995  
A:Title: Id gene activity during Xenopus embryogenesis.  
A:Reference number: I51316; MUID:95344988; PMID:7619724  
A:Accession: I51317

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA  
 A;Residues: 1-6 <ZHA>  
 A;Cross-references: GB:S79038; NID:gl042006; PIDN:AAD14294.1; PID:g4261994  
 C;Genetics:  
 A;Gene: XIDib

Query Match 16.7%; Score 3; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred.No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 EPF 14  
 ||||  
 Db 4 EPF 6

#### RESULT 7

XEYDGD  
 galactose oxidase inhibitor - fungus (Cladobotryum dendroides)  
 C;Species: Cladobotryum dendroides  
 C;Date: 30-Jun-1987 #sequence\_revision 30-Jun-1997 #text\_change 31-Dec-1993  
 C;Accession: A01341  
 R;Avigad, G.; Markus, Z.  
 Fed. Proc. 31, 447, 1972  
 A;Reference number: A01341  
 A;Accession: A01341  
 A;Molecule type: protein  
 A;Residues: 1-7 <AVI>  
 C;Comment: The mycelia of this imperfect fungus produce the metalloenzyme galactose oxidase, which may inactivate the enzyme by binding to its prosthetic copper group.  
 C;Superfamily: galactose oxidase inhibitor  
 C;Keywords: copper

Query Match 16.7%; Score 3; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred.No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TES 17  
 ||||  
 Db 5 TES 7

#### RESULT 8

S33244  
 neuromodulatory peptide Wamide-1 - giant African snail  
 C;Species: Achatina fulica (giant African snail)  
 C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Jul-1997  
 C;Accession: S33244  
 R;Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.  
 FEBS Lett. 323, 104-108, 1993  
 A;Title: Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of the giant African snail Achatina fulica.  
 A;Reference number: S33244; MUID:93265912; PMID:8495720  
 A;Accession: S33244  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-7 <MIN>

Query Match 16.7%; Score 3; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred.No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KEM 4  
 ||||  
 Db 2 KEM 4

#### RESULT 9

A32523  
 peptidyl-dipeptidase A (EC 3.4.15.1) - bovine (fragment)  
 N;Alternate names: angiotensin I-converting enzyme; peptidyl-dipeptidase I  
 C;Species: Bos primigenius taurus (cattle)  
 C;Date: 18-Oct-1989 #sequence\_revision 18-Oct-1989 #text\_change 11-May-2000  
 C;Accession: A32523

R;Harris, R.B.

Adv. Exp. Med. Biol. 198, 513-521, 1986  
 A;Title: Isolation and sequencing of an active-site peptide from angiotensin I-converting enzyme.  
 A;Reference number: A32523; MUID:87123961; PMID:3028071  
 A;Accession: A32523  
 A;Molecule type: protein  
 A;Residues: 1-8 <HAR>  
 C;Superfamily: mammalian peptidyl-dipeptidase A  
 C;Keywords: alternative splicing; blood pressure control; peptidyl-dipeptide hydrolase

Query Match 16.7%; Score 3; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred.No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 FTE 16  
 ||||  
 Db 1 FTE 3

#### RESULT 10

S20162  
 leghemoglobin III - Sesbania rostrata (fragment)  
 C;Species: Sesbania rostrata  
 C;Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 04-Mar-2000  
 C;Accession: S20162  
 R;Metz, B.A.; Welters, P.; Hoffmann, H.J.; Jensen, E.O.; Schell, J.; de Bruijn, F.J.  
 Mol. Gen. Genet. 214, 181-191, 1988  
 A;Title: Primary structure and promoter analysis of leghemoglobin genes of the stem-nodulated legume Sesbania rostrata.  
 A;Reference number: S08322; MUID:89181515; PMID:3237206  
 A;Accession: S20162  
 A;Molecule type: DNA  
 A;Residues: 1-8 <MET>  
 A;Cross-references: EMBL:X13504; NID:g21383; PIDN:CAA31858.1; PID:g579482  
 C;Genetics:  
 A;Gene: glb3  
 C;Superfamily: globin; globin homology  
 C;Keywords: heme; oxygen carrier

Query Match 16.7%; Score 3; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred.No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 FTE 16  
 ||||  
 Db 3 FTE 5

#### RESULT 11

PD0443  
 3-oxoacid CoA-transferase (EC 2.8.3.5) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 05-Feb-1999 #sequence\_revision 05-Feb-1999 #text\_change 05-Feb-1999  
 C;Accession: PD0443  
 R;Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Tsugita, A.  
 submitted to JIPID, August 1998  
 A;Description: Proteome analysis of mouse brain.  
 A;Reference number: PD0441  
 A;Contents: Striatum  
 A;Accession: PD0443  
 A;Molecule type: protein  
 A;Residues: 1-9 <KAW>  
 C;Keywords: CoA-transferase

Query Match 16.7%; Score 3; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred.No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PVE 12  
 ||||  
 Db 7 PVE 9

#### RESULT 12

A60410  
beta-neoendorphin / dynorphin precursor - guinea pig  
N;Alternate names: alpha-neoendorphin; proenkephalin B precursor  
C;Species: Cavia porcellus (guinea pig)  
C;Date: 03-Feb-1993 #sequence\_revision 03-Feb-1993 #text\_change 21-Jan-2000  
C;Accession: A60410  
R;Murphy, R.; Turner, C.A.  
Peptides 11, 65-68, 1990  
A;Title: Isolation and microsequence analysis of guinea pig alpha-neo-endorphin.  
A;Reference number: A60410; MUID:90259864; PMID:2342991  
A;Accession: A60410  
A;Molecule type: protein  
A;Residues: 1-10 <MUR>  
C;Superfamily: proenkephalin  
C;Keywords: neuropeptide; opioid peptide

Query Match 16.7%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0;

QY 8 KYP 10  
|||  
Db 7 KYP 9

RESULT 13  
S65728  
hemoglobin, extracellular, chain d1 - earthworm (Lumbricus terrestris) (fragment)  
C;Species: Lumbricus terrestris (common earthworm)  
C;Date: 06-Dec-1996 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997  
C;Accession: S65728  
R;Fushitani, K.; Higashiyama, K.; Asao, M.; Hosokawa, K.  
Biochim. Biophys. Acta 1292, 273-280, 1996  
A;Title: Characterization of the constituent polypeptides of the extracellular hemoglobin  
A;Reference number: S65721; MUID:96176855; PMID:8597573  
A;Accession: S65728  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-10 <FUS>

Query Match 16.7%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0;

QY 15 TES 17  
|||  
Db 5 TES 7

RESULT 14  
A37268  
IG heavy chain C region (129) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 19-Mar-1997 #sequence\_revision 13-Mar-1998 #text\_change 13-Mar-1998  
C;Accession: A37268  
R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.  
J. Biol. Chem. 265, 6607-6613, 1991  
A;Title: Heavy and light chain variable region sequences and antibody properties of anti  
A;Reference number: A38740; MUID:91177923; PMID:1706720  
A;Accession: A37268  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-10 <RUF>

Query Match 16.7%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0;

QY 16 ESQ 18  
|||  
Db 1 ESQ 3

RESULT 15  
F58501  
43.5K bile stone protein - unidentified bacterium (fragment)  
C;Species: unidentified bacterium  
C;Date: 07-Feb-1997 #sequence\_revision 07-Feb-1997 #text\_change 10-Jul-1998  
C;Accession: F58501  
R;Binette, J.P.; Binette, M.B.  
submitted to the Protein Sequence Database, October 1996  
A;Description: The proteins of kidney and gallbladder stones.  
A;Reference number: A58501  
A;Accession: F58501  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-11 <BIN>  
A;Experimental source: human bile with stones  
A;Note: 6-Asn and 8-Ala were also found

Query Match 16.7%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0;

QY 10 PVE 12  
|||  
Db 9 PVE 11

RESULT 16  
PA0028  
protein QA300042 - Arabidopsis thaliana (fragment)  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 06-Jun-1997  
C;Accession: PA0028  
R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.  
submitted to JIPID, July 1994  
A;Description: Separation and characterization of Arabidopsis proteins by two-dimens  
A;Reference number: PA0001  
A;Accession: PA0028  
A;Molecule type: protein  
A;Residues: 1-11 <KAM>  
A;Experimental source: seed  
C;Keywords: seed

Query Match 16.7%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0;

QY 5 PFP 7  
|||  
Db 6 PFP 8

RESULT 17  
PC4267  
ribosomal protein L12.1 - rice (fragment)  
C;Species: Oryza sativa (rice)  
C;Date: 28-May-1997 #sequence\_revision 18-Jul-1997 #text\_change 18-Jul-1997  
C;Accession: PC4267  
R;Kawakami, T.; Kamo, M.; Chen, M.C.; Tsugita, A.  
submitted to JIPID, April 1997  
A;Reference number: PC4267  
A;Accession: PC4267  
A;Molecule type: protein  
A;Residues: 1-11 <KAW>  
A;Experimental source: strain Japonica Nihonbare

Query Match 16.7%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0;

QY 15 TES 17  
|||  
Db 4 TES 6



## RESULT 18

PQ0731  
 unidentified 5.7/35K protein [imported] - rice (fragment)  
 C:Species: Oryza sativa (rice)  
 C>Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
 C:Accession: PQ0731  
 R:Komatsu, S.; Kajiwara, H.; Hirano, H.  
 Theor. Appl. Genet. 86, 935-942, 1993  
 A>Title: A rice protein library; a data-file of rice proteins separated by two-dimension  
 A:Reference number: PQ0696  
 A:Accession: PQ0731  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-11 <KOM>

Query Match 16.7%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PKY 9  
 ||||  
 Db 6 PKY 8

## RESULT 19

154193  
 Rhesus blood group CcEe protein - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 06-Sep-1996 #sequence\_revision 06-Sep-1996 #text\_change 21-Jul-2000  
 C:Accession: I54193  
 R:Charif-Zahar, B.; Le Van Kim, C.; Rouillac, C.; Raynal, V.; Cartron, J.P.; Colin, Y.  
 Genomics 19, 68-74, 1994  
 A>Title: Organization of the gene (RHCE) encoding the human blood group RhCcEe antigens  
 A:Reference number: I54193; MUID:94245182; PMID:8188244  
 A:Accession: I54193  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-11 <RES>  
 A:Cross-references: GB:S70456; MID:g546795; PIDN:AAD14061.1; PID:g4261761  
 C:Genetics:  
 A:Gene: GDB:RHCE  
 A:Cross-references: GDB:229957; OMIM:111700  
 A:Map position: 1p36.2-1p34

Query Match 16.7%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KYP 10  
 ||||  
 Db 4 KYP 6

## RESULT 20

A54348  
 N-acetylglucosamine-6-sulfatase (EC 3.1.6.14) - bovine (fragment)  
 C:Species: Bos primigenius taurus (cattle)  
 C>Date: 05-Jan-1996 #sequence\_revision 05-Jan-1996 #text\_change 05-Jan-1996  
 C:Accession: A54348  
 R:Shilatfard, A.; Cummings, R.D.  
 Biochemistry 33, 4273-4282, 1994  
 A>Title: Purification and characterization of N-acetylglucosamine-6-sulfate sulfatase fr  
 A:Reference number: A54348; MUID:94206936; PMID:8155645  
 A:Accession: A54348  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-11 <SHI>  
 C:Keywords: sulfuric ester hydrolase

Query Match 16.7%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 EPF 14  
 ||||  
 Db 2 EPF 4

## RESULT 21

PQ0491  
 self-incompatibility locus glycoprotein delta - wild cabbage (fragment)  
 C:Species: Brassica oleracea (wild cabbage)  
 C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 31-Oct-1997  
 C:Accession: PQ0491  
 R:Gaude, T.; Friry, A.; Heizmann, P.; Mariac, C.; Rougier, M.; Fobis, I.; Dumas, C.  
 Plant Cell 5, 75-86, 1993  
 A>Title: Expression of a self-incompatibility gene in a self-compatible line of Brass  
 A:Reference number: JQ1733; MUID:93177215; PMID:8439745  
 A:Accession: PQ0491  
 A:Molecule type: protein  
 A:Residues: 1-13 <GAU>  
 A:Experimental source: stigma, var. acephala P57Si  
 C:Superfamily: S-receptor kinase; protein kinase homology; S-locus-specific glycoprot  
 C:Keywords: glycoprotein

Query Match 16.7%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TES 17  
 ||||  
 Db 7 TES 9

## RESULT 22

A44818  
 extracellular lipase - Pseudomonas aeruginosa (fragment)  
 C:Species: Pseudomonas aeruginosa  
 C>Date: 31-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 31-Oct-1997  
 C:Accession: A44818  
 R:Gilbert, B.J.; Cornish, A.; Jones, C.W.  
 J. Gen. Microbiol. 137, 2223-2229, 1991  
 A>Title: Purification and properties of extracellular lipase from Pseudomonas aerugin  
 A:Reference number: A44818; MUID:92085040; PMID:1748875  
 A:Accession: A44818  
 A>Status: preliminary; not compared with conceptual translation  
 A:Molecule type: nucleic acid  
 A:Residues: 1-13 <GIL>  
 A:Experimental source: strain F53285  
 A>Note: sequence extracted from NCBI backbone (NCBIP:70395)  
 C:Superfamily: Pseudomonas triacylglycerol lipase

Query Match 16.7%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KYP 10  
 ||||  
 Db 7 KYP 9

## RESULT 23

A28953  
 alpha-conotoxin SI - cone shell (Conus striatus)  
 C:Species: Conus striatus (striated cone)  
 C>Date: 30-Jun-1989 #sequence\_revision 25-Apr-1997 #text\_change 23-May-1997  
 C:Accession: A28953  
 R:Zafaralla, G.C.; Ramilo, C.; Gray, W.R.; Karlstrom, R.; Olivera, B.M.; Cruz, L.J.  
 Biochemistry 27, 7102-7105, 1988  
 A>Title: Phylogenetic specificity of cholinergic ligands: alpha-conotoxin SI.  
 A:Reference number: A28953; MUID:89062448; PMID:3196703  
 A:Accession: A28953  
 A:Molecule type: protein  
 A:Residues: 1-13 <ZAF>  
 A>Note: this sequence was confirmed by chemical synthesis

C;Comment: This paralytic toxin from a fish-hunting cone snail inhibits the acetylcholinesterase activity of the acetylcholine receptor.  
 C;Superfamily: alpha-conotoxin  
 C;Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neurotoxin; 2-7, 3-13/disulfide bonds; #status experimental  
 F;13/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 16.7%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PKY 9  
 ||||  
 Db 9 PKY 11

## RESULT 24

S21152  
 tryptophyllin-related peptide - two-colored leaf frog  
 C;Species: Phyllomedusa bicolor (two-colored leaf frog)  
 C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 18-Aug-2000

C;Accession: S21152  
 R;Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G.  
 FEBS Lett. 302, 151-154, 1992  
 A;Title: Identification and characterization of two dermorphins from skin extracts of the two-colored leaf frog  
 A;Reference number: S21152; MUID:92339502; PMID:1633846

A;Accession: S21152  
 A;Molecule type: protein  
 A;Residues: 1-13 <MIG>  
 A;Experimental source: skin  
 C;Superfamily: unassigned animal peptides

Query Match 16.7%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPV 11  
 ||||  
 Db 11 YPV 13

## RESULT 25

A60458  
 protocatechuate 3,4-dioxygenase (EC 1.13.11.13) alpha chain - Moraxella sp. (strain GU2)

N;Alternate names: protocatechuate oxygenase

C;Species: Moraxella sp.

C;Date: 20-Feb-1993 #sequence\_revision 20-Feb-1993 #text\_change 07-May-1999

C;Accession: A60458

R;Stergiades, R.; Pelmont, J.

Appl. Environ. Microbiol. 55, 340-347, 1989

A;Title: Occurrence of two different forms of protocatechuate 3,4-dioxygenase in a Moraxella sp.

A;Reference number: A60458; MUID:89245845; PMID:2541659

A;Accession: A60458

A;Molecule type: protein

A;Residues: 1-13 <STE>

A;Note: two forms P and G of the alpha subunit yielded identical amino terminal sequence

C;Keywords: iron; oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPV 11  
 ||||  
 Db 11 YPV 13

## RESULT 26

PC2371  
 probable endopeptidase Clp ATP-binding chain C [similarity] - Bacillus cereus (strain ts-1)

N;Contains: adenosinetriphosphatase (EC 3.6.1.3)

C;Species: Bacillus cereus

C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000

C;Accession: PC2371

R;Matsuno, K.; Miyamoto, T.; Yamaguchi, K.; Sayed, M.A.; Kajiwara, T.; Hatano, S.  
 Biosci. Biotechnol. Biochem. 59, 231-235, 1995  
 A;Title: Identification of DNA-binding proteins changed after induction of sporulation in Bacillus subtilis  
 A;Reference number: PC2369; MUID:95218265; PMID:7766022

A;Accession: PC2371

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-13 <MAS>

C;Keywords: ATP; hydrolase; nucleotide binding

Query Match 16.7%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FTE 16  
 ||||  
 Db 6 FTE 8

## RESULT 27

D56661

S-locus specific glycoprotein (allele S3) - wild cabbage (fragment)

C;Species: Brassica oleracea (wild cabbage)

C;Date: 05-Jan-1996 #sequence\_revision 05-Jan-1996 #text\_change 05-Jan-1996

C;Accession: D56661

R;Gaudet, T.; Denoroy, L.; Dumas, C.

Electrophoresis 12, 646-653, 1991

A;Title: Use of a fast protein electrophoretic purification procedure for N-terminal sequencing of glycoproteins

A;Reference number: A56661; MUID:92090397; PMID:1752245

A;Accession: D56661

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-13 <GAU>

A;Experimental source: stigma extracts, var. acephala

A;Note: sequence extracted from NCBI backbone (NCBIP:72300)

C;Comment: This glycoprotein, expressed only in stigmas, plays an important role in the development of the stigma

C;Keywords: glycoprotein; polymorphism

Query Match 16.7%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17  
 ||||  
 Db 7 TES 9

## RESULT 28

B61620

locustamytropin IV - migratory locust

C;Species: Locusta migratoria (migratory locust)

C;Date: 21-Jul-1995 #sequence\_revision 28-Jul-1995 #text\_change 11-Jul-1997

C;Accession: B61620

R;Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; Kochansky, J.P.; De Loof, A.

Insect Biochem. Mol. Biol. 22, 447-452, 1992

A;Title: Isolation, identification and synthesis of locustamytropin III and IV, two peptides that induce the release of histamine from mast cells

A;Reference number: A61620

A;Accession: B61620

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-13 <SCH>

C;Keywords: amidated carboxyl end; neuropeptide

F;13/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 16.7%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MPF 6  
 ||||  
 Db 7 MPF 9

## RESULT 29

D61458  
Ig kappa chain V-IV region (DEP) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 15-Oct-1994 #sequence\_revision 15-Oct-1994 #text\_change 16-Aug-1996  
C:Accession: D61458; PLO158  
R:Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.  
J. Exp. Med. 170, 1551-1558, 1989  
A:Title: Expression of a public idiotype by human monoclonal IgM directed to myelin-associated glycoprotein  
A:Reference number: A61458; PMID:90039128; PMID:2478651  
A:Accession: D61458  
A:Molecule type: protein  
A:Residues: 1-13 <BRO>  
C:Comment: This protein is one of monoclonal IgM reactive with myelin-associated glycoprotein  
C:Keywords: heterotetramer; immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17  
|||  
Db 5 TES 7

## RESULT 30

E61458  
Ig kappa chain V-IV region (FUE) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 15-Oct-1994 #sequence\_revision 15-Oct-1994 #text\_change 16-Aug-1996  
C:Accession: E61458  
R:Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.  
J. Exp. Med. 170, 1551-1558, 1989  
A:Title: Expression of a public idiotype by human monoclonal IgM directed to myelin-associated glycoprotein  
A:Reference number: A61458; PMID:90039128; PMID:2478651  
A:Accession: E61458  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-13 <BRO>  
C:Keywords: heterotetramer; immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17  
|||  
Db 5 TES 7

## RESULT 31

PH1772  
T cell receptor alpha chain V region (clone 2V alpha 23-3) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C:Accession: PH1772  
R:Porcell, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.  
J. Exp. Med. 178, 1-16, 1993  
A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A:Reference number: PH1754; PMID:93301585; PMID:8391057  
A:Accession: PH1772  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-13 <POR>

Query Match 16.7%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEP 13  
|||  
Db 4 VEP 6

## RESULT 32

PT0026  
calotropin DI - mudar (fragment)  
C:Species: Calotropis gigantea (mudar, madar)  
C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 05-Aug-1994  
C:Accession: PT0026  
R:Bhattacharya, D.; Sengupta, A.; Sinha, N.K.  
Phytochemistry 26, 633-636, 1987  
A:Title: Chemical modification and amino terminal sequence of calotropin DI from Calotropis gigantea  
A:Reference number: PT0026  
A:Accession: PT0026  
A:Molecule type: protein  
A:Residues: 1-14 <BHA>  
C:Comment: This enzyme is classified as a plant cysteine protease.  
C:Keywords: pyroglutamic acid  
F1/Modified site: pyroglutamic acid (Gln) #status experimental

Query Match 16.7%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPV 11  
|||  
Db 5 YPV 7

## RESULT 33

E33098  
214K exoantigen (version 2) - malaria parasite (Plasmodium falciparum) (fragments)  
C:Species: Plasmodium falciparum  
C:Date: 24-Aug-1990 #sequence\_revision 24-Aug-1990 #text\_change 09-Jun-2000  
C:Accession: E33098  
R:Nichols, J.H.; Hager, L.P.  
submitted to the Protein Sequence Database, May 1990  
A:Reference number: A33098  
A:Accession: E33098  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-14 <NIC>

Query Match 16.7%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPV 11  
|||  
Db 12 YPV 14

## RESULT 34

PA0024  
protein QA300050 - Arabidopsis thaliana (fragment)  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 06-Jun-1997  
C:Accession: PA0024  
R:Kamo, M.; Kawakami, T.; Miyatake, N.; Teugita, A.  
submitted to JIPID, July 1994  
A:Description: Separation and characterization of Arabidopsis proteins by two-dimensional gel electrophoresis  
A:Reference number: PA0001  
A:Accession: PA0024  
A:Molecule type: protein  
A:Residues: 1-15 <RAM>  
A:Experimental source: seed

Query Match 16.7%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PFP 7  
|||  
Db 6 PFP 8

Db 4 PPT 6

RESULT 35  
PS0452  
32K protein 3306 - rice (strain Nihonbare) (fragment)  
C:Species: Oryza sativa (rice)  
C>Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 11-Apr-1995  
C:Accession: PS0452  
R:Tsuigita, A.; Miyatake, N.  
submitted to JIPID, April 1993  
A:Reference number: PS0208  
A:Accession: PS0452  
A:Molecule type: protein  
A:Residues: 1-15 <TSU>  
A:Experimental source: bran, strain Nihonbare  
C:Comment: molecular weight 32K, pI 5.3.

Query Match 16.7%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PPP 7  
|||  
Db 6 PFP 8

RESULT 36  
PA0062  
fumarate hydratase (EC 4.2.1.2) - fungus (Fusarium sporotrichioides) (fragment)  
C:Species: Fusarium sporotrichioides  
C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001  
C:Accession: PA0062  
R:Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.  
submitted to JIPID, October 1994  
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides  
A:Reference number: PA0051  
A:Accession: PA0062  
A:Molecule type: protein  
A:Residues: 1-15 <CHO>  
C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 16.7%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17  
|||  
Db 5 TES 7

RESULT 37  
B61457  
alpha-glucosidase (EC 3.2.1.20) - Tetrahymena pyriformis (strain W) (fragment)  
C:Species: Tetrahymena pyriformis  
C>Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 07-Dec-1999  
C:Accession: B61457  
R:Banno, Y.; Sasaki, N.; Yoshino, T.; Mochizuki, J.I.; Hirata, H.; Nozawa, Y.  
J. Protozool. 36, 562-567, 1989  
A:Title: A thermostable acid alpha-glucosidase from Tetrahymena thermophila: purification  
A:Reference number: B61457; MUID:90095988; PMID:2689637  
A:Accession: B61457  
A:Molecule type: protein  
A:Residues: 1-15 <BAN>  
C:Genetics:  
A:Genetic code: SGC5  
C:Keywords: extracellular protein; glycoprotein; glycosidase; hydrolase; lysosome; monomeric

Query Match 16.7%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PPT 15  
|||

Db 4 PPT 6

RESULT 38  
A36527  
juvenile-hormone esterase (EC 3.1.1.59) - tobacco hornworm (fragment)  
C:Species: Manduca sexta (tobacco hornworm)  
C>Date: 12-Apr-1991 #sequence\_revision 12-Apr-1991 #text\_change 03-Feb-1994  
C:Accession: A36527  
R:Venkatesh, K.; Abdel-Aal, Y.A.I.; Armstrong, F.B.; Roe, R.M.  
J. Biol. Chem. 265, 21727-21732, 1990  
A:Title: Characterization of affinity-purified juvenile hormone esterase from the pl.  
A:Reference number: A36527; MUID:91072375; PMID:2254326  
A:Accession: A36527  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-15 <VEN>  
C:Keywords: carboxylic ester hydrolase

Query Match 16.7%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17  
|||  
Db 12 TES 14

RESULT 39  
A49480  
major immunophilin hsp56 - chicken (fragment)  
C:Species: Gallus gallus (chicken)  
C>Date: 06-Oct-1994 #sequence\_revision 18-Nov-1994 #text\_change 28-Apr-1995  
C:Accession: A49480  
R:Yem, A.W.; Reardon, I.M.; Leone, J.W.; Heinrikson, R.L.; Deibel Jr., M.R.  
Biochemistry 32, 12571-12576, 1993  
A:Title: An active FK506-binding domain of 17,000 daltons is isolated following limited proteolysis of chicken immunophilin hsp56  
A:Reference number: A49480; MUID:94072550; PMID:7504525  
A:Accession: A49480  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-15 <YEM>  
A:Experimental source: thymus  
A:Note: sequence extracted from NCBI backbone (NCBIP:142438)

Query Match 16.7%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17  
|||  
Db 7 TES 9

RESULT 40  
PT0205  
insulin-like growth factor-binding protein, bone - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 08-Dec-1994  
C:Accession: PT0205; A33175  
R:Bautista, C.M.; Baylink, D.J.; Mohan, S.  
Biochem. Biophys. Res. Commun. 176, 756-763, 1991  
A:Title: Isolation of a novel insulin-like growth factor (IGF) binding protein from human placenta  
A:Reference number: PT0205; MUID:91222244; PMID:1709017  
A:Accession: PT0205  
A:Molecule type: protein  
A:Residues: 1-15 <BAU>

Query Match 16.7%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEP 13  
|||

```

Db          7 VEP 9
|||
RESULT 41
B45115
peptidylprolyl isomerase (EC 5.2.1.8) FKBP51 - human (fragment)
N/Alternate names: FK506-binding protein FKBP51; peptidylprolyl cis-trans isomerase FKBP
C/Species: Homo sapiens (man)
C/Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 16-Feb-1997
C/Accession: B45115
R/Wiederrecht, G.; Hung, S.; Chan, H.K.; Marcy, A.; Martin, M.; Calaycay, J.; Boulton, D
J. Biol. Chem. 267, 21753-21760, 1992
A/Title: Characterization of high molecular weight FK-506 binding activities reveals a n
A/Reference number: A45115; MUID:93016131; PMID:1383226
A/Accession: B45115
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-15 <WIE>
A/Experimental source: JURKAT cells
A/Note: sequence extracted from NCBI backbone (NCBIP:116748)
C/Keywords: cis-trans-isomerase; cyclosporin A binding

Query Match          16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          15 TES 17
|||
Db          2 TES 4

RESULT 42
B42324
cytochrome P450c27/25 - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Mar-1999
C/Accession: B42324
R/Shayig, R.M.; Avadhani, N.G.
J. Biol. Chem. 267, 2421-2428, 1992
A/Title: Sequence complementarity between the 5'-terminal regions of mRNAs for rat mitoc
ap.
A/Reference number: A42324; MUID:92129322; PMID:1733943
A/Accession: B42324
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-16 <SHA>
A/Note: sequence extracted from NCBI backbone (NCBIN:78408, NCBIP:88990)
C/Superfamily: human cytochrome P450 CYP11B1; cytochrome P450 homology
C/Keywords: heme; transmembrane protein

Query Match          16.7%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          8 KYP 10
|||
Db          10 KYP 12

RESULT 43
C45133
casein kinase II (EC 2.7.1.1-) alpha chain - dog (fragment)
C/Species: Canis lupus familiaris (dog)
C/Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 03-Jun-1996
C/Accession: C45133
R/Ou, W.J.; Thomas, D.Y.; Bell, A.W.; Bergeron, J.J.
J. Biol. Chem. 267, 23789-23796, 1992
A/Title: Casein kinase II phosphorylation of signal sequence receptor alpha and the asso
A/Reference number: A45133; MUID:93054738; PMID:1331100
A/Accession: C45133
A/Status: preliminary
A/Molecule type: protein

A:Residues: 1-16 <OUI>
A:Experimental source: endoplasmic reticulum, pancreas
A/Note: sequence extracted from NCBI backbone (NCBIP:118799)
C/Superfamily: kinase-related transforming protein; protein kinase homology
C/Keywords: ATP; heterotetramer; phosphotransferase; serine/threonine-specific protei

Query Match          16.7%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          12 EPF 14
|||
Db          6 EPF 8

RESULT 44
I40065
shikimate 5-dehydrogenase (EC 1.1.1.25) - Buchnera aphidicola (fragment)
C/Species: Buchnera aphidicola
C/Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 08-Oct-1999
C/Accession: I40065
R/Rouhbakhsh, D.; Baumann, P.
Gene 155, 107-112, 1995
A/Title: Characterization of a putative 23S-5S rRNA operon of Buchnera aphidicola (er
A/Reference number: I40065; MUID:95212914; PMID:7535281
A/Accession: I40065
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-16 <RES>
A/Cross-references: EMBL:U10499; NID:g854717; PIDN:AAA79128.1; PID:g854718
A/Genetics: aroB
A/Gene: aroB
C/Keywords: oxidoreductase

Query Match          16.7%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          6 FPK 8
|||
Db          9 FPK 11

RESULT 45
C53113
Lys-gingipain form 2, 17K - Porphyromonas gingivalis (fragment)
N/Alternate names: lysine-specific cysteine proteinase 2, 17K
C/Species: Porphyromonas gingivalis
C/Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 05-Apr-1995
C/Accession: C53113
R/Pike, R.; McGraw, W.; Potempa, J.; Travis, J.
J. Biol. Chem. 269, 406-411, 1994
A/Title: Lysine- and arginine-specific proteinases from Porphyromonas gingivalis. Isc
A/Reference number: A53113; MUID:94103245; PMID:8276827
A/Accession: C53113
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-16 <PIK>
A/Experimental source: H66
A/Note: sequence extracted from NCBI backbone (NCBIP:141693)

Query Match          16.7%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          14 FTE 16
|||
Db          3 FTE 5

RESULT 46
S05671
hirudin Ia - medicinal leech (fragment)

```

N:Alternate names: thrombin inhibitor  
 C:Species: Hirudo medicinalis (medicinal leech)  
 C>Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 17-Jul-1998  
 C:Accession: S05671  
 R:Scharf, M.; Engels, J.; Tripiet, D.  
 FEBS Lett. 255, 105-110, 1989

A:Title: Primary structures of new 'iso-hirudins'.  
 A:Reference number: S05671; MUID:90005945; PMID:2792365  
 A:Accession: S05671  
 A:Molecule type: protein  
 A:Residues: 1-17 <SCH>  
 C:Superfamily: thrombin inhibitor  
 C:Keywords: anticoagulant; serine proteinase inhibitor; sulfoprotein  
 F:6-14/Disulfide bonds: #status predicted

Query Match 16.7%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17  
 ||||  
 Db 7 TES 9

RESULT 47  
 S05033  
 photosystem II protein psbL - Synechococcus sp. (strain Copeland) (fragment)  
 N:Alternate names: photosystem II 5K protein  
 C:Species: Synechococcus sp.  
 C>Date: 01-Dec-1989 #sequence\_revision 01-Dec-1989 #text\_change 18-Jun-1993  
 C:Accession: S05033  
 R:Ikeuchi, M.; Koike, H.; Inoue, Y.  
 FEBS Lett. 251, 155-160, 1989

A:Title: Identification of psbI and psbL gene products in cyanobacterial photosystem II  
 A:Reference number: S05030  
 A:Molecule type: protein  
 A:Residues: 1-17 <IKE>  
 A:Note: the source is designated as Synechococcus vulcanus  
 C:Genetics:  
 A:Gene: psbL  
 C:Keywords: photosynthesis; photosystem II; thylakoid

Query Match 16.7%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PVE 12  
 ||||  
 Db 9 PVE 11

RESULT 48  
 B31769  
 T-cell receptor delta-2 chain J region - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 05-Nov-1999  
 C:Accession: B31769  
 R:Loch, E.Y.; Cwirla, S.; Serafini, A.T.; Phillips, J.H.; Lanier, L.L.  
 Proc. Natl. Acad. Sci. U.S.A. 85, 9714-9718, 1988  
 A:Title: Human T-cell-receptor delta chain: genomic organization, diversity, and expression  
 A:Reference number: A94221; MUID:8901766; PMID:2974163  
 A:Accession: B31769  
 A:Molecule type: DNA  
 A:Residues: 1-17 <LOH>  
 A:Cross-references: GB:L36386; NID:g540455; PIDN:AAA61108.1; PID:g540456  
 C:Keywords: T-cell receptor

Query Match 16.7%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11-VEP 13

Db 15 VEP 17  
 ||||

RESULT 49  
 G85956  
 hypothetical protein Z4331 [imported] - Escherichia coli (strain O157:H7, substrain 1)  
 C:Species: Escherichia coli  
 C>Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001  
 C:Accession: G85956  
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Maier, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamocis, K.; Apod, Nature 409, 529-533, 2001  
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
 A:Reference number: A85480; MUID:21074935; PMID:11206551  
 A:Accession: G85956  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-17 <STO>  
 A:Cross-references: GB:AE005174; NID:gl2517539; PIDN:AAG58115.1; GSPDB:GN00145; UWGP  
 A:Experimental source: strain O157:H7, substrain EDL933  
 C:Genetics:  
 A:Gene: Z4331

Query Match 16.7%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PFP 7  
 ||||  
 Db 6 PFP 8

RESULT 50  
 S29264  
 ovohemerythrin - duck leech (fragment)  
 N:Alternate names: 14K yolk protein  
 C:Species: Theromyzon tessulatum (duck leech)  
 C>Date: 19-Mar-1997 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C:Accession: S29264  
 R:Baert, J.L.; Britel, M.; Sautiere, P.; Malecha, J.  
 Eur. J. Biochem. 209, 563-569, 1992  
 A:Title: Ovohemerythrin, a major 14-kDa yolk protein distinct from vitellogenin in 1  
 A:Reference number: S29264; MUID:93049299; PMID:1425663  
 A:Accession: S29264  
 A:Molecule type: protein  
 A:Residues: 1-18 <BAE>  
 A:Cross-references: PIDN:AAB23969.1; PID:g258980  
 C:Superfamily: hemerythrin  
 C:Keywords: egg yolk; oxygen carrier

Query Match 16.7%; Score 3; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EFP 14  
 ||||  
 Db 5 EFP 7

RESULT 51  
 H64711  
 hypothetical protein HPI536 - Helicobacter pylori (strain 26695)  
 C:Species: Helicobacter pylori  
 C>Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 08-Oct-1999  
 C:Accession: H64711  
 R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khaliq, H.G.; Glodek, A.; McK son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey Nature 388, 539-547, 1997  
 A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.  
 A:Reference number: A64520; MUID:97394467; PMID:9252185

A;Accession: H64711  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-18 <TOM>  
A;Cross-references: GB:AE000651; GB:AE000511; NID:g2314708; PIDN:AA08578.1; PID:g2314711

Query Match 16.7%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PKY 9  
Db 15 PKY 17

RESULT 52  
S58277  
insulin-like growth factor receptor type II - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1996 #sequence\_revision 01-Mar-1996 #text\_change 05-Nov-1999  
C;Accession: S58277  
R;Smrzka, O.W.; Stoger, R.; Kurbauer, R.; Fae, I.; Fischer, G.F.; Barlow, D.P.  
submitted to the EMBL Data Library, January 1995  
A;Description: Conservation of a methylation imprint and a putative imprinting box at the 5' end of the human insulin-like growth factor receptor gene.  
A;Reference number: S58277  
A;Accession: S58277  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-18 <SMR>  
A;Cross-references: EMBL:X83702; NID:g929644; PIDN:CAA58675.1; PID:g929645  
C;Keywords: growth factor receptor

Query Match 16.7%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TES 17  
Db 5 TES 7

RESULT 53  
S71592  
serine proteinase inhibitor, 31K - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 19-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 13-Sep-1998  
C;Accession: S71592  
R;Rao, C.N.; Liu, Y.Y.; Peavey, C.L.; Woodley, D.T.  
Arch. Biochem. Biophys. 317, 311-314, 1995  
A;Title: Novel extracellular matrix-associated serine proteinase inhibitors from human skin.  
A;Reference number: S71592; MUID:95177668; PMID:7872799  
A;Accession: S71592  
A;Molecule type: protein  
A;Residues: 1-18 <RAO>  
C;Function:  
A;Description: involved in turnover of connective tissues  
C;Keywords: serine proteinase inhibitor

Query Match 16.7%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 EPF 14  
Db 5 EPF 7

RESULT 54  
I46653  
T-cell receptor delta-chain J-delta-2 - pig (fragment)  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 30-May-1997  
C;Accession: I46653

R;Yang, Y.G.; Ohta, S.; Yamada, S.; Shimizu, M.; Takagaki, Y.  
J. Immunol. 155, 1981-1993, 1995  
A;Title: Diversity of T cell receptor delta-chain cDNA in the thymus of a one-month-old mouse.  
A;Reference number: I46623; MUID:95363165; PMID:7636249  
A;Accession: I46653  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-18 <YAN>  
A;Cross-references: GB:DA9561; NID:g1041174; PID:g1041175  
C;Keywords: T-cell receptor

Query Match 16.7%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VEP 13  
Db 16 VEP 18

RESULT 55  
A59137  
protein Pil - golden needle mushroom (fragment)  
C;Species: Flammulina velutipes (golden needle mushroom)  
C;Date: 12-Nov-1999 #sequence\_revision 12-Nov-1999 #text\_change 12-Nov-1999  
C;Accession: A59137  
R;Sakamoto, Y.; Ando, A.; Tamai, Y.; Miura, K.  
submitted to the Protein Sequence Database, November 1999  
A;Description: Differences of proteins expressed in the fruiting dikaryon and the non-fruited dikaryon of the golden needle mushroom.  
A;Reference number: A59137  
A;Accession: A59137  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-18 <SAK>

Query Match 16.7%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PFT 15  
Db 15 PFT 17

RESULT 56  
BWSMCN  
cinnamycin - Streptovorticillium cinnamomeum  
N;Alternate names: lanthiopeptin; lantibiotic Ro 09-0198  
C;Species: Streptovorticillium cinnamomeum  
C;Date: 30-Sep-1993 #sequence\_revision 12-May-1994 #text\_change 07-May-1999  
C;Accession: A45767  
R;Naruse, N.; Tenmyo, O.; Tomita, K.; Konishi, M.; Miyaki, T.; Kawaguchi, H.; Fukase, J.  
Antibiot. 42, 837-845, 1989  
A;Title: Lanthiopeptin, a new peptide antibiotic. Production, isolation and properties.  
A;Reference number: A45767; MUID:89291558; PMID:2544544  
A;Accession: A45767  
A;Molecule type: protein  
A;Residues: 1-19 <NAR>  
R;Wakamiya, T.; Fukase, K.; Naruse, N.; Konishi, M.; Shiba, T.  
Tetrahedron Lett. 29, 4771-4772, 1988  
A;Title: Lanthiopeptin, a new peptide effective against Herpes simplex virus: structural analysis.  
A;Reference number: A53359  
A;Contents: annotation; strain L337-2  
C;Superfamily: cinnamycin precursor  
C;Keywords: antibiotic; beta-hydroxyaspartic acid; lanthionine  
F;1-18/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Cys-Thr) #status experimental  
F;4-14/Cross-link: sn-(2S,6R)-lanthionine (Ser-Cys) #status experimental  
F;5-11/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Cys-Thr) #status experimental  
F;6-19/Cross-link: (2xi,9S)-lysinoalanine (Ser-Lys) #status experimental  
F;15/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental

Query Match 16.7%; Score 3; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFT 15  
|||  
Db 9 PFT 11

RESULT 57  
S59485  
hyoxyproline-rich cell wall glycoprotein (42K and others) - kidney bean (fragment)  
C;Species: Phaseolus vulgaris (kidney bean)  
C;Date: 27-Apr-1996 #sequence\_revision 26-Jul-1996 #text\_change 05-Dec-1998  
C;Accession: S59485; S59484; S59483  
R;Wojtaszek, P.; Trethowan, J.; Bolwell, G.P.  
Plant Mol. Biol. 28, 1075-1087, 1995  
A;Title: Specificity in the immobilisation of cell wall proteins in response to different  
A;Reference number: S59481; MUID:96011753; PMID:7548825  
A;Accession: S59485  
A;Molecule type: protein  
A;Residues: 1-19 <WOJ>  
A;Note: hyoxyproline-rich cell wall glycoprotein, 42K  
A;Accession: S59484  
A;Molecule type: protein  
A;Residues: 1-15 <WOW>  
A;Note: hyoxyproline-rich cell wall glycoprotein, 84K  
A;Accession: S59483  
A;Molecule type: protein  
A;Residues: 1-14 <WOP>  
A;Note: hyoxyproline-rich cell wall glycoprotein, 136K, minor component  
C;Superfamily: proline-rich protein 3  
C;Keywords: glycoprotein; hydroxyproline  
F;6,11,16/Modified site: hydroxyproline (pro) #status experimental

Query Match 16.7%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PVE 12  
|||  
Db 6 PVE 8

RESULT 58  
S43641  
carboxylesterase (EC 3.1.1.1), thermostable - Alicyclobacillus acidocaldarius (fragment)  
C;Species: Alicyclobacillus acidocaldarius  
C;Date: 19-Mar-1997 #sequence\_revision 01-Aug-1997 #text\_change 17-Mar-1999  
C;Accession: S43641  
R;Manco, G.; di Gennaro, S.; de Rosa, M.; Rossi, M.  
Eur. J. Biochem. 221, 965-972, 1994  
A;Title: Purification and characterization of a thermostable carboxylesterase from the  
A;Reference number: S43641; MUID:94237161; PMID:8181479  
A;Accession: S43641  
A;Molecule type: protein  
A;Residues: 1-19 <MAN>  
A;Experimental source: strain MT3  
A;Note: the source is designated as Bacillus acidocaldarius  
C;Keywords: carboxylic ester hydrolase; monomer

Query Match 16.7%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PVE 12  
|||  
Db 4 PVE 6

RESULT 59  
C56661  
S-locus specific glycoprotein (allele S9) - wild cabbage (fragment)  
C;Species: Brassica oleracea (wild cabbage)  
C;Date: 05-Jan-1996 #sequence\_revision 05-Jan-1996 #text\_change 05-Jan-1996

C;Accession: C56661  
R;Gaude, T.; Denoroy, L.; Dumas, C.  
Electrophoresis 12, 646-653, 1991  
A;Title: Use of a fast protein electrophoretic purification procedure for N-terminal  
A;Reference number: A56661; MUID:92090397; PMID:1752245  
A;Accession: C56661  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-19 <GAU>  
A;Experimental source: stigma extracts, var. acephala  
A;Note: sequence extracted from NCBI backbone (NCBIP:72301)  
C;Comment: This glycoprotein, expressed only in stigmas, plays an important role in  
C;Keywords: glycoprotein; polymorphism

Query Match 16.7%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17  
|||  
Db 7 TES 9

RESULT 60  
PQ0492  
self-incompatibility locus glycoprotein epsilon - wild cabbage (fragment)  
C;Species: Brassica oleracea (wild cabbage)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 03-Mar-1995  
C;Accession: PQ0492  
R;Gaude, T.; Friry, A.; Heizmann, P.; Mariac, C.; Rougier, M.; Fobis, I.; Dumas, C.  
Plant Cell 5, 75-86, 1993  
A;Title: Expression of a self-incompatibility gene in a self-compatible line of Bras  
A;Reference number: JQ1733; MUID:93177215; PMID:8439745  
A;Accession: PQ0492  
A;Molecule type: protein  
A;Residues: 1-19 <GAU>  
A;Experimental source: stigma, var. acephala P57S1  
C;Keywords: glycoprotein

Query Match 16.7%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17  
|||  
Db 7 TES 9

RESULT 61  
A61144  
probable flagellar protein (clone FCH-F8-4) - Trypanosoma cruzi (fragment)  
C;Species: Trypanosoma cruzi  
C;Date: 10-Mar-1994 #sequence\_revision 07-Apr-1994 #text\_change 24-Feb-1995  
C;Accession: A61144  
R;Bua, J.; Bontempi, E.J.; Levin, M.; Orn, A.; Velasco, D.; Moreno, M.; Levi-Yeyati,  
Exp. Parasitol. 72, 54-62, 1991  
A;Title: Trypanosoma cruzi: cellular and antibody response against the parasite in m  
A;Reference number: A61144; MUID:91130571; PMID:1993465  
A;Accession: A61144  
A;Molecule type: mRNA  
A;Residues: 1-19 <BUA>

Query Match 16.7%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEP 13  
|||  
Db 17 VEP 19

RESULT 62  
C39305



```

neurotoxin Tx3 - spider (Phoneutria nigriventer) (fragment)
C:Species: Phoneutria nigriventer
C>Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 07-Feb-1997
C:Accession: C39305
R:Rezende Jr., L.; Cordeiro, M.N.; Oliveira, E.B.; Diniz, C.R.
Toxinon 29, 1225-1233, 1991
A>Title: Isolation of neurotoxic peptides from the venom of the 'armed' spider Phoneutria
A:Reference number: A39305; MUID:92196803; PMID:1801316
A:Accession: C39305
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-19 <REZ>
C:Keywords: neurotoxin

Query Match      16.7%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ESQ 18
   |||
Db 7 ESQ 9

RESULT 63
I46654
T-cell receptor delta-chain J-delta-3 - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 05-Nov-1999
C:Accession: I46654
R:Yang, Y.G.; Ohta, S.; Yamada, S.; Shimizu, M.; Takagaki, Y.
J. Immunol. 155, 1981-1993, 1995
A>Title: Diversity of T cell receptor delta-chain cDNA in the thymus of a one-month-old
A:Reference number: I46623; MUID:95363165; PMID:7636249
A:Accession: I46654
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-19 <YAN>
A:Cross-references: GB:D49562; NID:gl041176; PIDN:BAA08506.1; PID:gl041177
C:Keywords: T-cell receptor

Query Match      16.7%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEP 13
   |||
Db 17 VEP 19

RESULT 64
S69166
ferredoxin b - Japanese radish (fragments)
C:Species: Kaiware daikon (Japanese radish)
C>Date: 10-Mar-1998 #sequence_revision 10-Mar-1998 #text_change 17-Apr-1998
C:Accession: S69166
R:Obata, S.; Nishimura, M.; Nagai, K.; Sakihama, N.; Shin, M.
Arch. Biochem. Biophys. 316, 797-802, 1995
A>Title: Four ferredoxins from Japanese radish leaves.
A:Reference number: S69164; MUID:95168867; PMID:7864635
A:Accession: S69166
A:Molecule type: protein
A:Residues: 1-19 <OBA>
C:Keywords: 2Fe-2S; electron transfer; iron-sulfur protein

Query Match      16.7%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKE 3
   |||
Db 13 HKE 15

```

```

RESULT 65
S11611
ribosomal protein S2 [validated] - Halobacterium salinarum (fragment)
N:Alternate names: ribosomal protein HSSA
C:Species: Halobacterium salinarum
C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jul-2000
C:Accession: S11611
R:Yaguchi, M.; Visentin, L.P.; Zuker, M.; Matheson, A.T.; Roy, C.; Strom, A.R.
Zbl. Bakt. Hyg. I. Abt. Orig. C 3, 200-208, 1982
A>Title: Amino-terminal sequences of ribosomal proteins from the 30S subunit of archa
A:Reference number: S11609
A:Accession: S11611
A:Molecule type: protein
A:Residues: 1-19 <YAG>
A>Note: the protein is designated as ribosomal protein HSSA
C:Keywords: protein biosynthesis; ribosome

Query Match      16.7%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17
   |||
Db 7 TES 9

RESULT 66
S06466
T-cell receptor alpha chain J segment (DO) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 06-Jun-1997
C:Accession: S06466
R:Rague, J.; Blackman, M.; Born, W.; Marrack, P.; Kappler, J.; Palmer, E.
Nucleic Acids Res. 16, 11355-11364, 1988
A>Title: The structure of V-alpha and J-alpha segments in the mouse.
A:Reference number: S06466; MUID:89083566; PMID:2849763
A:Accession: S06466
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-20 <YAG>
A:Experimental source: strain Balb/c
C:Genetics:
A:Map position: 14
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein; heterodimer; T-cell receptor
F:1-18/Domain: J segment <JSE>
F:19-20/Domain: C region (fragment) <CRE>

Query Match      16.7%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEP 13
   |||
Db 16 VEP 18

RESULT 67
JP0059
ribosomal protein L30 - Thermoactinomyces intermedius (fragment)
C:Species: Thermoactinomyces intermedius
C>Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 03-May-1996
C:Accession: JP0059
R:Ochi, K.
submitted to JPIID, February 1994
A:Description: Phylogenetic diversity in the genus Bacillus and comparative ribosomal
A:Reference number: JP0042
A:Accession: JP0059
A:Molecule type: protein
A:Residues: 1-20 <OCH>
C:Superfamily: Escherichia coli ribosomal protein L30
C:Keywords: protein biosynthesis; ribosome

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Query Match 16.7%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 16 ESQ 18  
Db 17 ESQ 19

RESULT 68  
PL0145  
carbon-monoxide dehydrogenase (EC 1.2.99.2) small chain - Pseudomonas carboxydoflava (fr  
C/Species: Pseudomonas carboxydoflava  
C/Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 28-Apr-1993  
C/Accession: PL0145  
R/Kraut, M.; Hugendieck, I.; Herwig, S.; Meyer, O.  
Arch. Microbiol. 152, 335-341, 1989  
A/Title: Homology and distribution of CO dehydrogenase structural genes in carboxydotrop  
A/Reference number: PL0138; MUID:90055678; PMID:2818128  
A/Accession: PL0145  
A/Molecule type: protein  
A/Residues: 1-20 <K2A>  
C/Comment: Carbon-monoxide dehydrogenase consists of three polypeptide chains: large, me  
C/Keywords: oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 11 VEP 13  
Db 18 VEP 20

RESULT 69  
PQ0046  
citrate (si)-synthase (EC 4.1.3.7) - Streptomyces hygroscopicus (fragment)  
N/Alternate names: citrate condensing enzyme; citrogenase; condensing enzyme; oxaloaceta  
C/Species: Streptomyces hygroscopicus  
C/Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 05-May-2000  
C/Accession: PQ0046  
R/Shimotomo, K.W.; Imai, S.; Murakami, T.; Seto, H.  
Agric. Biol. Chem. 54, 463-470, 1990  
A/Title: Purification and characterization of citrate synthase from Streptomyces hygrosc  
A/Reference number: PS0106; MUID:90334852; PMID:1368511  
A/Accession: PQ0046  
A/Molecule type: protein  
A/Residues: 1-20 <SHI>  
A/Experimental source: strain SF-1293  
C/Comment: This enzyme catalyzes the synthesis of citric acid.  
C/Keywords: carbon-carbon lyase; coenzyme A; oxo-acid-lyase; tricarboxylic acid cycle

Query Match 16.7%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 9 YPV 11  
Db 16 YPV 18

RESULT 70  
S29635  
jacalin beta chain - Artocarpus tonkinensis  
C/Species: Artocarpus tonkinensis  
C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Jul-1997  
C/Accession: S29635  
R/Ngoc, L.D.; Brillard, M.; Hoebeke, J.  
Biochim. Biophys. Acta 1156, 219-222, 1993  
A/Title: The alpha- and beta-subunits of the jacalins are cleavage products from a 17-kD  
A/Reference number: S29635; MUID:93152601; PMID:8427879  
A/Accession: S29635  
A/Status: preliminary

Query Match 16.7%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 PFP 7  
Db 12 PFP 14

RESULT 71  
B30208  
hypothetical protein 1 (cpc-1 5' region) - Neurospora crassa  
C/Species: Neurospora crassa  
C/Date: 01-Dec-1989 #sequence\_revision 01-Dec-1989 #text\_change 18-Jun-1993  
C/Accession: B30208  
R/Faluh, J.L.; Orbach, M.J.; Legerton, T.L.; Yanofsky, C.  
Proc. Natl. Acad. Sci. U.S.A. 85, 3728-3732, 1988  
A/Title: The cross-pathway control gene of Neurospora crassa, cpc-1, encodes a prote  
A/Reference number: A30208; MUID:88234499; PMID:2967496  
A/Accession: B30208  
A/Molecule type: DNA  
A/Residues: 1-20 <PAL>  
A/Cross-references: GB:J03262

Query Match 16.7%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 PFP 7  
Db 6 PFP 8

RESULT 72  
S58382  
hypothetical protein 1 - human  
C/Species: Homo sapiens (man)  
C/Date: 12-Feb-1998 #sequence\_revision 20-Feb-1998 #text\_change 08-Oct-1999  
C/Accession: S58382  
R/Dirks, R.P.H.; Onnekink, C.; Jansen, H.J.; de Jong, A.; Bloemers, H.P.J.  
Nucleic Acids Res. 23, 2815-2822, 1995  
A/Title: A novel human c-sis mRNA species is transcribed from a promoter in c-sis in  
A/Reference number: S58382; MUID:95388493; PMID:7659502  
A/Accession: S58382  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-20 <DIR>  
A/Cross-references: EMBL:X83705; NID:g951023; PIDN:CAA58678.1; PID:g951024

Query Match 16.7%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 PFP 7  
Db 12 PFP 14

RESULT 73  
I46652  
T-cell receptor delta-chain J-delta-1 segment - pig (fragment)  
C/Species: Sus scrofa domestica (domestic pig)  
C/Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 05-Nov-1999  
C/Accession: I46652  
R/Yang, Y.G.; Ohta, S.; Yamada, S.; Shimizu, M.; Takagaki, Y.  
J. Immunol. 155, 1981-1993, 1995  
A/Title: Diversity of T cell receptor delta-chain cDNA in the thymus of a one-month-  
A/Reference number: I46623; MUID:95363165; PMID:7636249  
A/Accession: I46652  
A/Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA  
A:Residues: 1-20 <YAN>  
A:Cross-references: GB:D49560; NID:g1041172; PIDN:BA08504.1; PID:g1041173  
C:Keywords: T-cell receptor

Query Match 16.7%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred.No. 3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VEP 13  
|||  
Db 18 VEP 20

RESULT 74  
A41439  
acid ribonuclease (EC 3.1.1.-) - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)  
C>Date: 21-Apr-1992 #sequence\_revision 21-Apr-1992 #text\_change 21-Mar-1996  
C:Accession: A41439  
R:Ohgi, K.; Sanda, A.; Takizawa, Y.; Irie, M.  
J. Biochem. 103, 267-273, 1988  
A:Title: Purification of acid ribonucleases from bovine spleen.  
A:Reference number: A41439; MUID:88227899; PMID:3131316  
A:Accession: A41439  
A>Status: Preliminary  
A:Molecule type: protein  
A:Residues: 1-20 <OHG>  
C:Keywords: hydrolase

Query Match 16.7%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred.No. 3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FPK 8  
|||  
Db 12 FPK 14

RESULT 75  
GKHU  
growth-modulating peptide - human  
C:Species: Homo sapiens (man)  
C>Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C:Accession: A01421  
R:Schlesinger, D.H.; Pickart, L.; Thaler, M.M.  
Experientia 33, 324-325, 1977  
A:Title: Growth-modulating serum tripeptide is glycyl-histidyl-lysine.  
A:Reference number: A01421; MUID:77162369; PMID:858356  
A:Accession: A01421  
A:Molecule type: protein  
A:Residues: 1-3 <SCH>  
A>Note: this serum tripeptide is found to stimulate growth of some cell types and to inhibit growth of others.  
C:Superfamily: unassigned animal peptides

Query Match 11.1%; Score 2; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred.No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HK 2  
||  
Db 2 HK 3

Search completed: November 25, 2003, 19:36:08  
Job time : 12.3488 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:17:40 ; Search time 6.38372 Seconds  
(without alignments)  
132.600 Million cell updates/sec

Title: US-09-641-801-22  
Perfect score: 18  
Sequence: 1 HKEMPPFKYVPEPTESQ 18

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3  
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	16.7	7	1	IGAO_DACDE
2	3	16.7	7	1	WMA3_ACHFU
3	3	16.7	10	1	UHA3_HUMAN
4	3	16.7	11	1	EPG_GLOPA
5	3	16.7	13	1	LMT4_LOGMI
6	3	16.7	13	1	UHA3_CANFA
7	3	16.7	13	1	YPE2_LACLC
8	3	16.7	14	1	CAL1_CALGI
9	3	16.7	15	1	ESTJ_MANSE
10	3	16.7	15	1	UC08_MAIZE
11	3	16.7	15	1	UC16_MAIZE
12	3	16.7	15	1	UC25_MAIZE
13	3	16.7	16	1	H5_COTJA
14	3	16.7	16	1	ODPB_SOLTU
15	3	16.7	17	1	ITHB_HIRME
16	3	16.7	17	1	PSBL_SYNVU
17	3	16.7	18	1	D7AI_ACASC
18	3	16.7	18	1	HEMH_THETS
19	3	16.7	18	1	LCTN_LANGL
20	3	16.7	19	1	DURA_STRGV
21	3	16.7	19	1	TX3_PHONI
22	3	16.7	20	1	CSYJ_STRHY
23	3	16.7	20	1	SB60_MAIZE
24	2	11.1	3	1	GRWM_HUMAN
25	2	11.1	5	1	PAP2_PARMA
26	2	11.1	5	1	RE31_LITRU
27	2	11.1	5	1	RE32_LITRU
28	2	11.1	5	1	SUGA_ACHDO
29	2	11.1	6	1	ASF2_LACSN
30	2	11.1	7	1	ALL3_CARMA
31	2	11.1	7	1	CARP_MYTED
32	2	11.1	7	1	E105_LITRU
33	2	11.1	7	1	FAR1_HELTI

RESULT 1

34	2	11.1	7	1	FAR5_HIRME	P42564	hirudo medi
35	2	11.1	7	1	UF04_MOUSE	P38642	mus musculus
36	2	11.1	7	1	UN06_PIPES	P81675	pinus pinas
37	2	11.1	7	1	WWA1_ACHFU	P35919	achatina fu
38	2	11.1	8	1	AKH_LIBAU	P25418	libellula a
39	2	11.1	8	1	AKH_TABAT	P14595	tabanus atr
40	2	11.1	8	1	ANG2_BOTJA	O10582	bothrops ja
41	2	11.1	8	1	CLP_THICU	P80488	thiobacillu
42	2	11.1	8	1	HTF2_PERAM	P04549	periplaneta
43	2	11.1	8	1	LMT2_LOGMI	P22396	locusta mig
44	2	11.1	8	1	LPK_LEUMA	P13049	leucophaea
45	2	11.1	8	1	ORMY_ORCLI	P82455	orconectes
46	2	11.1	8	1	PPK2_PERAM	P82692	periplaneta
47	2	11.1	8	1	PPK3_PERAM	P82618	periplaneta
48	2	11.1	8	1	RS7_MYCIT	P33564	mycobacteri
49	2	11.1	8	1	UC26_MAIZE	P80632	zea mays (m
50	2	11.1	8	1	UF06_MOUSE	P38644	mus musculu
51	2	11.1	8	1	UPA1_HUMAN	P30087	homo sapien
52	2	11.1	8	1	UPAA_HUMAN	P30096	homo sapien
53	2	11.1	9	1	CCAP_CARMA	P38556	carcinus ma
54	2	11.1	9	1	CONO_CONGE	P05486	conus geogr
55	2	11.1	9	1	COXE_THUOB	P80975	thunus obe
56	2	11.1	9	1	FAR2_CALVO	P41857	calliphora
57	2	11.1	9	1	FAR3_CALVO	P41858	calliphora
58	2	11.1	9	1	FAR4_PENMO	P83313	penaeus mon
59	2	11.1	9	1	FAR5_PENMO	P83320	penaeus mon
60	2	11.1	9	1	FIBB_MACFU	P19345	macaca fusc
61	2	11.1	9	1	FRF1_SARBU	P83350	sarcophaga
62	2	11.1	9	1	HUTU_KLEAE	P12381	klebsiella
63	2	11.1	9	1	KNL3_BOMVA	P83058	bombina var
64	2	11.1	9	1	LMT3_LOGMI	P41489	locusta mig
65	2	11.1	9	1	OXYA_SCYCA	P42996	scyllorhinu
66	2	11.1	9	1	OXIF_SCYCA	P42997	scyllorhinu
67	2	11.1	9	1	OXIV_SQUAC	P43000	squalus aca
68	2	11.1	9	1	SAMP_MUSCA	P19095	mustelus ca
69	2	11.1	9	1	THYF_PIG	P01255	sus scrofa
70	2	11.1	9	1	UHA2_HUMAN	P40929	homo sapien
71	2	11.1	9	1	UN19_CLOPA	P81355	clostridium
72	2	11.1	9	1	UPA3_HUMAN	P30089	homo sapien
73	2	11.1	10	1	ANG1_BOTJA	O10581	bothrops ja
74	2	11.1	10	1	ANGT_BOVIN	P10117	bos taurus
75	2	11.1	10	1	ANGT_CHICK	P10118	gallus gall
76	2	11.1	10	1	BPP_VIPAS	P31351	vipera aspi
77	2	11.1	10	1	COXA_ONCMY	P80328	oncorhynch
78	2	11.1	10	1	FAR6_PANRE	P82660	panagrellus
79	2	11.1	10	1	GAJU_HUMAN	P01358	homo sapien
80	2	11.1	10	1	GON2_CHICK	P37043	gallus gall
81	2	11.1	10	1	HTF1_ROMMI	P18110	romalea mic
82	2	11.1	10	1	HTF2_CARMO	P11385	carausius m
83	2	11.1	10	1	HTF_TABAT	P14596	tabanus atr
84	2	11.1	10	1	LPK2_LOGMI	P41488	locusta mig
85	2	11.1	10	1	ODP2_BOVIN	P11180	bos taurus
86	2	11.1	10	1	PNEU_HUMAN	P22103	homo sapien
87	2	11.1	10	1	PNEU_RAT	P21996	rattus norv
88	2	11.1	10	1	PPCK_PASHE	P80525	fasciola he
89	2	11.1	10	1	PPCK_LOGMI	P83382	locusta mig
90	2	11.1	10	1	RL16_ACHLA	P80465	comamonas t
91	2	11.1	10	1	RT02_BOVIN	P29221	acholeplasm
92	2	11.1	10	1	RT02_BOVIN	P29221	acholeplasm
93	2	11.1	10	1	SLAP_BACTG	P49325	bacillus th
94	2	11.1	10	1	SYK_CAMUP	Q46464	campylobact
95	2	11.1	10	1	TKNB_CHICK	P19851	gallus gall
96	2	11.1	10	1	TKNB_ONCMY	P28500	oncorhynch
97	2	11.1	10	1	TKNB_RANRI	P29135	rana ridibu
98	2	11.1	10	1	TKU1_UREUN	P40751	urechis uni
99	2	11.1	10	1	UH05_RAT	P56573	rattus norv
100	2	11.1	10	1	UPA5_HUMAN	P30091	homo sapien

ALIGNMENTS

IGAO\_DACDE  
 ID IGAO\_DACDE STANDARD; PRT; 7 AA.  
 AC P06294;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 01-OCT-1994 (Rel. 30, Last annotation update)  
 DE Galactose oxidase inhibitor.  
 OS Dactylium dendroides (Cladobotryum dendroides).  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypomyces.  
 OX NCBI\_TaxID=5132;  
 RN [1]\_TaxID=5132;  
 RP SEQUENCE.  
 RA Avidad G., Markus Z.;  
 RT "Identification of a peptide inhibitor of galactose oxidase from  
 RT Dactylium dendroides.";  
 RL Fed. Proc. 31:447-447(1972).  
 CC -!- FUNCTION: BINDS ONE COPPER ION PER MOLECULE BUT DOES NOT BIND THE  
 CC GALACTOSE OXIDASE APOENZYME. IT MAY INACTIVATE THE ENZYME BY  
 CC BINDING TO ITS PROSTHETIC COPPER GROUP.  
 DR PIR; A01341; XEYDGD.  
 KW Copper; Metalloenzyme inhibitor.  
 SQ SEQUENCE 7 AA; 706 MW; 75BB01A456D87DB0 CRC64;  
 Query Match 16.7%; Score 3; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 15 TES 17  
 DB 5 TES 7  
 RESULT 2  
 ID WFA3\_ACHFU STANDARD; PRT; 7 AA.  
 AC P35921;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-OCT-1994 (Rel. 30, Last annotation update)  
 DE Wamide-3.  
 OS Achatina fulica (Giant African snail).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
 OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.  
 OX NCBI\_TaxID=6530;  
 RN [1]\_TaxID=6530;  
 RP SEQUENCE.  
 RC TISSUE=Ganglion;  
 RX MEDLINE=93265912; PubMed=8495720;  
 RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;  
 RT "Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from  
 RT ganglia of the African giant snail, Achatina fulica.";  
 RL FEBS Lett. 323:104-108(1993).  
 DR PIR; S33244; S33244.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 7 7  
 SQ SEQUENCE 7 AA; 965 MW; 7362D5B69B132310 CRC64;  
 Query Match 16.7%; Score 3; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 KEM 4  
 DB 2 KEM 4  
 RESULT 3  
 ID UHA3\_HUMAN STANDARD; PRT; 10 AA.  
 AC P40910;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Unknown protein from 2D-page of heart (Spot 7513) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]\_TaxID=9606;  
 RP SEQUENCE.  
 RC TISSUE=Heart;  
 RX MEDLINE=95203287; PubMed=7895732;  
 RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;  
 RT "The human myocardial two-dimensional gel protein database: update  
 RT 1994.";  
 RL Electrophoresis 15:1459-1465(1994).  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 6.8, ITS MW IS: 47.3 kDa.  
 FT NON TER 10 10  
 SQ SEQUENCE 10 AA; 1049 MW; 6BBCDE41A041B76B CRC64;  
 Query Match 16.7%; Score 3; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 11 VEP 13  
 DB 2 VEP 4  
 RESULT 4  
 ID EFG\_CLOPA STANDARD; PRT; 11 AA.  
 AC P81350;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Elongation factor G (EF-G) (CP 5) (Fragment).  
 GN FUSA.  
 OS Clostridium pasteurianum.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium.  
 OX NCBI\_TaxID=1501;  
 RN [1]\_TaxID=1501;  
 RP SEQUENCE.  
 RC STRAIN=WS;  
 RX MEDLINE=98291870; PubMed=9629918;  
 RA Flengsrud R., Skjeldal L.;  
 RT "Two-dimensional gel electrophoresis separation and N-terminal  
 RT sequence analysis of proteins from Clostridium pasteurianum W5.";  
 RL Electrophoresis 19:802-806(1998).  
 CC -!- FUNCTION: This protein promotes the GTP-dependent translocation of  
 CC the nascent protein chain from the A-site to the P-site of the  
 CC ribosome.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.  
 CC EF-G/EF-2 SUBFAMILY.  
 DR InterPro; IPR000795; EF\_GTPbind.  
 KW PROSITE; PS00301; EFATOR\_GTP; PARTIAL.  
 KW Elongation factor; Protein biosynthesis; GTP-binding.  
 FT NON TER 11 11  
 SQ SEQUENCE 11 AA; 1337 MW; 412E71FD9C33B17 CRC64;  
 Query Match 16.7%; Score 3; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 KYP 10  
 DB 1 KYP 3  
 RESULT 5  
 ID LMT4\_LOCMI STANDARD; PRT; 13 AA.

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AC P41490;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Locustamytotropin 4 (LOW-MT-4).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,
RA de Loof A.,
RT IV, two additional neuropeptides of Locusta migratoria: members of the
RT Locustamytotropin peptide family."
RL Insect Biochem. Mol. Biol. 22:447-452(1992).
CC -I- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY). LOW-MT IV SEEMS TO BE A MORE POTENT MUSCLE
CC STIMULATOR THAN LOW-MT I, II AND III.
CC -I- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR PIR: B61620; B61620.
DR InterPro: IPR001484; Pyrokinin.
DR PROSITE: PS00539; PYROKININ: 1.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 13 13
FT AMIDATION.
SQ SEQUENCE 13 AA; 1553 MW; 20861943824D6698 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MPF 6
DB 7 MPF 9

RESULT 6
UHA3 CANFA
ID UHA3 CANFA STANDARD; PRT; 13 AA.
AC P56535;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Unknown protein from 2D-page of heart tissue (Spot 7520) (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins."
RL Electrophoresis 18:2795-2802(1997).
CC -I- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.9. ITS MW IS: 55.4 kDa.
DR HSC-2DPAGE; P56535; DOG.
FT NON_TER 13 13
FT
SQ SEQUENCE 13 AA; 1457 MW; 9F5BD94B9306D76A CRC64;

Query Match 16.7%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PVE 12
DB 7 PVE 9
```

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RESULT 7
YPE2_LACLC
ID YPE2_LACLC STANDARD; PRT; 13 AA.
AC P42021;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in PEPT 5'region (ORF2) (Fragment).
OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1359;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94245610; PubMed=8188586;
RA Mierau I., Haandrikman A.J., Veltrop O., Tan P.S.T., Leenhouts K.L.,
RA Konings W.N., Venema G., Kok J.;
RT "Tripeptidase gene (pepT) of Lactococcus lactis: molecular cloning
RT and nucleotide sequencing of pepT and construction of a chromosomal
RT deletion mutant";
RL J. Bacteriol. 176:2854-2861(1994).
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: L27596; AAA20625.1; -
KW Hypothetical protein.
FT NON_TER 1
FT
SQ SEQUENCE 13 AA; 1392 MW; 3671D53271B459D7 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EPF 14
DB 5 EPF 7

RESULT 8
CAL1 CALGI
ID CAL1 CALGI STANDARD; PRT; 14 AA.
AC P20728;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Calotropin DI (EC 3.4.22.-) (Fragment).
OS Calotropis gigantea (Madar) (Bowstring hemp).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Gentianales; Apocynaceae; Asclepiadoideae;
OC Asclepiadeae; Calotropis.
OX NCBI_TaxID=4066;
RN [1]
RP SEQUENCE.
RA Bhattacharya D., Sengupta A., Sinha N.K.;
RT "Chemical modification and amino terminal sequence of calotropin DI
RT from Calotropis gigantea."
RL Phytochemistry 26:633-636(1987).
CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
DR PIR: PT0026; PT0026.
DR MEROPS: C01.011; -.
DR InterPro: IPR000169; SHprot_accsite.
DR PROSITE: PS00139; THIOI_PROTEASE_CYS; PARTIAL.
DR PROSITE: PS00639; THIOI_PROTEASE_HIS; PARTIAL.
DR PROSITE: PS00640; THIOI_PROTEASE_ASN; PARTIAL.
KW Hydrolase; Thiol protease; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1
FT PYRROLIDONE CARBOXYLIC ACID.
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FT  NON_TER      14      14
SQ  SEQUENCE     14 AA;  1715 MW;  D993F0276CDA4662 CRC64;

Query Match
Best Local Similarity 16.7%; Score 3; DB 1; Length 14;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  9 YPV 11
DB  5 YPV 7

RESULT 9
ESTJ MANSE
ID  ESTJ MANSE      STANDARD;      PRT;      15 AA.
AC  P19985;
DT  01-FEB-1991 (Rel. 17, Created)
DT  01-FEB-1991 (Rel. 17, Last sequence update)
DT  01-FEB-1994 (Rel. 28, Last annotation update)
DE  Juvenile hormone esterase (EC 3.1.1.59) (JH esterase) (Fragment).
OS  Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC  Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Spingioidea;
OC  Spingidae; Spinginae; Manduca.
OX  NCBI_TaxID=7130;
RN  [1]

RP  SEQUENCE.
RC  TISSUE=Larval plasma;
RX  MEDLINE=91072375; PubMed=2254326;
RA  Venkatesh K., Abdel-Aal Y.A.I., Armstrong F.B., Roe R.M.;
RT  "Characterization of affinity-purified juvenile hormone esterase from
the plasma of the tobacco hornworm, Manduca sexta.";
RL  J. Biol. Chem. 265:21727-21732(1990).
CC  -1- FUNCTION: JH ESTERASE PLAYS A CRUCIAL ROLE IN THE DECREASE OF
JH ACTIVITY IN LEPIDOPTERAN INSECTS, BY HYDROLYZING THE METHYL
ESTER OF JH. IT IS ALSO INVOLVED IN THE TRANSPORT OF JH.
CC  -1- CATALYTIC ACTIVITY: Methyl (2E,6E)-(10R,11S)-10,11-epoxy-3,7,11-
trimethyltrideca-2,6-dienoate + H(2)O = (2E,6E)-(10R,11S)-10,11-
epoxy-3,7,11-trimethyltrideca-2,6-dienoate + methanol.
CC  -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC  PIR; A36527; A36527.
DR  InterPro; IPR020218; CarbesteraseB.
DR  PROSITE; PS00122; CARBOXYLESTERASE_B_1; PARTIAL.
DR  PROSITE; PS00941; CARBOXYLESTERASE_B_2; PARTIAL.
KW  Hydrolase; Serine esterase.
FT  NON_TER      15
SQ  SEQUENCE     15 AA;  1659 MW;  D321EA432E58B848 CRC64;

Query Match
Best Local Similarity 16.7%; Score 3; DB 1; Length 15;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  15 TES 17
DB  12 TES 14

RESULT 10
UC08 MAIZE
ID  UC08 MAIZE      STANDARD;      PRT;      15 AA.
AC  P80614;
DT  01-OCT-1996 (Rel. 34, Created)
DT  01-OCT-1996 (Rel. 34, Last sequence update)
DT  15-JUL-1999 (Rel. 38, Last annotation update)
DE  Unknown protein from 2D-page of etiolated coleoptile (Spot 159)
DE  (Fragment).
OS  Zea mays (Maize).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC  PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX  NCBI_TaxID=4577;
RN  [1]

RP  SEQUENCE.
RC  TISSUE=Coleoptile;
RA  Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA  Pernollet J.-C., Zivy M., de Vienne D.;
RT  "The maize two dimensional gel protein database: towards an integrated
genome analysis program.";
RL  Theor. Appl. Genet. 93:997-1005(1996).
CC  -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 6.4, ITS MW IS: 38.8 kDa.
CC  -1- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
family.
CC  Maize-2DPAGE; P80614; COLEOPTILE.
DR  MaizeDB; 123934; -.
FT  NON_TER      15
SQ  SEQUENCE     15 AA;  1796 MW;  D331A518F7440BE7 CRC64;

Query Match
Best Local Similarity 16.7%; Score 3; DB 1; Length 15;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  11 VEP 13
DB  12 VEP 14

RESULT 12
UC25 MAIZE
ID  UC25 MAIZE      STANDARD;      PRT;      15 AA.
AC  P80631;
DT  01-OCT-1996 (Rel. 34, Created)
DT  01-OCT-1996 (Rel. 34, Last sequence update)
DT  15-JUL-1999 (Rel. 38, Last annotation update)
DE  Unknown protein from 2D-page of etiolated coleoptile (Spot 77)
DE  (Fragment).

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RC  TISSUE=Coleoptile;
RA  Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA  Pernollet J.-C., Zivy M., de Vienne D.;
RT  "The maize two dimensional gel protein database: towards an integrated
genome analysis program.";
RL  Theor. Appl. Genet. 93:997-1005(1996).
CC  -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 6.4, ITS MW IS: 38.8 kDa.
CC  -1- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
family.
CC  Maize-2DPAGE; P80614; COLEOPTILE.
DR  MaizeDB; 123934; -.
FT  NON_TER      15
SQ  SEQUENCE     15 AA;  1785 MW;  1978B1D6AB4DDF8D CRC64;

Query Match
Best Local Similarity 16.7%; Score 3; DB 1; Length 15;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  9 YPV 11
DB  8 YPV 10

RESULT 11
UC16 MAIZE
ID  UC16 MAIZE      STANDARD;      PRT;      15 AA.
AC  P80622;
DT  01-OCT-1996 (Rel. 34, Created)
DT  01-OCT-1996 (Rel. 34, Last sequence update)
DT  15-JUL-1999 (Rel. 38, Last annotation update)
DE  Unknown protein from 2D-page of etiolated coleoptile (Spot 308)
DE  (Fragment).
CC  Zea mays (Maize).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC  PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX  NCBI_TaxID=4577;
RN  [1]

RP  SEQUENCE.
RC  TISSUE=Coleoptile;
RA  Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA  Pernollet J.-C., Zivy M., de Vienne D.;
RT  "The maize two dimensional gel protein database: towards an integrated
genome analysis program.";
RL  Theor. Appl. Genet. 93:997-1005(1996).
CC  -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 5.9, ITS MW IS: 18.6 kDa.
CC  Maize-2DPAGE; P80622; COLEOPTILE.
DR  MaizeDB; 123948; -.
FT  NON_TER      15
SQ  SEQUENCE     15 AA;  1796 MW;  D331A518F7440BE7 CRC64;

Query Match
Best Local Similarity 16.7%; Score 3; DB 1; Length 15;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  11 VEP 13
DB  12 VEP 14

RESULT 12
UC25 MAIZE
ID  UC25 MAIZE      STANDARD;      PRT;      15 AA.
AC  P80631;
DT  01-OCT-1996 (Rel. 34, Created)
DT  01-OCT-1996 (Rel. 34, Last sequence update)
DT  15-JUL-1999 (Rel. 38, Last annotation update)
DE  Unknown protein from 2D-page of etiolated coleoptile (Spot 77)
DE  (Fragment).

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OS Zea mays (Maize).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 OX NCBI\_TaxID=4577;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Coleoptile;  
 RA Touzet P., Ricciardi F., Morin C., Danerval C., Huet J.-C.,  
 RA Pernollet J.-C., Zivy M., de Vienne D.;  
 RT "The maize two dimensional gel protein database: towards an integrated  
 RT genome analysis program.";  
 RL Theor. Appl. Genet. 93:997-1005(1996).  
 CC -1- MISCCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 4.9, ITS MW IS: 31.6 kDa.  
 CC Maize-2DPAGE; P80631; COLEOPTILE.  
 DR MaizeDB; 123957; -.  
 FT NON TER 1 15  
 FT NON TER 15 15  
 SQ SEQUENCE 15 AA; 1580 MW; 83C54CFOCE1614D0 CRC64;  
 Query Match 16.7%; Score 3; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 10 PVE 12  
 Db |||  
 10 PVE 12  
 Db |||  
 RESULT 13  
 H5\_COTJA STANDARD; PRT; 16 AA.  
 AC P18638;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Histone H5 (Fragment).  
 OS Coturnix coturnix japonica (Japanese quail).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Coturnix.  
 OX NCBI\_TaxID=93934;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=76277939; PubMed=962913;  
 RA Seligy V., Roy C., Dove M., Yaguchi M.;  
 RT "Species variability of N-terminal sequence of avian erythrocyte-  
 RT specific histone H5.";  
 RL Biochem. Biophys. Res. Commun. 71:196-202(1976).  
 CC -1- FUNCTION: HISTONE H5 PERFORMS THE SAME FUNCTION AS H1, BEING  
 CC NECESSARY FOR THE CONDENSATION OF NUCLEOSOME CHAINS INTO HIGHER  
 CC ORDER STRUCTURES, AND REPLACES HISTONE H1 IN CERTAIN CELLS.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- TISSUE SPECIFICITY: ERYTHROID CELLS.  
 CC -1- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.  
 KW Chromosomal protein; Nuclear protein; DNA-binding; DNA condensation.  
 FT NON TER 16 16  
 FT NON TER 16 16  
 SQ SEQUENCE 16 AA; 1665 MW; DB528219B3074D3C CRC64;  
 Query Match 16.7%; Score 3; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 15 TES 17  
 Db |||  
 1 TES 3  
 Db |||  
 RESULT 14  
 ODPE\_SOLTU STANDARD; PRT; 16 AA.  
 ID\_ODPB\_SOLTU  
 AC P81419;

DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Pyruvate dehydrogenase E1 component beta subunit, mitochondrial  
 DE (EC 1.2.4.1) (PDHE1-B) (Fragment).  
 OS Solanum tuberosum (Potato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; lamiids; Solanales; Solanaceae; Solanum.  
 OX NCBI\_TaxID=4113;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=cv. Romano; TISSUE=Tuber;  
 RX MEDLINE=98399821; PubMed=9729464;  
 RA Millar A.H., Knorr C., Leaver C.J., Hill S.A.;  
 RT "Plant mitochondrial pyruvate dehydrogenase complex: purification and  
 RT identification of catalytic components in potato.";  
 RL Biochem. J. 334:571-576(1998).  
 CC -1- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall  
 CC conversion of pyruvate to acetyl-CoA and CO(2). It contains  
 CC multiple copies of three enzymatic components: pyruvate  
 CC dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and  
 CC lipoamide dehydrogenase (E3).  
 CC -1- CATALYTIC ACTIVITY: Pyruvate + lipoamide = S-  
 CC acetyldihydrolipoamide + CO(2).  
 CC -1- COFACTOR: THIAMINE PYROPHOSPHATE.  
 CC -1- SUBUNIT: Tetramer of two alpha and two beta subunits (by  
 CC similarity).  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.  
 KW Glycolysis; Oxidoreductase; Flavoprotein; Thiamine pyrophosphate;  
 KW Phosphorylation; Mitochondrion.  
 FT NON TER 16 16  
 FT NON TER 16 16  
 SQ SEQUENCE 16 AA; 1705 MW; FF6ED80EC804F797 CRC64;  
 Query Match 16.7%; Score 3; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2 KEM 4  
 Db |||  
 5 KEM 7  
 Db |||  
 RESULT 15  
 ITHB\_HIRME STANDARD; PRT; 17 AA.  
 AC P28502;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Hirudin IA (Fragment).  
 OS Hirudo medicinalis (Medicinal leech).  
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;  
 OC Arynchobellida; Hirudiniformes; Hirudinidae; Hirudo.  
 OX NCBI\_TaxID=6421;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=90005945; PubMed=2792365;  
 RA Scharf M., Engels J., Tripiet D.;  
 RT "Primary structures of new 'iso-hirudins'.";  
 RL FEBS Lett. 255:105-110(1989).  
 CC -1- FUNCTION: Hirudin is a potent thrombin-specific protease  
 CC inhibitor. It forms a stable non-covalent complex with alpha-  
 CC thrombin, thereby abolishing its ability to cleave fibrinogen.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.  
 CC PIR; S05671; S05671.  
 DR HSSP; P01050; IHIC.  
 DR InterPro; IPR000429; Hirudin.  
 DR Pfam; PF00713; Hirudin; 1.  
 KW Serine protease inhibitor; Sulfation; Multigene family.  
 FT NON TER 17 17  
 FT NON TER 17 17  
 SQ SEQUENCE 17 AA; 1877 MW; 8904C6786C301CE7 CRC64;



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Query Match      16.7%; Score 3; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 TES 17
DB      7 TES 9

RESULT 16
ID PSBL_SYNNU STANDARD; PRT; 17 AA.
AC P12241;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Photosystem II reaction center L protein (PSII 5 kDa protein)
DE (Fragment).
DE PSBL.
GN PSBL.
OS Synechococcus vulcanus (Thermosynechococcus vulcanus).
OC Bacteria; Cyanobacteria; Chroococcales; Thermosynechococcus.
OX NCBI_TaxID=32053;
RN [1]
RP SEQUENCE.
RA Ikeuchi M., Koike H., Inoue Y.;
RT "Identification of psbI and psbL gene products in cyanobacterial
RT photosystem II reaction center preparation.";
RL FEBS Lett. 251:155-160(1989).
CC -!- FUNCTION: NOT KNOWN. POSSIBLY A PERIPHERAL COMPONENT OF CYTOCHROME
CC B559.
CC -!- SIMILARITY: BELONGS TO THE PSBL FAMILY.
CC PIR; S05033; S05033.
DR InterPro: IPR003372; PSII_PsbL.
DR Pfam; PF02419; PSBL; 1.
KW Photosynthesis; Photosystem II.
FT NON TER 17
SQ SEQUENCE 17 AA; 2018 MW; A86FD372B70B9847 CRC64;

Query Match      16.7%; Score 3; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 PVE 12
DB      9 PVE 11

RESULT 17
D7A1 ACASC STANDARD; PRT; 18 AA.
AC P83402;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Aldehyde dehydrogenase family 7 member A1 (EC 1.2.1.3) (Antiquitin 1)
DE (Fragment).
OS Acanthopagrus schlegelii (Black porgy).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Percoidae;
OC Sparidae; Acanthopagrus.
OX NCBI_TaxID=72011;
RN [1]
RP SEQUENCE, ACTIVITY, COFACTOR, AND SUBUNIT.
RC TISSUE=Liver;
RX MEDLINE=21956475; PubMed=11959129;
RA Tang W.-K., Cheng C.H.K., Fong W.-P.;
RT "First purification of the antiquitin protein and demonstration of its
RT enzymatic activity.";
RL FEBS Lett. 516:183-186(2002).
CC -!- CATALYTIC ACTIVITY: An aldehyde + NAD(+) + H(2)O = an acid +
CC NADH.

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CC -!- SUBUNIT: Homotetramer.
CC -!- MISCELLANEOUS: Optimal pH is 9-10. The Km for acetaldehyde is
CC 2.0 mM and Vmax is 1.3 micromol/min x mg enzyme.
CC -!- SIMILARITY: Belongs to the aldehyde dehydrogenase family.
DR GO; GO:0004029; F:aldehyde dehydrogenase (NAD+) activity; IDA.
DR GO; GO:0006081; P:aldehyde metabolism; IDA.
DR InterPro; IPR002086; Aldehyde dehydr.
DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; PARTIAL.
DR PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; PARTIAL.
KW Oxidoreductase; NAD.
FT NON TER 18
SQ SEQUENCE 18 AA; 2059 MW; BFF8C3EF1A9B4047 CRC64;

Query Match      16.7%; Score 3; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PKY 9
DB      8 PKY 10

RESULT 18
HEMH THETS STANDARD; PRT; 18 AA.
ID PSBL_THETS
AC P80155;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ovohemerythrin (vp14) (Fragment).
OS Theromyzon tessulatum (Leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Rhynchobdellida; Glossiphoniidae; Theromyzon.
OX NCBI_TaxID=13286;
RN [1]
RP SEQUENCE.
RC TISSUE=Oocyte;
RX MEDLINE=93049299; PubMed=1425663;
RA Baert J.-L., Britel M., Sautiere P., Malecha J.;
RT "Ovohemerythrin, a major 14-kDa yolk protein distinct from
RT vitellogenin in leech.";
RL Eur. J. Biochem. 209:563-569(1992).
CC -!- FUNCTION: MAJOR YOLK PROTEIN. THIS IRON PROTEIN MAY PLAY A ROLE
CC IN THE DETOXIFICATION OF FREE IRON AFTER A BLOOD MEAL.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the hemerythrin family.
DR PIR; S29264; S29264.
DR HSP; P02247; 2MHR.
DR InterPro; IPR002063; Hemerythrin.
DR Pfam; PF01814; Hemerythrin; 1.
DR PROSITE; PS00550; HEMERYTHRINS; PARTIAL.
KW Oxygen transport; Metal-binding; Iron; Yolk.
FT NON TER 18
SQ SEQUENCE 18 AA; 2368 MW; 33397EE587C81F1 CRC64;

Query Match      16.7%; Score 3; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 EPF 14
DB      5 EPF 7

RESULT 19
ID LCTN_LAMGL STANDARD; PRT; 18 AA.
AC P83315;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lactophorin (Whey protein) (Fragment).
OS Lama glama (Llama).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.  
 OX NCBI\_TaxID=9844;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=20000588; PubMed=10531593;  
 RA Kappeler S., Farah Z., Puhon Z.;  
 RT "Alternative splicing of lactophorin mRNA from lactating mammary gland  
 of the camel (Camelus dromedarius).";  
 RL J. Dairy Sci. 82:1-10(1999).  
 CC -!- SIMILARITY: BELONGS TO THE PP3 / GLYCAM-1 FAMILY.  
 DR GO:000576; C:extracellular; ISS.  
 DR Pfam: PF05242; GLYCAM-1; 1.  
 FT NON TER 18  
 FT SEQUENCE 18 AA; 2079 MW; CD596165B236AC6 CRC64;  
 SQ  
 Query Match 16.7%; Score 3; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred.No. 1.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 16 ESQ 18  
 Db [1]  
 15 ESQ 17

RESULT 20  
 DURA\_STRGV STANDARD; PRT; 19 AA.  
 AC P36504;  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Lanthibiotic duramycin (leucopeptin) (Antibiotic PA48009).  
 OS Streptovorticillium griseovirgatum.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomycineae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=68215;  
 RN [1]  
 RP SEQUENCE, AND STRUCTURE BY NMR.  
 RC STRAIN=PA-48009;  
 RX MEDLINE=91107438; PubMed=2272918;  
 RA Hayashi F., Nagashima K., Terui Y., Kawamura Y., Matsumoto K.,  
 RA Itazaki H.;  
 RT "The structure of PA48009: the revised structure of duramycin.";  
 RL J. Antibiot. 43:1421-1430(1990).  
 RN [2]  
 RP SEQUENCE.  
 RX MEDLINE=91107436; PubMed=2125590;  
 RA Fredenhagen A., Fendrich G., Marki F., Gruner J.,  
 RA Raschdorf F., Peter H.H.;  
 RT "Duramycins B and C, two new lanthionine containing antibiotics as  
 inhibitors of phospholipase A2. Structural revision of duramycin and  
 cinnamycin.";  
 RL J. Antibiot. 43:1403-1412(1990).  
 CC -!- FUNCTION: ACTS AS INHIBITOR OF PHOSPHOLIPASE A2.  
 CC -!- PTM: Maturation of lantibiotics involves the enzymic conversion of  
 Thr, and Ser into dehydrated AA and the formation of thioether  
 bonds with cysteine or the formation of dialkylamine bonds with  
 lysine. This is followed by membrane translocation and cleavage of  
 the modified precursor.  
 CC -!- SIMILARITY: STRUCTURAL SIMILARITY TO OTHER TYPE B LANTIBIOTICS.  
 KW Antibiotic; Bacteriocin; Lantibiotic; D-amino acid; Thioether bond.  
 FT CROSSLINK 1 18 Beta-methylanthionine (Cys-Thr).  
 FT CROSSLINK 4 14 Lanthionine (Ser-Cys).  
 FT CROSSLINK 5 11 Beta-methylanthionine (Cys-Thr).  
 FT CROSSLINK 6 19 Lysinoalanine (Ser-Lys).  
 FT CROSSLINK 6 19 Lysinoalanine (Ser-Lys).  
 SQ SEQUENCE 19 AA; 2069 MW; 012951AE27362F00 CRC64;  
 Query Match 16.7%; Score 3; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred.No. 1.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 13 PFT 15

Db [1]  
 9 PFT 11

RESULT 21  
 TX3\_PHONI STANDARD; PRT; 19 AA.  
 AC P31010;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Neurotoxin Tx3 (Fragment).  
 OS Phoneutria nigriventer (Brazilian armed spider).  
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;  
 OC Araneomorphae; Entelegynae; Lycosoidea; Ctenidae; Phoneutria.  
 OX NCBI\_TaxID=6918;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=92196803; PubMed=1801316;  
 RA Rezende L. Jr., Cordeiro M.N., Oliveira E.B., Diniz C.R.;  
 RT "Isolation of neurotoxic peptides from the venom of the 'armed'  
 spider Phoneutria nigriventer.";  
 RL Toxicon 29:1225-1233(1991).  
 CC -!- FUNCTION: ANTAGONIST OF L-TYPE CALCIUM CHANNELS (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.  
 CC -!- SIMILARITY: BELONGS TO THE SPIDER TOXIN TX3 FAMILY.  
 DR PIR; C39305; C39305.  
 KW Calcium channel inhibitor; Toxin; Neurotoxin; Ionic channel inhibitor.  
 FT NON TER 19  
 FT SEQUENCE 19 AA; 2244 MW; 3214E89CF10F7587 CRC64;  
 SQ  
 Query Match 16.7%; Score 3; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred.No. 1.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 16 ESQ 18  
 Db [1]  
 7 ESQ 9

RESULT 22  
 CISY\_STRHY STANDARD; PRT; 20 AA.  
 ID CISY\_STRHY STANDARD; PRT; 20 AA.  
 AC P20903;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Citrate synthase (EC 2.3.3.1) (Fragment).  
 GN GUTA.  
 OS Streptomyces hygroscopicus.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomycineae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=1912;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=SF1293;  
 RX MEDLINE=90334852; PubMed=1368511;  
 RA Shimotohno K.W., Inai S., Murakami T., Seto H.;  
 RT "Purification and characterization of citrate synthase from  
 Streptomyces hygroscopicus SF-1293 and comparison of its properties  
 with those of 2-phosphoenolpyruvate carboxykinase.";  
 RL Agric. Biol. Chem. 54:463-470(1990).  
 CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + oxaloacetate = citrate +  
 CoA.  
 CC -!- ENZYME REGULATION: ALLOSTERICALLY INHIBITED BY NADH.  
 CC -!- PATHWAY: Tricarboxylic acid cycle.  
 CC -!- SUBUNIT: Homohexamer.  
 CC -!- MISCELLANEOUS: CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS  
 CAPABLE OF OXIDATIVE METABOLISM.  
 CC -!- SIMILARITY: Belongs to the citrate synthase family.  
 DR PIR; PQ0046; PQ0046.

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DR InterPro; IPR002020; Citrate_synt.
KW PROSITE; PS00480; CITRATE SYNTHASE; PARTIAL.
KW Transferase; Tricarboxylic acid cycle; Allosteric enzyme.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2234 MW; C527EC7A87119597 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 YPV 11
   |||
Db 16 YPV 18

RESULT 23
SB60 MAIZE STANDARD; PRT; 20 AA.
AC P82868,
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative 60 kDa spermidine-binding protein (Fragment).
OS Zea mays (Maize)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE, AND SUBCELLULAR LOCATION
RC STRAIN=cv. Cecilia; TISSUE=Coleoptile;
RX MEDLINE=21948208; PubMed=11950979;
RA Tassoni A., Napier R.M., Franceschetti M., Venis M.A., Bagni N.;
RT "Spermidine-binding proteins. Purification and expression analysis in
   maize.";
RL Plant Physiol. 128:1303-1312(2002).
CC -!- FUNCTION: May have spermidine-binding activity.
CC -!- SUBUNIT: Dimer of 18 kDa and 60 kDa subunit (Probable).
CC -!- SUBCELLULAR LOCATION: Mitochondrial membrane.
CC -!- MISCELLANEOUS: On the 2D-gel its MW is: 60 kDa.
DR GO; GO:0005792; C:microsome; NAS.
KW Membrane; Microsome.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2093 MW; 7FD730C00391579A CRC64;

Query Match 16.7%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 YEP 13
   |||
Db 6 YEP 8

RESULT 24
GRWM HUMAN STANDARD; PRT; 3 AA.
AC P01157;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last annotation update)
DE Growth-modulating peptide.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77162369; PubMed=858356;
RA Schlesinger D.H., Pickart L., Thaler M.M.;
RT "Growth-modulating serum tripeptide is glycyl-histidyl-lysine.";
RL Experientia 33:324-325(1977).
CC -!- MISCELLANEOUS: THIS SERUM TRIPEPTIDE HAS BEEN FOUND TO STIMULATE

CC GROWTH OF SOME CELL TYPES AND TO INHIBIT OTHER TYPES IN VITRO.
DR GO; GO:0001558; P:regulation of cell growth; NAS.
SQ SEQUENCE 3 AA; 340 MW; 6331E81000000000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 3;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HK 2
   ||
Db 2 HK 3

RESULT 25
PAP2_PARMA STANDARD; PRT; 5 AA.
AC P81864;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pardaxin II (PXII) (Fragment).
OS Pardachirus marmoratus (Red sea mores sole).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Soleoidei; Soleidae; Pardachirus.
OX NCBI_TaxID=31087;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=87057369; PubMed=3782138;
RA Lazarovici P., Primor N., Loew L.M.;
RT "Purification and pore-forming activity of two hydrophobic
   polypeptides from the secretion of the Red sea mores sole (Pardachirus
   marmoratus).";
RL J. Biol. Chem. 261:16704-16713(1986).
CC -!- FUNCTION: Exhibits unusual shark repellent and surfactant
   properties. Forms voltage-dependent, ion-permeable channels
   in membranes. At high concentration causes cell membrane lysis.
CC -!- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE PARDAXIN FAMILY.
KW Toxin.
FT NON_TER 5
SQ SEQUENCE 5 AA; 614 MW; 7769C9C9C8100000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7
   ||
Db 4 PP 5

RESULT 26
RE31_LITRU STANDARD; PRT; 5 AA.
AC P82072;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Rubellidin 3.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Steinbörner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
   Tyler M.J., Wallace J.C.;

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RP "The structure of new peptides from the Australin red tree frog
RT 'Litoria rubella'. The skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -1- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -1- MASS SPECTROMETRY: MW=655; METHOD=PEP.
KW Amphibian defense peptide; Amidation.
FT MOD_RES 5 5
SQ SEQUENCE 5 AA; 656 MW; 71A9C9CB1030000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FT 15
DB 4 FT 5

RESULT 27
RE32 LITRU
ID RE32 LITRU STANDARD; PRT; 5 AA.
AC P82073;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Rubellidin 3.2.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -1- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
KW Amphibian defense peptide.
SQ SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FT 15
DB 4 FT 5

RESULT 28
SUGA ACHDO
ID SUGA ACHDO STANDARD; PRT; 5 AA.
AC P19991;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Subesophageal ganglion pentapeptide.
OS Acheta domestica (House cricket).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
OC Acheta.
OX NCBI_TaxID=6997;
RN [1]

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RP SEQUENCE.
RA Wicker C., Wicker C.;
RT "Isolation and structure of a peptide isolated from the
RT subesophageal ganglion of Acheta domestica (orthoptera).";
RL Comp. Biochem. Physiol. 88C:185-187(1987).
CC -1- SUBCELLULAR LOCATION: MAIN PEPTIDE FROM THE SUBESOPHAGEAL
CC GANGLIA.
DR PIR; JS0319; JS0319.
SQ SEQUENCE 5 AA; 476 MW; 69D76DDDDDB000000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PF 6
DB 4 PF 5

RESULT 29
ASP2 LACSN
ID ASP2 LACSN STANDARD; PRT; 6 AA.
AC P82655;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Acid shock protein 2 (Fragment).
OS Lactobacillus sanfranciscensis (lactobacillus sanfrancisco).
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1625;
RN [1]
RP SEQUENCE.
RC STRAIN=CB1;
RX MEDLINE=21322712; PubMed=11429463;
RA De Angelis M., Bini L., Pallini V., Cocconcelli P.S., Gobetti M.;
RT "The acid-stress response in Lactobacillus sanfranciscensis CB1.";
RL Microbiology 147:1863-1873(2001).
CC -1- INDUCTION: Overexpressed in acid environments.
FT NON_TER 6 6
SQ SEQUENCE 6 AA; 778 MW; 6AA45B5B132A8000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3
DB 2 KE 3

RESULT 30
ALL3 CARMA
ID ALL3 CARMA STANDARD; PRT; 7 AA.
AC P81806;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 3.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).

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CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 KW Neuropeptide; Multigene family.  
 SQ SEQUENCE 7 AA; 796 MW; 672879CDCB476B70 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;  
 Matches 2; Conservative 0; Mismatches 0;

Qy 12 EP 13  
 ||  
 Db 1 EP 2

RESULT 31  
 CARP MYTED STANDARD; PRT; 7 AA.  
 AC P10420;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 DT 01-MAR-1989 (Rel. 10, Last annotation update)  
 DE Catch-relaxing peptide (CARP).  
 OS Mytilus edulis (Blue mussel).  
 CC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;  
 CC Mytiloidea; Mytilidae; Mytilus.  
 OX NCBI\_TaxID=6550;  
 RN [1]

RP SEQUENCE.  
 RX MEDLINE=88052022; PubMed=3676797;  
 RA Hirata T., Kubota I., Takabatake I., Kawahara A., Shimamoto N.,  
 RA Mueoka Y.,  
 RT "Catch-relaxing peptide isolated from Mytilus pedal ganglia."  
 RL Brain Res. 422:374-376(1987).  
 CC -!- FUNCTION: THIS PEPTIDE EXHIBITS BOTH POTENTIATING (CONTRACTION)  
 AND INHIBITORY (RELAXATION) EFFECTS ON THE ANTERIOR BYSSUS  
 CC RETRACTOR MUSCLE.  
 DR PIR. A29342; ECMUCR.  
 KW Hormone; Amidation.  
 FT MOD RES 7  
 SQ SEQUENCE 7 AA; 831 MW; 6734072687669DB0 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;  
 Matches 2; Conservative 0; Mismatches 0;

Qy 4 MP 5  
 ||  
 Db 2 MP 3

RESULT 32  
 EI05 LITRU STANDARD; PRT; 7 AA.  
 AC P82101;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Electrin 5.  
 OS Litoria rubella (Desert tree frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hyliidae;  
 CC Pelodyadinae; Litoria.  
 OX NCBI\_TaxID=104895;  
 RN [1]

RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
 RT "Peptides from the skin glands of the Australian buzzing tree frog  
 RT Litoria electrica. Comparison with the skin peptides from Litoria  
 RT rubella."  
 RL Aust. J. Chem. 52:639-645(1999).  
 CC -!- SUBCELLULAR LOCATION: Secretd.  
 CC -!- TISSUE SPECIFICITY: Skin.

KW Amphibian defense peptide; Amidation.  
 FT MOD RES 7  
 SQ SEQUENCE 7 AA; 834 MW; 6DD05B076B0B5030 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;  
 Matches 2; Conservative 0; Mismatches 0;

Qy 12 EP 13  
 ||  
 Db 3 EP 4

RESULT 33  
 FAR1 HELTI STANDARD; PRT; 7 AA.  
 AC P41871;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE FMRFamide-like neuropeptide GDFPLRF-amide.  
 OS Helisoma trivolvis (Snail).  
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;  
 CC Lymnaeidae; Planorbidae; Helisoma.  
 OX NCBI\_TaxID=27815;  
 RN [1]

RP SEQUENCE.  
 RC TISSUE=Kidney;  
 RX MEDLINE=94286417; PubMed=7912428;  
 RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;  
 RA "FMRFamide-related peptides from the kidney of the snail, Helisoma  
 RT trivolvis."  
 RL Peptides 15:31-36(1994).  
 CC -!- FUNCTION: APPEARS TO BE INVOLVED IN OSMOREGULATION BY AFFECTING  
 THE KIDNEY, MANTLE AND SKIN.  
 CC -!- TISSUE SPECIFICITY: KIDNEY, SKIN, MANTLE AND THE HEMOLYMPH.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 7  
 SQ SEQUENCE 7 AA; 851 MW; 69D40729D76AA810 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;  
 Matches 2; Conservative 0; Mismatches 0;

Qy 5 PF 6  
 ||  
 Db 3 PF 4

RESULT 34  
 FAR5 HIRME STANDARD; PRT; 7 AA.  
 AC P42564;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE FMRFamide-like neuropeptide GGYMRF-amide.  
 OS Hirudo medicinalis (Medicinal leech).  
 CC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;  
 CC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.  
 OX NCBI\_TaxID=6421;  
 RN [1]

RP SEQUENCE.  
 RX MEDLINE=92195954; PubMed=1686933;  
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;  
 RT "Identification of Rfamide neuropeptides in the medicinal leech."  
 RL Peptides 12:897-908(1991).  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 7  
 SQ SEQUENCE 7 AA; 851 MW; 69D40729D76AA810 CRC64;

SQ SEQUENCE 7 AA; 858 MW; 69D4068B53387810 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KY 9  
||  
3 KY 4

Db

RESULT 35

UF04 MOUSE STANDARD; PRT; 7 AA.

ID UF04\_MOUSE

AC P38642; (Rel. 30, Last sequence update)

DT 01-OCT-1994 (Rel. 30, Last sequence update)

DT 01-FEB-1995 (Rel. 31, Last annotation update)

DE Unknown protein from 2D-page of fibroblasts (P46) (Fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE.

RC TISSUE=Fibroblast; PubMed=7523108;

RX MEDLINE=35009907; Wichter L.L., He C., Selkirk J.K.;

RA "Separation and sequencing of familial and novel murine proteins

RT using preparative two-dimensional gel electrophoresis.;"

RL Electrophoresis 15:735-745(1994).

CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN

CC PROTEIN IS: 5.0, ITS MW IS: 46 kDa.

FT NON TER 7

SQ SEQUENCE 7 AA; 766 MW; 68640AB77632700 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PK 8  
||  
1 PK 2

Db

RESULT 36

UN06 PINPS STANDARD; PRT; 7 AA.

ID UN06\_PINPS

AC P81675; (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Unknown protein from 2D-page of needles (N141) (Fragment).

OS Pinus pinaster (Maritime pine).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.

OX NCBI\_TaxID=71647;

RN [1]

RP SEQUENCE.

RC TISSUE=Needle; PubMed=10344291;

RX MEDLINE=99274088; Bauw G., Dubos C., Bahrman N., Kremer A.,

RA Costa P., Plomion C.;

RA Frigerio J.-M., Plomion C.;

RT "Separation and characterization of needle and xylem maritime pine

RT proteins.;"

RL Electrophoresis 20:1098-1108(1999).

CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN

CC PROTEIN IS: 6.6, ITS MW IS: 25 kDa.

CC NON TER 1

FT NON TER 7

SQ SEQUENCE 7 AA; 823 MW; 69D76724486B5740 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;

SQ SEQUENCE 7 AA; 993 MW; 7362D5B69B041310 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EM 4  
||  
3 EM 4

Db

RESULT 37

WWAL ACHFU STANDARD; PRT; 7 AA.

ID WWAL\_ACHFU

AC P35919; (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 01-OCT-1994 (Rel. 30, Last annotation update)

DB WWamide-1.

OS Achatina fulica (Giant African snail).

OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;

OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.

OX NCBI\_TaxID=6530;

RN [1]

RP SEQUENCE.

RC TISSUE=Ganglion; PubMed=8495720;

RX MEDLINE=93265912; Muneoka Y., Kobayashi M., Nomoto K.;

RA Minakata H., Ikeda T., novel neuromodulatory peptides isolated from

RT "WWamide-1, 2 and -3: novel neuromodulatory peptides isolated from

RL PBES Lett. 323:104-108(1993).

CC -1- FUNCTION: EXHIBITS MODULATORY EFFECTS ON THE PERIPHERAL NERVOUS

CC SYSTEM. INHIBITS ACTIVITY ON A CENTRAL NEURON.

CC PIR; S33245; S33245.

DR Neuropeptide; Amidation.

KW MOD RES 7

FT MOD RES 7

SQ SEQUENCE 7 AA; 993 MW; 7362D5B69B041310 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EM 4  
||  
3 EM 4

Db

RESULT 38

AKH LIBAU STANDARD; PRT; 8 AA.

ID AKH\_LIBAU

AC P25418; (Rel. 22, Created)

DT 01-MAY-1992 (Rel. 22, Last sequence update)

DT 01-FEB-1994 (Rel. 28, Last annotation update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Adipokinetic hormone (AKH).

OS Libellula auripennis (Skimmer dragonfly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Palaeoptera; Odonata; Anisoptera; Libellulidae; Libellula.

OX NCBI\_TaxID=6966;

RN [1]

RP SEQUENCE, AND SYNTHESIS.

RC TISSUE=Corpora cardiaca; PubMed=2390213;

RX MEDLINE=90359055; Gaede G.;

RA "The putative ancestral peptide of the adipokinetic/red-pigment-

RT concentrating hormone family isolated and sequenced from a

RT dragonfly.;"

RL Biol. Chem. Hoppe-Seyler 371:475-483(1990).

CC -1- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA

CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF

CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT

CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.

CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.

DR PIR; S10596; S10596.

DR InterPro; IPR002047; AKH.

DR PROSITE; PS00256; AKH; 1.

KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 978 MW; 8665A771A9C452D6 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FT 15  
 DB 4 FT 5

RESULT 39  
 AKH TABAT  
 ID AKH TABAT STANDARD; PRT; 8 AA.  
 AC P14595;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Adipokinetic hormone (AKH) (Dipteran corpora cardiaca factor I) (DCC I).  
 OS Tabanus atratus (Horse fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae;  
 OC Tabanus.  
 OX NCBI\_TaxID=7207;  
 RN [1]  
 RP SEQUENCE.  
 RX TISSUE=Corpora cardiaca;  
 RC MEDLINE=90046758; PubMed=2813385;  
 RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,  
 RA Vogel V.W., Zhang Y.-S., Hayes D.K.;  
 RT "Primary structure of two neuropeptide hormones with adipokinetic and  
 RT hypotrehalosemic activity isolated from the corpora cardiaca of horse  
 RT flies (Diptera).";  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164 (1989).  
 CC -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA  
 CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF  
 CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT  
 CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.  
 CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.  
 CC PIR; A33995; A33995.  
 DR InterPro; IPR002047; AKH.  
 DR PROSITE; PS00256; AKH; 1.  
 KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 949 MW; 86786771A9D1A736 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FT 15  
 DB 4 FT 5

RESULT 40  
 ANG2 BOTJA  
 ID ANG2 BOTJA STANDARD; PRT; 8 AA.  
 AC Q10582;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Angiotensin-like peptide II (Fragment).  
 OS Bothrops jararaca (Jarakaraca).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Bothrops.  
 OX NCBI\_TaxID=8724;

[1]  
 RN SEQUENCE.  
 RP TISSUE=Plasma;  
 RC MEDLINE=96208932; PubMed=8829801;  
 RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;  
 RT "Isolation and identification of angiotensin-like peptides from the  
 RT plasma of the snake Bothrops jararaca.";  
 RL Comp. Biochem. Physiol. 113B:467-473 (1996).  
 CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
 DR InterPro; IPR00215; Serpin.  
 DR PROSITE; PS00284; SERPIN; PARTIAL.  
 KW Vasoconstrictor; Plasma; Serpin.  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 1046 MW; DDD761E04B42D40A CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PF 6  
 DB 7 PF 8

RESULT 41  
 CLP THICU  
 ID CLP THICU STANDARD; PRT; 8 AA.  
 AC P80488;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Chemolithotroph-specific protein (Fragment).  
 OS Thiothraupis cuprinus.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 OC Comamonadaceae; Thiomonas.  
 OX NCBI\_TaxID=36860;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=DSM 5494;  
 RA Marin I., Amaro A.M., Jerez C.A., Amils R., Abad J.P.;  
 RL Submitted (SEP-1995) to the SWISS-PROT data bank.  
 CC -!- MISCELLANEOUS: FOUND SPECIFICALLY IN CELLS CULTURED  
 CC CHEMOLITHOTROPHICALLY.  
 CC FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 785 MW; 91487B06DDC2D76D CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PV 11  
 DB 2 PV 3

RESULT 42  
 HTF2 PERAM  
 ID HTF2 PERAM STANDARD; PRT; 8 AA.  
 AC P04549;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Hypertrahaloemic factor II (Neuropeptide M-II) (Periplanetin CC-2)  
 DE (Pea-CAH-II) (IleD-CC-II) (Hypertrahaloemic neuropeptide II).  
 OS Periplaneta americana (American cockroach).  
 OS Leptinotarsa decemlineata (Colorado potato beetle), and  
 OS Blatta orientalis (Oriental cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
 OC Blattidae; Periplaneta.  
 OX NCBI\_TaxID=6978, 7539, 6976;  
 RN [1]  
 RP SEQUENCE.

RC SPECIES=P.americana;  
RX MEDLINE=85046530; PubMed=6548628;  
RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,  
RA Rinehart K.L. Jr.;  
RT "Structures of two cockroach neuropeptides assigned by fast atom  
RT bombardment mass spectrometry.";  
RL Biochem. Biophys. Res. Commun. 124:350-358(1984).  
RN [2]  
RN SEQUENCE.  
RP SPECIES=P.americana;  
RC MEDLINE=84298179; PubMed=6591205;  
RX Scarbrough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,  
RA Miller C.A., Schooley D.A.;  
RT "Isolation and primary structure of two peptides with  
RT cardioceleratory and hyperglycemic activity from the corpora  
RT cardiaca of *Periplaneta americana*.";  
RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).  
RN [3]  
RN SEQUENCE.  
RP SPECIES=L.deceimlineata; TISSUE=Corpora cardiaca;  
RC MEDLINE=90160053; PubMed=2576128;  
RX Gaede G., Kellner R.;  
RA "The metabolic neuropeptides of the corpus cardiaca from the potato  
RT beetle and the American cockroach are identical.";  
RL Peptides 10:1287-1289(1989).  
RN [4]  
RN SEQUENCE.  
RP SPECIES=B.orientalis; TISSUE=Corpora cardiaca;  
RC MEDLINE=90253659; PubMed=2340112;  
RX Gaede G., Rinehart K.L. Jr.;  
RA "Primary structures of hypertrehalosaemic neuropeptides isolated from  
RT the corpora cardiaca of the cockroaches *Leucophaea maderae*,  
RT *Gromphadorhina portentosa*, *Blattella germanica* and *Blatta orientalis*  
RT and of the stick insect *Extatosoma tiaratum* assigned by tandem fast  
RT atom bombardment mass spectrometry.";  
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).  
CC CC -1- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT  
CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLymph OF INSECTS).  
CC THE MAJOR CARBOHYDRATE IN THE HEMOLymph OF INSECTS).  
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.  
DR PIR; B44960; B44960.  
DR PIR; B49823; B49823.  
DR PIR; S08996; S08996.  
DR IncerPro; IPR002047; AKH.  
DR PROSITE; PS00256; AKH; 1.  
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA; 1006 MW; 86745771A9D1A736 CRC64;  
Query Match 11.1%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 14 FT 15  
Db 4 FT 5

RESULT 43  
LMT2\_LOCMI  
ID LMT2\_LOCMI STANDARD; PRT; 8 AA.  
AC P22396;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 01-AUG-1991 (Rel. 19, Last annotation update)  
DE Locustamigratorin 2 (LOM-MT-2).  
OS Locusta migratoria (Migratoria locust).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
OX NCBI\_TaxID=7004;  
RN [1]

RP SEQUENCE.  
RC TISSUE=Corpora cardiaca;  
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;  
RT "Isolation, identification and synthesis of locustamigratorin II, an  
RT additional neuropeptide of *Locusta migratoria*. Member of the  
RT cephalomyotrophic peptide family.";  
RL Insect Biochem. 20:479-484(1990).  
CC CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
CC (MYOTROPIC ACTIVITY).  
CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
DR InterPro; IPR001484; Pyrokinin.  
DR PROSITE; PS00539; PYROKININ; 1.  
KW Neuropeptide; Amidation; Pyrokinin.  
FT MOD\_RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA; 934 MW; 26341771A9CAA87B CRC64;  
Query Match 11.1%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 14 FT 15  
Db 4 FT 5

RESULT 44  
LPK\_LEUMA  
ID LPK\_LEUMA STANDARD; PRT; 8 AA.  
AC P13049;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Leucopyrokinin (LPK) (LEM-PK).  
OS Leucophaea maderae (Madeira cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;  
OC Blaberidae; Leucophaea.  
OX NCBI\_TaxID=6988;  
RN [1]  
RN SEQUENCE.  
RP MEDLINE=86269041; PubMed=3015140;  
RX Nachman R.J., Holman G.M., Cook B.J.;  
RA "Active fragments and analogs of the insect neuropeptide  
RT leucopyrokinin: structure-function studies.";  
RL Biochem. Biophys. Res. Commun. 137:936-942(1986).  
CC CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
CC (MYOTROPIC ACTIVITY).  
CC -1- MISCELLANEOUS: AN ANALOG WITHOUT THE N-TERMINAL PCA RESIDUE WAS  
CC SYNTHESIZED AND FOUND TO EXHIBIT GREATER ACTIVITY (144%) THAN THE  
CC PARENT NEUROPEPTIDE. THE PORTION OF THE SEQUENCE OF LPK MOST  
CC CRITICAL FOR THE MYOTROPIC PROPERTIES IS LIMITED TO THE  
CC PENTAPEPTIDE FRAGMENT FTPL.  
CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
DR PIR; A23967; A23967.  
DR InterPro; IPR001484; Pyrokinin.  
DR PROSITE; PS00539; PYROKININ; 1.  
KW Neuropeptide; Amidation; Pyrokinin; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA; 949 MW; 92341771A9D5A1B6 CRC64;  
Query Match 11.1%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 14 FT 15  
||  
Db 4 FT 5

## RESULT 45

ID\_ORMY\_ORCLI STANDARD; PRT; 8 AA.  
AC P8245;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Orcomytropin (OMT).  
OS Orcomytes limosus (Spinycheek crayfish).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;  
OC Astacoidea; Cambaridae; Orconectes.  
OX NCBI\_TaxID=28379;  
RN [1]

RP SEQUENCE, MASS SPECTROMETRY, AND AMIDATION.

RC TISSUE=Hindgut;  
RX MEDLINE=20411310; PubMed=10952880;  
RA Dirksen H., Burdick S., Sauter A., Keller R.;  
RT "Two orokins and the novel octapeptide orcomytropin in the hindgut of the crayfish Orconectes limosus: identified myostimulatory neuropeptides originating together in neurones of the terminal abdominal ganglion.";  
RL J. Exp. Biol. 203:2807-2818(2000).  
CC -!- FUNCTION: MYOTROPIC PEPTIDE, ENHANCES BOTH THE FREQUENCY AND AMPLITUDE OF SPONTANEOUS HINDGUT CONTRACTIONS. IT IS SYNTHESIZED BY ABDOMINAL GANGLIONIC NEURONS.  
CC -!- MASS SPECTROMETRY: MW=904.8; METHOD=FAB.  
KW Amidation; Neuropeptide.  
FT MOD RES 8 8  
SQ SEQUENCE 8 AA; 905 MW; 87C861B1A9CDDAA9 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FT 15  
||  
Db 4 FT 5

## RESULT 46

ID\_PP2\_PERAM STANDARD; PRT; 8 AA.  
AC P82632;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Pyrokinin-2 (Pea-PK-2) (FXPRL-amide).  
OS Periplaneta americana (American cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
OC Blattidae; Periplaneta.  
OX NCBI\_TaxID=6978;  
RN [1]

RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.

RC TISSUE=Corpora cardiaca;  
RX MEDLINE=97353923; PubMed=9210163;  
RA Predel R., Eckert M., Kaufmann R., Penzlin H., Gaede G.;  
RT "Isolation and structural elucidation of two pyrokinins from the retrocerebral complex of the American cockroach.";  
RL Peptides 18:473-478(1997).  
RN [2]  
CC TISSUE SPECIFICITY.  
RP RS7 MYCIT  
ID MEDLINE=20189894; PubMed=10723010;  
RX Predel R., Eckert M.;  
RA "Tagma-specific distribution of FXPRLamides in the nervous system of the American cockroach.";  
RT J. Comp. Neurol. 419:352-363(2000).

CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY (MYOTROPIC ACTIVITY).  
CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.  
CC -!- MASS SPECTROMETRY: MW=883; METHOD=MALDI.  
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
DR InterPro; IPR001484; Pyrokinin.  
DR PROSITE; PS00539; PYROKININ; FALSE NEG.  
KW Neuropeptide; Amidation; Pyrokinin.  
FT MOD RES 8 8  
SQ SEQUENCE 8 AA; 884 MW; C834176DD9D7775 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PF 6  
||  
Db 3 PF 4

## RESULT 47

PPK3 PERAM STANDARD; PRT; 8 AA.  
ID PPK3 PERAM  
AC P82518;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Pyrokinin-3 (Pea-PK-3) (FXPRL-amide).  
OS Periplaneta americana (American cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
OC Blattidae; Periplaneta.  
OX NCBI\_TaxID=6978;  
RN [1]  
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
RC TISSUE=Retrocerebral complex;  
RX MEDLINE=99212469; PubMed=10196736;  
RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;  
RT "Differential distribution of pyrokinin-isoforms in cerebral and abdominal neurohemal organs of the American cockroach.";  
RL Insect Biochem. Mol. Biol. 29:139-144(1999).  
RN [2]  
CC TISSUE SPECIFICITY.  
RP MEDLINE=20189894; PubMed=10723010;  
RX Predel R., Eckert M.;  
RT "Tagma-specific distribution of FXPRLamides in the nervous system of the American cockroach.";  
RL J. Comp. Neurol. 419:352-363(2000).  
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY (MYOTROPIC ACTIVITY).  
CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.  
CC -!- MASS SPECTROMETRY: MW=996.5; METHOD=MALDI.  
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
KW Neuropeptide; Amidation; Pyrokinin.  
FT MOD RES 8 8  
SQ SEQUENCE 8 AA; 997 MW; 0B34177409D772C7 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PF 6  
||  
Db 3 PF 4

## RESULT 48

RS7 MYCIT  
ID RS7 MYCIT STANDARD; PRT; 8 AA.  
AC P33564;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE 30S ribosomal protein S7 (Fragment).

GN RPS3.

OS Mycobacterium intracellulare.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.

OX NCBI\_TaxID=1767;

RN (1)

RP SEQUENCE FROM N.A. PubMed=8451173;

RX MEDLINE=93197130; PubMed=8451173;

RA Nair J., Rouse D.A., Morris S.L.;

RT "Nucleotide sequence analysis of the ribosomal S12 gene of

RT Mycobacterium intracellulare.";

RL Nucleic Acids Res. 21:1039-1039(1993).

CC -!- FUNCTION: One of the primary rRNA binding proteins, it binds

CC directly to 16S rRNA where it nucleates assembly of the head

CC domain of the 30S subunit. Is located at the subunit interface

CC close to the decoding center, probably blocks exit of the E-site

CC tRNA (By similarity).

CC -!- SUBUNIT: Part of the 30S ribosomal subunit. Contacts proteins S9

CC and S11 (By similarity).

CC -!- SIMILARITY: BELONGS TO THE S7P FAMILY OF RIBOSOMAL PROTEINS.

CC -----

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CC -----

DR EMBL: L08171; AAA25376.1; -.

DR PIR: S35538; S35538.

DR HAMAP: MF\_00480; -; 1.

DR InterPro: IPR000235; Ribosomal\_S7.

DR PROSITE: PS00052; RIBOSOMAL\_S7; PARTIAL.

KW Ribosomal protein; rRNA-binding; tRNA-binding; tRNA-binding.

FT INIT MET 0 0 BY SIMILARITY.

FT NON\_TER 8 8

SQ SEQUENCE 8 AA; 850 MW; 63276DC768732417 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PK 8

Db ||

7 PK 8

RESULT 49

ID UC26 MAIZE STANDARD; PRT; 8 AA.

AC P80632;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Unknown protein from 2D-page of etiolated coleoptile (Spot 907)

DE (Fragment).

OS Zea mays (Maize).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC PACCAD clade; Panicoideae; Andropogoneae; Zea.

OX NCBI\_TaxID=4577;

RN (1)

RP SEQUENCE.

RC TISSUE=Coleoptile;

RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,

RA Pernollet J.-C., Zivy M., de Vienne D.;

RT "The maize two dimensional gel protein database: towards an integrated

RT genome analysis program.";

RL Theor. Appl. Genet. 93:997-1005(1996).

CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN

CC PROTEIN IS: 7.0, ITS MW IS: 57.2 kDa.

DR Maize-2DPAGE; P80632; COLEOPTILE.

FT NON\_TER 1 1

FT NON\_TER 8 8

SQ SEQUENCE 8 AA; 990 MW; 9639D6DAB4176B1D CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 EP 13

Db ||

2 EP 3

RESULT 50

ID UF06 MOUSE STANDARD; PRT; 8 AA.

AC P38644;

DT 01-OCT-1994 (Rel. 30, Created)

DT 01-OCT-1994 (Rel. 30, Last sequence update)

DT 01-FEB-1995 (Rel. 31, Last annotation update)

DE Unknown protein from 2D-page of fibroblasts (P50) (Fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN (1)

RP SEQUENCE.

RC TISSUE=Fibroblast;

RX MEDLINE=95009907; PubMed=7523108;

RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;

RT "Separation and sequencing of familial and novel murine proteins

RT using preparative two-dimensional gel electrophoresis.";

RL Electrophoresis 15:735-745(1994).

CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN

CC PROTEIN IS: 5.2, ITS MW IS: 50 kDa.

FT NON\_TER 8 8

SQ SEQUENCE 8 AA; 817 MW; A35DD878676B05B1 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 EP 13

Db ||

3 EP 4

RESULT 51

ID UPAL HUMAN STANDARD; PRT; 8 AA.

AC P30087;

DT 01-APR-1993 (Rel. 25, Created)

DT 01-APR-1993 (Rel. 25, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Unknown protein from 2D-page of plasma (Spot 2) (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI\_TaxID=9606;

RN (1)

RP SEQUENCE.

RC TISSUE=Plasma;

RX MEDLINE=93092937; PubMed=1459097;

RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,

RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,

RA Hochstrasser D.F.;

RT "Plasma protein map: an update by microsequencing.";

RL Electrophoresis 13:707-714(1992).

CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN

CC PROTEIN IS: 4.9, ITS MW IS: 65 kDa.

DR SWISS-2DPAGE; P30087; HUMAN.

FT NON\_TER 1 1

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FT UNSURE      8      8
ST NON_TER     8      8
SQ SEQUENCE    8 AA; 944 MW; C01772C455BB06DA CRC64;

Query Match
Best Local Similarity 11.1%; Score 2; DB 1; Length 8;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ES 17
   ||
DB 3 ES 4

RESULT 52
UPAA HUMAN
ID UPAA HUMAN STANDARD; PRT; 8 AA.
AC P30096;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 36) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 7. ITS MW IS: 12 kDa.
DR SWISS-2DPAGE; P30096; HUMAN.
FT NON_TER 1
FT VARIANT 5 5 F -> P.
FT /FTID=VAR_000004.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 909 MW; 86677B59D1A72042 CRC64;

Query Match
Best Local Similarity 11.1%; Score 2; DB 1; Length 8;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YP 10
   ||
DB 6 YP 7

RESULT 53
CCAP CARMA
ID CCAP CARMA STANDARD; PRT; 9 AA.
AC P38556;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Cardioactive peptide (CCAP).
OS Carcinus maenas (Common shore crab) (Green crab),
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm),
OS Tenebrio molitor (Yellow mealworm), and
OS Spodoptera eridania (Southern armyworm).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759, 7130, 7067, 37547;
RN [1]
RP SEQUENCE.
RC SPECIES=C.maenas; TISSUE=Pericardial organs;
RA Stangler J., Halbach C., Beyreuther K., Keller R.;
RT "Unusual cardioactive peptide (CCAP) from pericardial organs of the

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RT shore crab Carcinus maenas.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:575-579(1987).
RN [2]
RP SEQUENCE.
RC SPECIES=M.sexta;
RX MEDLINE=93050243; PubMed=1426284;
RA Cheung C.C., Loi P.K., Sylwester A.W., Lee T.D., Tublitz N.J.;
RT "Primary structure of a cardioactive neuropeptide from the tobacco
RT hawkmoth, Manduca sexta.";
RL FEBS Lett. 313:165-168(1992).
RN [3]
RP SEQUENCE.
RC SPECIES=T.molitor, and S.eridania; TISSUE=Head;
RX MEDLINE=94176032; PubMed=8129851;
RA Furuya K., Liao S., Reynolds S.E., Ota R.B., Hackett M.,
RA Schooley D.A.;
RT "Isolation and identification of a cardioactive peptide from Tenebrio
RT molitor and Spodoptera eridania.";
RL Biol. Chem. Hoppe-Seyler 374:1065-1074(1993).
CC -!- FUNCTION: THE EFFECT OF CCAP IS BOTH INO- AND CHRONOTROPIC.
CC -!- TISSUE SPECIFICITY: STORED IN PERICARDIAL ORGANS AND RELEASED
CC INTO THE HEMOLYMPH.
DR PIR; A26363; A26363.
DR PIR; S27233; S27233.
KW Neuropeptide; Amidation.
FT DISULFID 3 9
FT MOD_RES 9 9 AMIDATION.
FT SEQUENCE 9 AA; 959 MW; C5A861A9CDD44EB9 CRC64;

Query Match
Best Local Similarity 11.1%; Score 2; DB 1; Length 9;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PF 6
   ||
DB 1 PF 2

RESULT 54
CONO CONGE STANDARD; PRT; 9 AA.
AC P05486;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lys-conopressin G.
OS Conus geographus (Geography cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hyposogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6491;
RN [1]
RP SEQUENCE.
RX MEDLINE=88058932; PubMed=3680228;
RA Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,
RA Gray W.R., Olivera B.M.;
RT "Invertebrate vasopressin/oxytocin homologs. Characterization of
RT peptides from Conus geographus and Conus straitus venoms.";
RN J. Biol. Chem. 262:15821-15824(1987).
RN [2]
RP REVIEW.
RX MEDLINE=89024586; PubMed=3052286;
RA Gray W.R., Olivera B.M., Cruz L.J.;
RT "Peptide toxins from venomous Conus snails.";
RL Annu. Rev. Biochem. 57:665-700(1988).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR; A28495; A28495.
DR InterPro; IPR000981; Neurhyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00364; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6

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FT  MOD RES          9          9          AMIDATION.
SQ  SEQUENCE 9 AA; 1037 MW;  DAFc276EB4540059 CRC64;

Query Match      11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 PK 8
      |||
Db      7 PK 8

RESULT 55
COXE_THIOB
ID _COXE_THIOB STANDARD; PRT; 9 AA.
AC P80975;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Cytochrome c oxidase polypeptide Via (EC 1.9.3.1) (Fragment).
OS Thunus obesus (Bigeye tuna).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8241;
RN [1]

RP  TISSUE=Heart;
RC  MEDLINE=97454291; PubMed=9310366;
RA  Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
RA  Kadenbach B.;
RT  "The subunit structure of cytochrome-c oxidase from tuna heart and
RT  liver.";
RL  Eur. J. Biochem. 248:99-103(1997).
CC  -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC  CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC  MITOCHONDRIAL ELECTRON TRANSPORT.
CC  -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome
CC  C + 2 H(2)O.
CC  -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC  -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIA FAMILY.
DR  PIR: S77984; S77984.
DR  IncerPro; IPR001349; COX6A.
DR  PROSITE; PS01329; COX6A; PARTIAL.
KW  Oxidoreductase; Inner membrane; Mitochondrion.
FT  NON_TER 1
FT  NON_TER 9
SQ  SEQUENCE 9 AA; 1136 MW;  62E072C9CB0776DB CRC64;

Query Match      11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 KE 3
      |||
Db      1 KE 2

RESULT 56
FAR2_CALVO
ID _FAR2_CALVO STANDARD; PRT; 9 AA.
AC P41857;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRFamide 2.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]

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RP  TISSUE=Thoracic ganglion;
RC  MEDLINE=92196111; PubMed=1549595;
RA  Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA  Rehfeld J.F., Thorpe A.;
RT  "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT  neuropeptides (designated calliFMRFamides) from the blowfly
RT  Calliphora vomitoria.";
RL  Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC  -!- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED
CC  SALIVARY GLAND OF CALLIPHORA.
CC  -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC  FAMILY.
DR  PIR: B41978; B41978.
KW  Neuropeptide; Amidation.
FT  MOD RES 9
SQ  SEQUENCE 9 AA; 1128 MW;  29D00699CAB6C5A7 CRC64;

Query Match      11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      17 SQ 18
      |||
Db      3 SQ 4

RESULT 57
FAR3_CALVO
ID _FAR3_CALVO STANDARD; PRT; 9 AA.
AC P41858;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRFamide 3.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP  TISSUE=Thoracic ganglion;
RC  MEDLINE=92196111; PubMed=1549595;
RA  Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA  Rehfeld J.F., Thorpe A.;
RT  "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT  neuropeptides (designated calliFMRFamides) from the blowfly
RT  Calliphora vomitoria.";
RL  Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC  -!- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED
CC  SALIVARY GLAND OF CALLIPHORA.
CC  -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC  FAMILY.
DR  PIR: C41978; C41978.
KW  Neuropeptide; Amidation.
FT  MOD RES 9
SQ  SEQUENCE 9 AA; 1114 MW;  2F0B0699CAB6C5A7 CRC64;

Query Match      11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      17 SQ 18
      |||
Db      3 SQ 4

RESULT 58
FAR4_PENMO
ID _FAR4_PENMO STANDARD; PRT; 9 AA.
AC P83319;
DT 28-FEB-2003 (Rel. 41, Created)

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DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE FMRPamide-like neuropeptide FLP4 (SQPSMLRPF-amide).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupum J., Krungkarn C., Longyant S.,
RA Chaivuthangkul P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRPamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Penaeus monodon."
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1119.8; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRPAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1121 MW; DA0B07340685A776 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 SQ 18
DB 1 SQ 2

RESULT 59
FAR5 PENMO
ID FAR5 PENMO STANDARD; PRT; 9 AA.
AC P83320;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE FMRPamide-like neuropeptide FLP5 (SMPSLRLPF-amide).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupum J., Krungkarn C., Longyant S.,
RA Chaivuthangkul P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRPamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Penaeus monodon."
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1121.1; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRPAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1106 MW; B60B07340735A766 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MP 5
DB 2 MP 3

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RESULT 60
FIBB MACFU
ID FIBB MACFU STANDARD; PRT; 9 AA.
AC P19345;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain (Contains: Fibrinopeptide B) (Fragment).
GN FGB.
OS Macaca fuscata fuscata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9543;
RN [1]
RP SEQUENCE.
RX MEDLINE=85289140; PubMed=3928610;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and
RT patas monkey (Erythrocebus patas): their amino acid sequences,
RT restricted mutations, and a molecular phylogeny for macaques,
RT guenons, and baboons."
RL J. Biochem. 97:1487-1492(1985).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
CC PIR; C24180; C24180.
DR InterPro; IPR002181; Fibrinogen_C.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1038 MW; 69FE65B9C735B1B CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ES 17
DB 3 ES 4

RESULT 61
FRFL SARBU
ID FRFL SARBU STANDARD; PRT; 9 AA.
AC P83350;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neb-FMRPamide 1.
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7385;
RN [1]
RP SEQUENCE, AMIDATION, AND FUNCTION.
RC TISSUE=CNS;
RX MEDLINE=22342733; PubMed=12438685;
RA Meusen T., Mertens I., Clynen E., Baggerman G., Nichols R.,
RA Nachman R.J., Huybrechts R., De Loof A., Schoofs L.;
RT "Identification in Drosophila melanogaster of the invertebrate G
RT protein-coupled FMRPamide receptor."
RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).
CC -!- FUNCTION: Has modulatory actions at skeletal neuromuscular
CC junctions.

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CC -|- SUBCELLULAR LOCATION: Secreted.  
 CC -|- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 9 9 AMIDATION.  
 SQ SEQUENCE 9 AA; 1155 MW; 2D810699CAB6C5A7 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 SQ 18  
 ||  
 Db 3 SQ 4

RESULT 62  
 HUTU KLEAE STANDARD; PRT; 9 AA.  
 ID HUTU KLEAE  
 AC P12381;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Urocanate hydratase (EC 4.2.1.49) (Urocanase) (Imidazolonepropionate  
 hydrolase) (Fragment).  
 GN HUTU.  
 OS Klebsiella aerogenes.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Klebsiella.  
 OX NCBI\_TaxID=28451;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=8819018; PubMed=2834335;  
 RA Nieuwkoop A.J., Baldauf S.A., Hudspeth M.E.S., Bender R.A.;  
 RT "Bidirectional promoter in the hut(P) region of the histidine  
 utilization (hut) operons from Klebsiella aerogenes.";  
 RL J. Bacteriol. 170:2240-2246(1988).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90368611; PubMed=2203754;  
 RA Schwacha A., Bender R.A.;  
 RT "Nucleotide sequence of the gene encoding the repressor for the  
 histidine utilization genes of Klebsiella aerogenes.";  
 RL J. Bacteriol. 172:5477-5481(1990).  
 CC -|- CATALYTIC ACTIVITY: 3-(5-oxo-4,5-dihydro-3-H-imidazol-4-  
 yl)propanoate = urocanate + H(2)O.  
 CC -|- COFACTOR: Binds 1 NAD per subunit (By similarity).  
 CC -|- PATHWAY: Histidine degradation; second step.  
 CC -|- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -|- SIMILARITY: BELONGS TO THE UROCANASE FAMILY.  
 CC  
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 CC  
 CC EMBL; M19665; AAA25078.1; -;  
 CC DR EMBL; M34604; AAA25076.1; -;  
 CC DR HAMAP; MF\_00577; -; 1.  
 CC DR InterPro; IPR000193; Urocanase.  
 CC DR PROSITE; PS01233; UROCANASE; PARTIAL.  
 KW Histidine metabolism; Lyase; NAD.  
 FT NON TER 9  
 SQ SEQUENCE 9 AA; 1140 MW; 970FC41B5325A6C5 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KY 9  
 ||  
 Db 5 KY 6

RESULT 63  
 KNL3 BOMVA STANDARD; PRT; 9 AA.  
 ID KNL3 BOMVA  
 AC P83058;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE [Thr6]bradykinin.  
 OS Bombina variegata (Yellow-bellied toad).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.  
 OX NCBI\_TaxID=8348;  
 RN [1]  
 RP SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.  
 RC TISSUE=Skin secretion;  
 RA Chen T.B., Orr D.F., Bjourson A.J., McLean S., Rao P.F., Shaw C.;  
 RT "Cloning and post-translational processing of frog skin kininogens.";  
 RL Submitted (JUL-2001) to the SWISS-PROT data bank.  
 CC -|- FUNCTION: [Thr6]bradykinin produces in vitro relaxation of rat  
 CC arterial smooth muscle and constriction of intestinal smooth  
 CC muscle.  
 CC -|- SUBCELLULAR LOCATION: Secreted.  
 CC -|- TISSUE SPECIFICITY: Skin.  
 CC -|- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.  
 KW Amphibian defense peptide; Vasodilator; Bradykinin.  
 SQ SEQUENCE 9 AA; 1074 MW; 3393D771A9C86777 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PF 6  
 ||  
 Db 7 PF 8

RESULT 64  
 LMT3 LOCM1 STANDARD; PRT; 9 AA.  
 ID LMT3 LOCM1  
 AC P41489;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Locustamyotropin 3 (LOM-WT-3).  
 OS Locusta migratoria (Migratory locust).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
 OX NCBI\_TaxID=7004;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Brain;  
 RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,  
 RA de Loof A.;  
 RT "Isolation, identification and synthesis of locustamyotropin III and  
 RT IV, two additional neuropeptides of Locusta migratoria: members of the  
 RT locustamyotropin peptide family.";  
 RL Insect Biochem. Mol. Biol. 22:447-452(1992).  
 CC -|- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY  
 CC (MYOTROPIC ACTIVITY).  
 CC -|- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
 CC PIR; A61620; A61620.  
 DR InterPro; IPR001484; Pyrokinin.  
 DR PROSITE; PS00539; PYROKININ; 1.  
 KW Neuropeptide; Amidation; Pyrokinin.  
 FT MOD\_RES 9 9 AMIDATION.  
 SQ SEQUENCE 9 AA; 1140 MW; D5AE1772C9D776C6 CRC64;

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Query Match      11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No.1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 PF 6
      ||
Db      4 PF 5

RESULT 65
OXYA SCYCA
ID OXYA SCYCA STANDARD; PRT; 9 AA.
AC P42996;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Asvatocin.
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyliorhinidae; Scyliorhinus.
OX NCBI_TaxID=7830;
RN [1]
RP SEQUENCE.
RC TISSUE=Pituitary;
RX MEDLINE=95062247; PubMed=7972045;
RA Chauvet J., Rouille Y., Chauveau C., Chauvet M.-T., Acher R.;
RT "Special evolution of neurohypophysial hormones in cartilaginous
RT fishes: asvatocin and phasvatocin, two oxytocin-like peptides
RT isolated from the spotted dogfish (Scyliorhinus caniculus).";
RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994)
CC -!- FUNCTION: DISPLAYS OXYTOCIC ACTIVITY ON RAT UTERUS.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro; IPR000981; Neurhyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 982 MW; 17EDD76EB44404B CRC64;

Query Match      11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No.1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 PV 11
      ||
Db      7 PV 8

RESULT 66
OXYF SCYCA
ID OXYF SCYCA STANDARD; PRT; 9 AA.
AC P42997;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Phasvatocin.
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyliorhinidae; Scyliorhinus.
OX NCBI_TaxID=7830;
RN [1]
RP SEQUENCE.
RC TISSUE=Pituitary;
RX MEDLINE=95062247; PubMed=7972045;
RA Chauvet J., Rouille Y., Chauveau C., Chauvet M.-T., Acher R.;
RT "Special evolution of neurohypophysial hormones in cartilaginous
RT fishes: asvatocin and phasvatocin, two oxytocin-like peptides
RT isolated from the spotted dogfish (Scyliorhinus caniculus).";
RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994)
CC -!- FUNCTION: DISPLAYS OXYTOCIC ACTIVITY ON RAT UTERUS.

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CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro; IPR000981; Neurhyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 1016 MW; 17EDD76EB44449DB CRC64;

Query Match      11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No.1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 PV 11
      ||
Db      7 PV 8

RESULT 67
OXYV SQUAC
ID OXYV SQUAC STANDARD; PRT; 9 AA.
AC P43000;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Valitocin.
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.
OX NCBI_TaxID=7797;
RN [1]
RP SEQUENCE.
RX MEDLINE=73031727; PubMed=5083097;
RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Phylogeny of the neurohypophysial hormones. Two new active peptides
RT isolated from a cartilaginous fish, Squalus acanthias.";
RL Eur. J. Biochem. 29:12-19(1972).
RN [2]
RP SEQUENCE.
RX MEDLINE=72128038; PubMed=4622083;
RA Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
RT "Identification of 2 new neurohypophyseal hormones, valitocin (Vala-
RT oxytocin) and asparatocin (Asn4-oxytocin) in a selachian fish, the
RT spiny dog-fish (Squalus acanthias).";
RL C. R. Acad. Sci., D, Sci. Nat. 274:313-316(1972).
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro; IPR000981; Neurhyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 996 MW; 17EDD76EB456D04B CRC64;

Query Match      11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No.1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 PV 11
      ||
Db      7 PV 8

RESULT 68
SAMP MUSCA
ID SAMP MUSCA STANDARD; PRT; 9 AA.
AC P19035;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serum amyloid P-component (SAP) (Fragment).
OS Mustelus canis (Smooth dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;

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OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharthiniiformes; Triakidae;
OC Mustelus.
OX NCBI_TaxID=7812;
RN [1]_
RP SEQUENCE
RX MEDLINE=83160932; PubMed=6403520;
RA Robey F.A., Tanaka T., Liu T.-Y.;
RT "Isolation and characterization of two major serum proteins from the
RT dogfish, Mustelus canis, C-reactive protein and amyloid P
RT component.";
RL J. Biol. Chem. 258:3889-3894(1983).
CC -!- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTRAXIN) HAVE A DISCOID
CC ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DISEASE: SAP IS A PRECURSOR OF AMYLOID COMPONENT P WHICH IS FOUND
CC IN BASEMENT MEMBRANE AND ASSOCIATED WITH AMYLOID DEPOSITS.
CC -!- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
DR PIR; B20569; B20569.
DR InterPro; IPR001759; Pentaxin.
DR PROSITE; PS00289; PENTAXIN; PARTIAL.
KW Lectin; Amyloid; Glycoprotein; Plasma; Pentaxin.
FT DOMAIN
FT NON TER 1 >9 PENTAXIN.
FT SEQUENCE 9 AA; 965 MW; D05B5735B3386769 CRC64;
SQ
Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 FP 7
DB 2 FP 3
RESULT 69
THYF_FIG
ID THYF_FIG STANDARD; PRT; 9 AA.
AC P01255;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Thymic factor.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]_
RP SEQUENCE.
RX MEDLINE=78026571; PubMed=914862;
RA Pleau J.-M., Dardenne M., Blouquit Y., Bach J.-F.;
RT "Structural study of circulating thymic factor: a peptide isolated
RT from pig serum. II. Amino acid sequence.";
RL J. Biol. Chem. 252:8045-8047(1977).
CC -!- MISCELLANEOUS: THE BIOLOGICAL SOURCE(S) AND PHYSIOLOGICAL
CC ACTIVITIES OF THIS PEPTIDE HAVE NOT BEEN DETERMINED.
DR PIR; A01523; YFPG.
KW Pyrrolidone carboxylic acid. PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 1 1
FT SEQUENCE 9 AA; 876 MW; D500B87866C5B33D CRC64;
SQ
Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 17 SQ 18
DB 4 SQ 5
RESULT 70
UHA2_HUMAN
ID UHA2_HUMAN STANDARD; PRT; 9 AA.
AC P40929;
DE Unknown protein from 2D-page of plasma (Spot 11) (Fragment).
```

```
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of heart (Spot 5603) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE.
RX TISSUE=Heart;
RX MEDLINE=95203287; PubMed=7895732;
RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
RT "The human myocardial two-dimensional gel protein database: update
RT 1994.";
RL Electrophoresis 15:1459-1465(1994).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.0, ITS MW IS: 55.3 kDa.
FT NON TER 9
FT SEQUENCE 9 AA; 1104 MW; 8874B1BBSB01B2CA CRC64;
SQ
Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 TE 16
DB 4 TE 5
RESULT 71
UN19_CLOPA
ID UN19_CLOPA STANDARD; PRT; 9 AA.
AC P81355;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Unknown protein CP 19 from 2D-page (Fragment).
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]_
RP SEQUENCE.
RX STRAIN=WS;
RX MEDLINE=98291870; PubMed=9629918;
RA Flengsrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC VARIANT PROTEIN IS: 6.5, ITS MW IS: 38.0 kDa.
FT NON TER 8 8 M -> D.
FT SEQUENCE 9 AA; 1128 MW; E33E9B0AF5BB19DA CRC64;
SQ
Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 EM 4
DB 7 EM 8
RESULT 72
UPA3_HUMAN
ID UPA3_HUMAN STANDARD; PRT; 9 AA.
AC P30089;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 11) (Fragment).
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OS Homo sapiens (Human).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RN SEQUENCE.  
 RC TISSUE=Plasma;  
 RX MEDLINE=93092937; PubMed=1459097;  
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,  
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,  
 RA Hochstrasser D.P.;  
 RT "Plasma protein map: an update by microsequencing.";  
 RL Electrophoresis 13:707-714(1992).  
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 4.6, ITS MW IS: 46 kDa.  
 DR SWISS-2DPAGE; P30089; HUMAN.  
 FT NON\_TER 1 1  
 FT NON\_TER 9 9  
 SQ SEQUENCE 9 AA; 1056 MW; 26F2B1BAF769C737 CRC64;  
 Query Match 11.1%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 PP 7  
 Db 4 PP 5  
 RESULT 73  
 ANGT\_BOVINA  
 ID ANGT\_BOVINA STANDARD; PRT; 10 AA.  
 AC Q10581;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Angiotensin-like peptide I (Fragment).  
 OS Bothrops jararaca (Jararaca).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Bothrops.  
 OX NCBI\_TaxID=8724;  
 RN [1]  
 RN SEQUENCE.  
 RC TISSUE=Plasma;  
 RX MEDLINE=96208932; PubMed=8829801;  
 RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;  
 RT "Isolation and identification of angiotensin-like peptides from the  
 RT plasma of the snake Bothrops jararaca.";  
 RL Comp. Biochem. Physiol. 113B:467-473(1996).  
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
 DR InterPro; IPR000215; Serpin.  
 DR PROSITE; PS00284; SERPIN; PARTIAL.  
 KW Vasoconstrictor; Plasma; Serpin; 3D-structure.  
 FT PEPTIDE 1 10 ANGIOTENSIN I.  
 FT PEPTIDE 1 8 ANGIOTENSIN II.  
 FT PEPTIDE 2 8 ANGIOTENSIN III.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1308 MW; CEP50DD761F2DB42 CRC64;  
 Query Match 11.1%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 9.4e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 PP 6  
 Db 7 PP 8  
 RESULT 74  
 ANGT\_BOVIN  
 ID ANGT\_BOVIN STANDARD; PRT; 10 AA.  
 AC P01017;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DE Angiotensin-like peptide I (Fragment).  
 OS Bothrops jararaca (Jararaca).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Bothrops.  
 OX NCBI\_TaxID=8724;  
 RN [1]  
 RN SEQUENCE.  
 RC TISSUE=Plasma;  
 RX MEDLINE=96208932; PubMed=8829801;  
 RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;  
 RT "Isolation and identification of angiotensin-like peptides from the  
 RT plasma of the snake Bothrops jararaca.";  
 RL Comp. Biochem. Physiol. 113B:467-473(1996).  
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
 DR InterPro; IPR000215; Serpin.  
 DR PROSITE; PS00284; SERPIN; PARTIAL.  
 KW Vasoconstrictor; Plasma; Serpin.  
 FT PEPTIDE 1 10 ANGIOTENSIN I.  
 FT PEPTIDE 1 8 ANGIOTENSIN II.  
 FT PEPTIDE 2 8 ANGIOTENSIN III.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1308 MW; CEP50DD761F2DB42 CRC64;  
 Query Match 11.1%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 9.4e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 PP 6  
 Db 7 PP 8  
 RESULT 75  
 ANGT\_CHICK  
 ID ANGT\_CHICK STANDARD; PRT; 10 AA.  
 AC P01018;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Angiotensinogen [Contains: Angiotensin I (Ang I); Angiotensin II (Ang  
 DE II); Angiotensin III (Ang III) (Des-Asp[1]-angiotensin II)]  
 (Fragment).  
 OS Gallus gallus (Chicken), and  
 OS Coturnix coturnix japonica (Japanese quail).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031, 93934;  
 RN [1]  
 RN SEQUENCE.  
 RC SPECIES=Chicken;  
 RX MEDLINE=74127845; PubMed=4361802;  
 RA Nakayama T., Nakajima T., Sokabe H.;  
 RT "Comparative studies on angiotensins. 3. Structure of fowl  
 RT angiotensin and its identification by DNS-method.";  
 RL Chem. Pharm. Bull. 21:2085-2087(1973).  
 RN [2]  
 RN SEQUENCE.  
 RC SPECIES=C.G.japonica;  
 RX MEDLINE=90284684; PubMed=2191893;

DE Angiotensinogen [Contains: Angiotensin I (Ang I); Angiotensin II (Ang  
 DE II); Angiotensin III (Ang III) (Des-Asp[1]-angiotensin II)]  
 (Fragment).  
 DE NCBI\_TaxID=9913;  
 GN AGT OR SERPINAS.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RN SEQUENCE.  
 RA Elliott D.F., Peart W.S.;  
 RT "The amino acid sequence in a hypertensin.";  
 RL Biochem. J. 65:246-254(1957).  
 CC -1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN  
 CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACR (ANGIOTENSIN  
 CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE  
 CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT  
 CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL  
 CC BALANCE OF BODY FLUIDS.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Synthesized by the liver and secreted in the  
 CC plasma.  
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
 DR PIR; A90345; A90345.  
 DR PDB; 3ER5; 15-JUL-92.  
 DR InterPro; IPR000215; Serpin.  
 DR PROSITE; PS00284; SERPIN; PARTIAL.  
 KW Vasoconstrictor; Plasma; Serpin; 3D-structure.  
 FT PEPTIDE 1 10 ANGIOTENSIN I.  
 FT PEPTIDE 1 8 ANGIOTENSIN II.  
 FT PEPTIDE 2 8 ANGIOTENSIN III.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1282 MW; CEEFDD761F2DB42 CRC64;  
 Query Match 11.1%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 9.4e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 PP 6  
 Db 7 PP 8

RESULT 75  
 ANGT\_CHICK  
 ID ANGT\_CHICK STANDARD; PRT; 10 AA.  
 AC P01018;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Angiotensinogen [Contains: Angiotensin I (Ang I); Angiotensin II (Ang  
 DE II); Angiotensin III (Ang III) (Des-Asp[1]-angiotensin II)]  
 (Fragment).  
 OS Gallus gallus (Chicken), and  
 OS Coturnix coturnix japonica (Japanese quail).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031, 93934;  
 RN [1]  
 RN SEQUENCE.  
 RC SPECIES=Chicken;  
 RX MEDLINE=74127845; PubMed=4361802;  
 RA Nakayama T., Nakajima T., Sokabe H.;  
 RT "Comparative studies on angiotensins. 3. Structure of fowl  
 RT angiotensin and its identification by DNS-method.";  
 RL Chem. Pharm. Bull. 21:2085-2087(1973).  
 RN [2]  
 RN SEQUENCE.  
 RC SPECIES=C.G.japonica;  
 RX MEDLINE=90284684; PubMed=2191893;

RA Takei Y., Hasegawa Y.;  
 RT "Vasopressor and depressor effects of native angiotensins and  
 inhibition of these effects in the Japanese qual.";  
 RL Gen. Comp. Endocrinol. 79:12-22(1990).  
 CC -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN  
 CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN  
 CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE  
 CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT  
 CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL  
 CC BALANCE OF BODY FLUIDS.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Synthesized by liver and secreted in plasma.  
 CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
 DR PIR; A60624; A60624.  
 DR PIR; A90917; A90917.  
 DR InterPro; IPR000215; Serpin.  
 DR PROSITE; PS00284; SERPIN; PARTIAL.  
 KW Vasoconstrictor; Plasma; Serpin.  
 FT PEPTIDE 1 10 ANGIOTENSIN I.  
 FT PEPTIDE 1 8 ANGIOTENSIN II.  
 FT PEPTIDE 2 8 ANGIOTENSIN III.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1232 MW; CEFBEDD761F2DB42 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 9.4e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PF 6  
 ||  
 Db 7 PF 8

Search completed: November 25, 2003, 19:28:22  
 Job time : 7.45515 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:25:50 ; Search time 33.8023 Seconds  
(without alignments)  
137.415 Million cell updates/sec

Title: US-09-641-801-22

Perfect score: 18

Sequence: 1 HKEMPPKYPVPEFTESQ 18

Scoring table: OLIGO

Gapex 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

SPTREMBL.23.\*

1: sp\_archaea.\*

2: sp\_bacteria.\*

3: sp\_fungi.\*

4: sp\_human.\*

5: sp\_invertebrate.\*

6: sp\_mammal.\*

7: sp\_mhc.\*

8: sp\_organelle.\*

9: sp\_phase.\*

10: sp\_plant.\*

11: sp\_rodent.\*

12: sp\_virus.\*

13: sp\_vertibrate.\*

14: sp\_unclassified.\*

15: sp\_rvirus.\*

16: sp\_bacteriap.\*

17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	22.2	8	11	P82598
2	4	22.2	13	5	Q9TWR4
3	4	22.2	15	2	Q9A5Z5
4	4	22.2	18	11	Q8CJD4
5	3	16.7	8	2	Q934S4
6	3	16.7	10	4	Q8WXB5
7	3	16.7	7	6	Q9N1X1
8	3	16.7	10	10	Q9FS93
9	3	16.7	10	11	Q9GVJ5
10	3	16.7	10	11	Q9QVJ6
11	3	16.7	10	13	Q73588
12	3	16.7	11	5	Q9UR95
13	3	16.7	11	3	P82700
14	3	16.7	12	4	Q9HBU4
15	3	16.7	12	10	Q9FSA9
16	3	16.7	12	11	Q9WUX1

17	3	16.7	12	15	O12036
18	3	16.7	13	4	Q9H4C1
19	3	16.7	13	5	Q9W5Q6
20	3	16.7	13	10	Q9FSA8
21	3	16.7	13	10	Q9FS94
22	3	16.7	13	10	Q8SAT3
23	3	16.7	13	10	Q9S922
24	3	16.7	13	10	Q8SAT4
25	3	16.7	14	2	P83159
26	3	16.7	14	10	Q9FS95
27	3	16.7	14	10	Q9FS81
28	3	16.7	14	10	Q9FS91
29	3	16.7	15	2	Q9R4M8
30	3	16.7	15	2	Q9R4U7
31	3	16.7	15	4	Q9UBK0
32	3	16.7	15	4	Q9BXQ0
33	3	16.7	15	4	Q8IZK4
34	3	16.7	15	6	Q8HZ79
35	3	16.7	15	8	Q9T2G9
36	3	16.7	15	9	Q38574
37	3	16.7	15	10	Q9FSA5
38	3	16.7	15	10	Q9FSB2
39	3	16.7	15	10	Q9FS98
40	3	16.7	15	10	Q9FEI3
41	3	16.7	15	10	Q9FSA0
42	3	16.7	15	10	Q9FS99
43	3	16.7	15	10	Q9FEI5
44	3	16.7	15	10	Q3FEI4
45	3	16.7	15	10	Q9FS80
46	3	16.7	15	10	Q9FSB0
47	3	16.7	15	13	Q9PRM3
48	3	16.7	16	2	Q9R4J0
49	3	16.7	16	2	Q9R4J4
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51	3	16.7	16	2	Q9R514
52	3	16.7	16	2	Q8KLP7
53	3	16.7	16	2	P82597
54	3	16.7	16	4	Q9UBQ9
55	3	16.7	16	6	Q9SM73
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57	3	16.7	16	8	Q8HU42
58	3	16.7	16	8	Q8HU29
59	3	16.7	16	10	P83511
60	3	16.7	16	11	Q8CI82
61	3	16.7	17	2	Q9R9C3
62	3	16.7	17	4	Q9Y3F6
63	3	16.7	17	4	Q9UC43
64	3	16.7	17	6	Q9TRH5
65	3	16.7	17	6	Q9SM49
66	3	16.7	17	8	Q36741
67	3	16.7	17	10	Q9S8Y2
68	3	16.7	17	11	Q9QVS7
69	3	16.7	17	12	Q9IHG7
70	3	16.7	17	12	Q9IHH9
71	3	16.7	17	12	Q9IHG4
72	3	16.7	17	12	Q9IH17
73	3	16.7	17	12	Q9IHH4
74	3	16.7	17	12	Q9IHH9
75	3	16.7	17	12	Q9IHH4
76	3	16.7	17	12	Q9IHH9
77	3	16.7	17	12	Q9IHH5
78	3	16.7	17	12	Q9IHH1
79	3	16.7	17	12	Q9IHH8
80	3	16.7	17	12	Q9IHH5
81	3	16.7	17	12	Q9IHH8
82	3	16.7	17	12	Q9IHH1
83	3	16.7	17	12	Q9IHH0
84	3	16.7	17	12	Q9IHH6
85	3	16.7	17	12	Q9IHH2
86	3	16.7	17	12	Q9IHH3
87	3	16.7	17	12	Q9IHH0
88	3	16.7	17	12	Q9IHH6
89	3	16.7	17	12	Q9IHH1

O12036	caprine art
Q9H4C1	homo sapien
Q9W5Q6	drosophila
Q9FSA8	silene bacc
Q9FS94	silene pent
Q8SAT3	flaveria ro
Q9S922	brassica ol
Q8SAT4	flaveria an
P83159	anabaena sp
Q9FS95	silene pent
Q9FS81	silene aega
Q9FS91	silene sedo
Q9R4M8	bacillus fi
Q9R4U7	acinetobact
Q9UBK0	homo sapien
Q9BXQ0	homo sapien
Q8IZK4	homo sapien
Q8HZ79	bos taurus
Q9T2G9	solanum tub
Q38574	bacterioph
Q9FSA5	silene cryp
Q9FSB2	silene aega
Q9FS98	silene laco
Q9FEI3	silene aega
Q9FSA0	silene haus
Q9FS99	silene inte
Q9FEI5	silene sedo
Q9FEI4	silene pent
Q9FS80	silene zawa
Q9FSB0	silene aega
Q9PRM3	gallus gall
Q9R4J0	arthrobacte
Q9R4J4	pseudomonas
Q44610	buchnera ap
Q9R514	porphyromon
P82597	streptomyce
Q9UBQ9	bacillus sp
Q9SM73	pan troglod
Q9TRK9	canis famli
Q8HU42	passiflora
Q8HU29	passiflora
P83511	delonix reg
Q8CI82	mus musculus
Q9R9C3	borrelia bu
Q9Y3F6	homo sapien
Q9UC43	homo sapien
Q9SM49	bos taurus
Q36741	bos taurus
Q9S8Y2	homo sapien
Q9QVS7	lupinus arb
Q9IHG7	mus sp. lac
Q9IHH9	human polio
Q9IHG4	human polio
Q9IH17	human polio
Q9IHH4	human polio
Q9IHH9	human polio
Q9IHH4	human polio
Q9IHH5	human polio
Q9IHH1	human polio
Q9IHH8	human polio
Q9IHH5	human polio
Q9IHH8	human polio
Q9IHH2	human polio
Q9IHH3	human polio
Q9IHH0	human polio
Q9IHH6	human polio
Q9IHH1	human polio

90 Q9Ih13 human polio  
 91 Q9Ih10 human polio  
 92 Q9Ih06 human polio  
 93 Q9Ih07 human polio  
 94 Q9Ih15 human polio  
 95 Q9Ih12 human polio  
 96 Q9Ih13 human polio  
 97 Q9Ih02 human polio  
 98 Q8x444 escherichia  
 99 Q9uc87 homo sapien  
 100 Q98365 myosurus mi

## ALIGNMENTS

RESULT 1  
 P82598  
 ID P82598 PRELIMINARY; PRT; 8 AA.  
 AC P82598,2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE 38kDa non-arginase growth inhibitory factor (NAGIF) (Fragment).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;  
 RX MEDLINE=20198203; PubMed=10731662;  
 RA Kim K.-Y., Choi I., Kim S.-S.;  
 RT "Purification and characterization of a novel inhibitor of the  
 proliferation of hepatic stellate cells.";  
 RL J. Biochem. 127:23-27(2000).  
 CC -1- FUNCTION: MAY ACT AS A NEGATIVE EFFECTOR IN THE REGULATION OF THE  
 HEPATIC STELLATE CELLS (HSC). ALSO INHIBITS THE GROWTH OF BOVINE  
 CC ENDOTHELIAL CELLS AND 3T6 FIBROBLASTS.  
 CC -1- SIMILARITY: IDENTICAL TO THE 63-70 AA REGION OF THE RAT ZAG  
 CC PROTEIN.  
 FT NON TER 8 8  
 SQ SEQUENCE 8 AA; 914 MW; 80A3676B02D76B1D CRC64;

Query Match 22.2%; Score 4; DB 11; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PVEP 13  
 Db 3 PVEP 6

RESULT 2  
 Q9TWR4  
 ID Q9TWR4 PRELIMINARY; PRT; 13 AA.  
 AC Q9TWR4,2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE Peptide T-BRADYKININ potentiator.  
 OS Tityus serrulatus (Brazilian scorpion).  
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;  
 OC Buthoidea; Buthidae; Tityus.  
 OX NCBI\_TaxID=6887;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=94024945; PubMed=8212046;  
 RA Ferreira L.A., Alves E.W., Henriques O.B.;  
 RT "Peptide T, a novel bradykinin potentiator isolated from Tityus  
 serrulatus scorpion venom.";  
 RL Toxicon 31:941-947(1993).  
 SQ SEQUENCE 13 AA; 1604 MW; 35770B0644FC02D7 CRC64;

Query Match 22.2%; Score 4; DB 5; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPVE 12  
 Db 5 YPVE 8

RESULT 3  
 Q9R5Z5  
 ID Q9R5Z5 PRELIMINARY; PRT; 15 AA.  
 AC Q9R5Z5,2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE Streptolysin O (Fragment).  
 OS Streptococcus equisimilis.  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 OC Streptococcus.  
 OX NCBI\_TaxID=119602;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93273535; PubMed=8500915;  
 RA Gerlach D., Kohler W., Gunther E., Mann K.;  
 RT "Purification and characterization of streptolysin O secreted by  
 RT Streptococcus equisimilis (group C).";  
 RL Infect. Immun. 61:2727-2731(1993).  
 SQ SEQUENCE 15 AA; 1716 MW; 7C02547F72FF85BE CRC64;

Query Match 22.2%; Score 4; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KEMP 5  
 Db 3 KEMP 6

RESULT 4  
 Q8CJD4  
 ID Q8CJD4 PRELIMINARY; PRT; 18 AA.  
 AC Q8CJD4,2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Podocin (Fragment).  
 GN NPHS2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Morita H., Yoshimura A., Makino R., Inui K., Nakao N., Usami T.,  
 RA Roselli S., Antignac C., Matsuyama M., Ideura T.;  
 RT "Rat genome fragment containing a part of exons and all of the 3'UTR  
 of Nphs2 as well as microsatellite sites.";  
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB094124; BAC23094.1; -.  
 FT NON TER 1 1  
 SQ SEQUENCE 18 AA; 2033 MW; D47829DCFF0EF4B CRC64;

Query Match 22.2%; Score 4; DB 11; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PVEP 13  
 Db 4 PVEP 7

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RESULT 5
Q934S4
ID Q934S4 PRELIMINARY; PRT; 8 AA.
AC Q934S4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MerD protein (Fragment).
GN MERD.
OS Thiobacillus ferrooxidans.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Acidithiobacillus.
OX NCBI_TaxID=920;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=G66; TRANSPOSON=Tn5037;
RA Kalyaeva E.S., Kholodii G.Y., Bass I.A., Gorlenko A.M., Yurieva O.V.,
RA Nikiforov V.G.;
RT "Tn5037, a Tn21-like mercury resistance transposon from Thiobacillus
RT ferrooxidans."
RL Russ. J. Genet. 37:972-975(2001).
DR EMBL; AJ251743; CAC69252.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 937 MW; ED15A2D77B5DD446 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPV 11
Db |||
4 YPV 6

RESULT 6
Q8WXB5
ID Q8WXB5 PRELIMINARY; PRT; 10 AA.
AC Q8WXB5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE EYA2B (Fragment).
GN EYA2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Fee B.E., Doyle C.A., Cleveland J.L.;
RT "A novel eyes absent protein is expressed in the human eye.";
RL Gene 0:0-0(2002)
DR EMBL; AF455148; AAL57875.1; -.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1298 MW; 18021202C69B132B CRC64;

Query Match 16.7%; Score 3; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KEM 4
Db |||
4 KEM 6

RESULT 7
Q9N1X1
ID Q9N1X1 PRELIMINARY; PRT; 10 AA.
AC Q9N1X1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Alcohol dehydrogenase 3 (Fragment).
GN ADH3.

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OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20082971; PubMed=10613847;
RA Caetano A.R., Shue Y.L., Lyons L.A., O'Brien S.J., Laughlin T.F.,
RA Bowling A.T., Murray J.D.;
RT "A comparative gene map of the horse (Equus caballus).";
RL Genome Res. 9:1239-1249(1999).
DR EMBL; AF134056; AAF31299.1; -.
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1144 MW; C4EA25676B02D6DD CRC64;

Query Match 16.7%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEP 13
Db |||
5 VEP 7

RESULT 8
Q9FS93
ID Q9FS93 PRELIMINARY; PRT; 10 AA.
AC Q9FS93;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE RNA polymerase II (Fragment).
GN RPB2.
OS Silene pentelica.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.
OX NCBI_TaxID=49735;
RN [1]
RP SEQUENCE FROM N.A.
RA POPP M., Oxelman B.;
RT "Inferring the history of the polyploid Silene aegaea
RT (Caryophyllaceae) using nuclear and chloroplast DNA sequence data.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ296133; CAC13025.1; -.
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1108 MW; CF1AB6D1B2CAB1A9 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFT 15
Db |||
2 PFT 4

RESULT 9
Q9QVJ5
ID Q9QVJ5 PRELIMINARY; PRT; 10 AA.
AC Q9QVJ5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Myo-inositol hexakisphosphate phosphohydrolase (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.

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RX MEDLINE=91370007; PubMed=1654110;
RA Yang W.J., Matsuda Y., Sano S., Masutani H., Nakagawa H.;
RT "Purification and characterization of phytase from rat intestinal
RT mucosa.";
RL Biochim. Biophys. Acta 1075:75-82(1991).
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1096 MW; 37A8EA4B1B1B02D7 CRC64;

Query Match      16.7%; Score 3; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 PVE 12
Db       3 PVE 5
      |||

RESULT 10
Q9QVJ6 PRELIMINARY; PRT; 10 AA.
ID Q9QVJ6
AC Q9QVJ6
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE MYO-inositol hexakisphosphate phosphohydrolase (fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE
RX MEDLINE=91370007; PubMed=1654110;
RA Yang W.J., Matsuda Y., Sano S., Masutani H., Nakagawa H.;
RT "Purification and characterization of phytase from rat intestinal
RT mucosa.";
RL Biochim. Biophys. Acta 1075:75-82(1991).
SQ SEQUENCE 10 AA; 1124 MW; 28B8EA4B1B1B02D7 CRC64;

Query Match      16.7%; Score 3; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 PVE 12
Db       3 PVE 5
      |||

RESULT 11
O73588 PRELIMINARY; PRT; 10 AA.
ID O73588
AC O73588
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Engrailed-3 (fragment).
GN EN-3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=White Leghorn; TISSUE=Embryo;
RX MEDLINE=98141813; PubMed=9473273;
RA Peale F.V. Jr., Mason K., Hunter A.W., Bothwell M.;
RT "Multiplex display polymerase chain reaction amplifies and resolves
RT related sequences sharing a single moderately conserved domain.";
RL Anal. Biochem. 256:158-168(1998).
DR EMBL; U26148; AAC06186.1; -.
FT NON_TER 1
FT NON_TER 10

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SQ SEQUENCE 10 AA; 1118 MW; 73C0BE144735B72B CRC64;

Query Match      16.7%; Score 3; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 ESQ 18
Db       8 ESQ 10
      |||

RESULT 12
Q9UR95 PRELIMINARY; PRT; 11 AA.
ID Q9UR95
AC Q9UR95;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Heat shock protein 60 homolog (fragment).
OS Pichia angusta (yeast) (Hansenula polymorpha).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Pichia.
OX NCBI_TaxID=4905;
RN [1]
RP SEQUENCE.
RX MEDLINE=93223840; PubMed=8096822;
RA Evers M.E., Hulse B., Titorenko V.I., Kunau W.H., Hartl F.U.,
RA Harder W., Veenhuis M.;
RT "Affinity purification of molecular chaperones of the yeast Hansenula
RT polymorpha using immobilized denatured alcohol oxidase.";
RL FEBS Lett. 321:32-36(1993).
SQ SEQUENCE 11 AA; 1230 MW; 71872C1779C3372B CRC64;

Query Match      16.7%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HKE 3
Db       2 HKE 4
      |||

RESULT 13
P82700 PRELIMINARY; PRT; 11 AA.
ID P82700
AC P82700;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Periviscerokinin-3 (LEM-FVK-3).
OS Leucophaea maderae (Madeira cockroach),
OS Nauphoeta cinerea (Cinereous cockroach) (Gray cockroach),
OS Blaberus craniifer,
OS Blaptica dubia (Argentinian wood cockroach), and
OS Gromphadorina portentosa (Cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988, 6990, 6982, 132935, 36953;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROSCOPY.
RC TISSUE=ABDOMINAL PERISYMPATHETIC ORGANS;
RX MEDLINE=20307624; PubMed=10849006;
RA Predel R., Kellner R., Baggerman G., Steinmetzer T., Schoofs L.;
RT "Identification of novel periviscerokinins from single neurohaemal
RT release sites in insects. MS/MS fragmentation complemented by Edman
RT degradation.";
RL Eur. J. Biochem. 267:3869-3873(2000).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- MASS SPECTROMETRY: MW=1146.6; METHOD=MALDI.
KW Neuropeptide; Amidation.
FT MOD_RES 11
FT AMIDATION.

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SQ SEQUENCE 11 AA; 1147 MW; 2F4D9FF2D7605698 CRC64;
Query Match 16.7%; Score 3; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PFP 7
Db |||
7 PFP 9

RESULT 14
Q9HBU4 PRELIMINARY; PRT; 12 AA.
AC Q9HBU4;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DE Caspase 8 isoform i (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Eckhart L., Fischer H., Bach J., Henry M., Ban J., Tschachler E.;
RT "Identification and characterization of novel splice variants of human
RT caspase-8";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF207672; AAG10682.1; -.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 12 AA; 1343 MW; 80F055095B6B02D1 CRC64;

Query Match 16.7%; Score 3; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEP 13
Db |||
6 VEP 8

RESULT 15
Q9FSA9 PRELIMINARY; PRT; 12 AA.
AC Q9FSA9;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DE RNA polymerase II (Fragment).
GN RPB2.
OS Silene aegaea.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllaceae; Caryophyllaceae; Silene.
OX NCBI_TaxID=49732;
RN [1]
RP SEQUENCE FROM N.A.
RA Popp M., Oxelman B.;
RT "Inferring the history of the polyploid Silene aegaea
RT (Caryophyllaceae) using nuclear and chloroplast DNA sequence data.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ296130; CAC13014.1; -.
FT NON TER 1
FT NON TER 1
FT NON TER 12
FT NON TER 12
SQ SEQUENCE 12 AA; 1304 MW; 83269695B441B2CA CRC64;

Query Match 16.7%; Score 3; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFT 15
Db |||

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Db 2 PFT 4

RESULT 16
Q9WUX1 PRELIMINARY; PRT; 12 AA.
AC Q9WUX1;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
DE APOBEC-1 protein (Fragment).
GN APOBEC-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98335789; PubMed=9672068;
RA Greeve J., Axelos D., Welker S., Schipper M., Greten H.;
RT "Distinct promoters induce APOBEC-1 expression in rat liver and
RT intestine.";
RL Arterioscler. Thromb. Vasc. Biol. 18:1079-1092 (1998).
DR EMBL; AJ006695; CAB44439.1; -.
FT NON TER 1
FT NON TER 12
FT NON TER 12
SQ SEQUENCE 12 AA; 1357 MW; 70FE1679699325BB CRC64;

Query Match 16.7%; Score 3; DB 11; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17
Db |||
4 TES 6

RESULT 17
O12036 PRELIMINARY; PRT; 12 AA.
AC O12036;
DT 01-JUL-1997 (TRENBLrel. 04, Created)
DT 01-JUL-1997 (TRENBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Envelope glycoprotein (fragment).
GN ENV.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroviruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97296261; PubMed=9151845;
RA Turelli P., Guiguen F., Mornex J.F., Vigne R., Querat G.;
RT "dUTPase-minus caprine arthritis-encephalitis virus is attenuated for
RT pathogenesis and accumulates G-to-A substitutions.";
RL J. Virol. 71:4522-4530 (1997).
DR EMBL; U81390; AAC57905.1; -.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 12 AA; 1398 MW; 8D24228CA3733455 CRC64;

Query Match 16.7%; Score 3; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKE 3
Db |||
2 HKE 4

RESULT 18
Q9H4C1 PRELIMINARY; PRT; 13 AA.
ID Q9H4C1
AC Q9H4C1;

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DT 01-MAR-2001 (TReMBLrel. 16, Created)  
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE Angiopoietin-2B (Fragment).  
GN ANGIOPOIETIN-2B.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=2042311; PubMed=10964717;  
RA Mezquita J., Mezquita P., Montserrat P., Mezquita B., Francane V.,  
RA Vilgrasa X., Mezquita C.;  
RT "Genomic structure and alternative splicing of chicken angiopoietin-  
RT 2";  
RL Biochem. Biophys. Res. Commun. 275:643-651(2000).  
DR EMBL; AJ289780; CAC08179.1; --  
FT NON\_TER 13 13  
SQ SEQUENCE 13 AA; 1548 MW; C3A19DA93EE95B02 CRC64;  
  
Query Match 16.7%; Score 3; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 7.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 KEM 4  
Db |||  
3 KEM 5  
  
RESULT 19  
Q9W5Q6 PRELIMINARY; PRT; 13 AA.  
ID Q9W5Q6;  
AC Q9W5Q6;  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-WAR-2001 (TReMBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
DE Snap25 protein.  
GN SNAP25 OR CG17676 OR CG17884.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RT STRAIN=BERKELEY;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
RA Abril J.F., Agayani A., An H.-J., Andrews-Prannkoch C., Baldwin D.,  
RA Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Fabios B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Flossler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster";  
RL Science 287:2185-2195(2000).  
DR EMBL; AB002931; AAF45394.2; --  
DR FlyBase; FBgn0011288; Snap25.  
SQ SEQUENCE 13 AA; 1483 MW; 47FD7CC5C0AF9B13 CRC64;  
  
Query Match 16.7%; Score 3; DB 5; Length 13;  
Best Local Similarity 100.0%; Pred. No. 7.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 KEM 4  
Db |||  
6 KEM 8  
  
RESULT 20  
Q9FSA8 PRELIMINARY; PRT; 13 AA.  
ID Q9FSA8;  
AC Q9FSA8;  
DT 01-MAR-2001 (TReMBLrel. 16, Created)  
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
DE RNA polymerase II (Fragment).  
GN RPB2.  
OS Silene baccifera (Berry catchfly) (Cucubalus baccifer).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.  
OX NCBI\_TaxID=54818;  
RN [1]  
RP SEQUENCE FROM N.A.  
RT Popp M., Oxelman B.;  
RT "Inferring the history of the polyploid Silene aegaea  
RT (Caryophyllaceae) using nuclear and chloroplast DNA sequence data";  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ296139; CAC13015.1; --  
FT NON\_TER 1 1  
FT NON\_TER 13 13  
SQ SEQUENCE 13 AA; 1437 MW; D931E2CF1AB6D1B2 CRC64;  
  
Query Match 16.7%; Score 3; DB 10; Length 13;  
Best Local Similarity 100.0%; Pred. No. 7.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 13 PFT 15  
Db |||  
2 PFT 4  
  
RESULT 21  
Q9FS94 PRELIMINARY; PRT; 13 AA.  
ID Q9FS94;  
AC Q9FS94;  
DT 01-MAR-2001 (TReMBLrel. 16, Created)  
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
DE RNA polymerase II (Fragment).  
GN RPB2.  
OS Silene pentelica.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.



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OX NCBI_TaxID=49735;
RN [1]
RP SEQUENCE FROM N.A.
RA Popp M., Oxelman B.;
RT "Inferring the history of the polyploid Silene aegaea
RL (Caryophyllaceae) using nuclear and chloroplast DNA sequence data.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ296132; CAC13024.1; -.
FT NON_TER 1
FT NON_TER 13
FT NON_TER 13
SQ SEQUENCE 13 AA; 1437 MW; D931E2CFIAB6D1B2 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFT 15
Db 2 PFT 4

RESULT 22
Q9S922 ID Q9S922 PRELIMINARY; PRT; 13 AA.
AC Q9S922
DT 01-JUN-2000 (TrEMBLrel. 13, Created)
DT 01-JUN-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Non-C4 chloroplastic NADP-malic enzyme (Fragment).
GN CHLME2-2.
OS Brassica oleracea (Cauliflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; campanulids; Asterales; Asteraceae; Tageteae;
OC Flaveria.
OX NCBI_TaxID=163089;
RN SEQUENCE FROM N.A.
RP MEDLINE=21648948; PubMed=11788758;
RA Lai L.B., Wang L., Nelson T.M.;
RT "Distinct But Conserved Functions for Two Chloroplastic NADP-Malic
RL Enzyme Isoforms in C(3) and C(4) Flaveria Species.";
RL Plant Physiol. 128:125-139(2002).
DR EMBL; AF288914; AAL74058.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 13 AA; 1697 MW; 95393F9D91422775 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PKY 9
Db 7 PKY 9

RESULT 23
Q9S922 ID Q9S922 PRELIMINARY; PRT; 13 AA.
AC Q9S922
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE S3 SGP=S-locus specific glycoprotein (Fragment).
OS Brassica oleracea (Cauliflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3712;
RN SEQUENCE.
RP Submitted (OCT-2001) to the SWISS-PROT data bank.
RL FUNCTION: ROD LINKER PROTEIN, ASSOCIATED WITH PHYCOCYANIN. LINKER
CC POLYPEPTIDES DETERMINE THE STATE OF AGGREGATION AND THE LOCATION
CC OF THE DISC-SHAPED PHYCOBILIPROTEIN UNITS WITHIN THE PHYCOBILISOME
CC AND MODULATE THEIR SPECTROSCOPIC PROPERTIES IN ORDER TO MEDIATE A
CC DIRECTED AND OPTIMAL ENERGY TRANSFER.

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RT "Use of a fast protein electrophoretic purification procedure for N-
RT terminal sequence analysis to identify S-locus related proteins in
RT stigmas of Brassica oleracea.";
RL Electrophoresis 12:646-653(1991).
FT NON_TER 1
FT NON_TER 13
FT NON_TER 13
SQ SEQUENCE 13 AA; 1351 MW; 9C23EDFF999601B5 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17
Db 7 TES 9

RESULT 24
Q8SAT4 ID Q8SAT4 PRELIMINARY; PRT; 13 AA.
AC Q8SAT4
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Non-C4 chloroplastic NADP-malic enzyme (Fragment).
GN CHLME2.
OS Flaveria angustifolia.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; campanulids; Asterales; Asteraceae; Tageteae;
OC Flaveria.
OX NCBI_TaxID=163088;
RN SEQUENCE FROM N.A.
RP MEDLINE=21648948; PubMed=11788758;
RA Lai L.B., Wang L., Nelson T.M.;
RT "Distinct But Conserved Functions for Two Chloroplastic NADP-Malic
RL Enzyme Isoforms in C(3) and C(4) Flaveria Species.";
RL Plant Physiol. 128:125-139(2002).
DR EMBL; AF288896; AAL74057.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 13 AA; 1697 MW; 95393F9D91422775 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PKY 9
Db 7 PKY 9

RESULT 25
P83159 ID P83159 PRELIMINARY; PRT; 14 AA.
AC P83159
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Phycobilisome 32.1 kDa linker polypeptide, phycocyanin-associated,
DE rod (Fragment).
OS Anabaena sp. (strain L31).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OX NCBI_TaxID=29412;
RN SEQUENCE.
RA Apte S.K., Uhlemann E., Schmid R., Altendorf K.;
RL Submitted (OCT-2001) to the SWISS-PROT data bank.
CC FUNCTION: ROD LINKER PROTEIN, ASSOCIATED WITH PHYCOCYANIN. LINKER
CC POLYPEPTIDES DETERMINE THE STATE OF AGGREGATION AND THE LOCATION
CC OF THE DISC-SHAPED PHYCOBILIPROTEIN UNITS WITHIN THE PHYCOBILISOME
CC AND MODULATE THEIR SPECTROSCOPIC PROPERTIES IN ORDER TO MEDIATE A
CC DIRECTED AND OPTIMAL ENERGY TRANSFER.

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CC -!- SUBCELLULAR LOCATION: THIS PROTEIN OCCURS IN THE ROD, IT IS  
 CC ASSOCIATED WITH PHYCOCYANIN (BY SIMILARITY).  
 CC -!- SIMILARITY: TO OTHER PHYCOBILISOME LINKER PROTEINS.  
 KW Phycobilisome; Photosynthesis.  
 FT NON\_TER 14 14  
 SQ SEQUENCE 14 AA; 1405 MW; 96823B44F60A3115 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 8.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EPF 14  
 ||||  
 Db 12 EPF 14

## RESULT 26

Q9FS95 PRELIMINARY; PRT; 14 AA.

AC Q9FS95;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DE RNA polymerase II (Fragment).  
 GN RPB2.  
 OS Silene pentelica.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.  
 OX NCBI\_TaxID=49735;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Popp M., Oxelman B.;  
 RT "Inferring the history of the polyploid Silene aegaea  
 (Caryophyllaceae) using nuclear and chloroplast DNA sequence data.";  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ296131; CAC13023.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 14 14  
 SQ SEQUENCE 14 AA; 1508 MW; 9B0931E2CF1AB6D1 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 8.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFT 15  
 ||||  
 Db 2 PFT 4

## RESULT 27

Q9FSB1 PRELIMINARY; PRT; 14 AA.

AC Q9FSB1;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DE RNA polymerase II (Fragment).  
 GN RPB2.  
 OS Silene aegaea.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.  
 OX NCBI\_TaxID=49732;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Popp M., Oxelman B.;  
 RT "Inferring the history of the polyploid Silene aegaea  
 (Caryophyllaceae) using nuclear and chloroplast DNA sequence data.";  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ296122; CAC13007.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 14 14

SQ SEQUENCE 14 AA; 1508 MW; 9B0931E2CF1AB6D1 CRC64;  
 Query Match 16.7%; Score 3; DB 10; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 8.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFT 15  
 ||||  
 Db 2 PFT 4

## RESULT 28

Q9FS91 PRELIMINARY; PRT; 14 AA.

AC Q9FS91;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DE RNA polymerase II (Fragment).  
 GN RPB2.  
 OS Silene sedoides.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.  
 OX NCBI\_TaxID=39790;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Popp M., Oxelman B.;  
 RT "Inferring the history of the polyploid Silene aegaea  
 (Caryophyllaceae) using nuclear and chloroplast DNA sequence data.";  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ296105; CAC13028.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 14 14  
 SQ SEQUENCE 14 AA; 1508 MW; 9B0931E2CF1AB6D1 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 8.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFT 15  
 ||||  
 Db 2 PFT 4

## RESULT 29

Q9R4M8 PRELIMINARY; PRT; 15 AA.

AC Q9R4M8;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DE Catalase isozyme I (Fragment).  
 OS Bacillus firmus.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1399;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=95267795; PubMed=7748885;  
 RA Hicks D.B.;  
 RT "Purification of three catalase isozymes from facultatively  
 alkaliphilic Bacillus firmus OF4.";  
 RL Biochim. Biophys. Acta 1229:347-355(1995).  
 SQ SEQUENCE 15 AA; 1677 MW; 12E47DC8F66876ED CRC64;

Query Match 16.7%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFT 15  
 ||||  
 Db 13 PFT 15

```

RESULT 30
Q9R4U7 PRELIMINARY; PRT; 15 AA.
ID Q9R4U7
AC Q9R4U7;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE Malonate decarboxylase gamma subunit (Fragment).
OS Acinetobacter calcoaceticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=471;
RN [1]_
RP SEQUENCE.
RX MEDLINE=95050812; PubMed=7961952;
RA Kim Y.S., Byun H.S.;
RT "Purification and properties of a novel type of malonate decarboxylase
RT from Acinetobacter calcoaceticus".
RL J. Biol. Chem. 269:29636-29641(1994).
SQ SEQUENCE 15 AA; 1816 MW; 4E14F10E389F9FEA CRC64;

Query Match 16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPK 8
DB 11 FPK 13

RESULT 31
Q9UEK0 PRELIMINARY; PRT; 15 AA.
ID Q9UEK0
AC Q9UEK0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE Renal tissue-nonspecific alkaline phosphatase (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE.
RX MEDLINE=93092315; PubMed=1458595;
RA Nishihara Y., Hayashi Y., Adachi T., Koyama I., Stigbrand T.,
RA Hirano K.;
RT "Chemical nature of intestinal-type alkaline phosphatase in human
RT kidney.";
RL Clin. Chem. 38:2539-2542(1992).
SQ SEQUENCE 15 AA; 1931 MW; 9A28FDE13F01F716 CRC64;

Query Match 16.7%; Score 3; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PKY 9
DB 9 PKY 11

RESULT 32
Q9BXQ0 PRELIMINARY; PRT; 15 AA.
ID Q9BXQ0
AC Q9BXQ0;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Tissue transglutaminase (BC 2.3.2.13) (Fragment).
GN TGM2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Citron B.A., Santa Cruz K.S., Davies P.J.A., Festoff B.W.;
RT "Intron-exon swapping of transglutaminase mRNA and neuronal tau
RT aggregation in Alzheimer's disease.";
RL J. Biol. Chem. 0:0-0(2001).
DR EMBL; AF311286; AAK15272.1; -.
RW Acyltransferase; Transferase.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1641 MW; C340982AFEF851 CRC64;

Query Match 16.7%; Score 3; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EPF 14
DB 2 EPF 4

RESULT 33
Q8IZK4 PRELIMINARY; PRT; 15 AA.
ID Q8IZK4
AC Q8IZK4;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Breast and ovarian cancer susceptibility protein (Fragment).
GN BRCA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RA Valarmathi M.T., Agarwal A., Deo S.S.V., Shukla N.K., Das S.N.;
RT "BRCA1 germline mutations in Indian breast cancer families.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY093484; AAM18218.1; -.
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1807 MW; D156E8F11AB530FB CRC64;

Query Match 16.7%; Score 3; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ESQ 18
DB 10 ESQ 12

RESULT 34
Q8HZ79 PRELIMINARY; PRT; 15 AA.
ID Q8HZ79
AC Q8HZ79;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Alpha-synuclein (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]_
RP SEQUENCE FROM N.A.
RA Tompkins M.M., Gai W.P., Douglas S., Bunn S.J.;
RT "Alpha-synuclein expression localizes to the Golgi apparatus in bovine
RT adrenal medullary chromaffin cells.";

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RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY124580; AM94359.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 15 AA; 1774 MW; 1715433C9115DADA CRC64;

Query Match 16.7%; Score 3; DB 6; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EMP 5  
 DB 1 EMP 3

## RESULT 35

Q9T2G9 ID Q9T2G9 PRELIMINARY; PRT; 15 AA.  
 AC Q9T2G9;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE Carbonic anhydrase (EC 4.2.1.1) (Fragment).  
 OS Solanum tuberosum (Potato).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; lamids; Solanales; Solanaceae; Solanum.  
 OX NCBI\_TaxID=4113;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=96327808; PubMed=8680307;  
 RA Rumeau D., Quine S., Fina L., Gault N., Nicole M., Peltier G.;  
 RT "Subcellular distribution of carbonic anhydrase in Solanum tuberosum  
 L. leaves: characterization of two compartment-specific isoforms.";  
 RL Planta 199;79-88(1996).  
 SQ SEQUENCE 15 AA; 1647 MW; CA5B7063CDD32976 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PVE 12  
 DB 10 PVE 12

## RESULT 36

Q38574 ID Q38574 PRELIMINARY; PRT; 15 AA.  
 AC Q38574;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Lysis protein (Fragment).  
 OS Bacteriophage Kurl.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;  
 OC Levivirus.  
 OX NCBI\_TaxID=12021;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96207403; PubMed=8615017;  
 RA Gronsveld H., Oudot F., van Duin J.V.;  
 RT "RNA phage Kurl has an insertion of 18 nucleotides in the start codon  
 of its lysis gene."  
 RL Virology 218;141-147(1996).  
 DR EMBL; S81763; AAD14372.1; -.  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1736 MW; EA4430EAC749D708 CRC64;

Query Match 16.7%; Score 3; DB 9; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKE 3  
 DB 8 HKE 10

## RESULT 37

Q9FSA5 ID Q9FSA5 PRELIMINARY; PRT; 15 AA.  
 AC Q9FSA5;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE RNA polymerase II (Fragment).  
 GN RPB2.  
 OS Silene cryptoneura.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.  
 OX NCBI\_TaxID=39877;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Popp M., Oxelman B.;  
 RT "Inferring the history of the polyploid Silene aegaea  
 (Caryophyllaceae) using nuclear and chloroplast DNA sequence data."  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ296138; CAC13016.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1621 MW; C96B0931E2CF1AB6 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PPT 15  
 DB 2 PPT 4

## RESULT 38

Q9FSB2 ID Q9FSB2 PRELIMINARY; PRT; 15 AA.  
 AC Q9FSB2;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE RNA polymerase II (Fragment).  
 GN RPB2.  
 OS Silene aegaea.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.  
 OX NCBI\_TaxID=49732;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Popp M., Oxelman B.;  
 RT "Inferring the history of the polyploid Silene aegaea  
 (Caryophyllaceae) using nuclear and chloroplast DNA sequence data."  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ296115; CAC13000.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1633 MW; D3420931E2CF1AB6 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PPT 15  
 DB 2 PPT 4

```
RESULT 39
Q9FS98
ID Q9FS98 PRELIMINARY; PRT; 15 AA.
AC Q9FS98;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE RNA polymerase II (Fragment).
GN RPB2.
OS Silene laconica.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.
OX NCBI_TaxID=49734;
RN [1]
RP SEQUENCE FROM N.A.
RA Popp M., Oxelman B.;
RT "Inferring the history of the polyploid Silene aegaea
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ296136; CAC13020.1; -.
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1596 MW; 2C2EBDCD29DD887C CRC64;

Query Match 16.7%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFT 15
Db 2 PFT 4

RESULT 40
Q9FE13
ID Q9FE13 PRELIMINARY; PRT; 15 AA.
AC Q9FE13;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE RNA polymerase II (Fragment).
GN RPB2.
OS Silene aegaea.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.
OX NCBI_TaxID=49732;
RN [1]
RP SEQUENCE FROM N.A.
RA Popp M., Oxelman B.;
RT "Inferring the history of the polyploid Silene aegaea
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ296128; CAC13013.1; -.
DR EMBL; AJ296113; CAC12998.1; -.
DR EMBL; AJ296116; CAC13001.1; -.
DR EMBL; AJ296117; CAC13002.1; -.
DR EMBL; AJ296118; CAC13003.1; -.
DR EMBL; AJ296119; CAC13004.1; -.
DR EMBL; AJ296120; CAC13005.1; -.
DR EMBL; AJ296121; CAC13006.1; -.
DR EMBL; AJ296123; CAC13008.1; -.
DR EMBL; AJ296125; CAC13010.1; -.
DR EMBL; AJ296126; CAC13011.1; -.
DR EMBL; AJ296127; CAC13012.1; -.
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1621 MW; C96B0931E2CF1AB6 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFT 15
Db 2 PFT 4

RESULT 41
Q9FSA0
ID Q9FSA0 PRELIMINARY; PRT; 15 AA.
AC Q9FSA0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE RNA polymerase II (Fragment).
GN RPB2.
OS Silene haussknechtii.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.
OX NCBI_TaxID=49733;
RN [1]
RP SEQUENCE FROM N.A.
RA Popp M., Oxelman B.;
RT "Inferring the history of the polyploid Silene aegaea
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ296137; CAC13018.1; -.
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1621 MW; C96B0931E2CF1AB6 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFT 15
Db 2 PFT 4

RESULT 42
Q9FS99
ID Q9FS99 PRELIMINARY; PRT; 15 AA.
AC Q9FS99;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE RNA polymerase II (Fragment).
GN RPB2.
OS Silene integrifolia.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Caryophyllaceae; Silene.
OX NCBI_TaxID=39889;
RN [1]
RP SEQUENCE FROM N.A.
RA Popp M., Oxelman B.;
RT "Inferring the history of the polyploid Silene aegaea
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ296135; CAC13019.1; -.
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1621 MW; C96B0931E2CF1AB6 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFT 15
Db 2 PFT 4
```

## RESULT 43

Q9FE15 PRELIMINARY; PRT; 15 AA.  
 AC Q9FE15; (Created)  
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)  
 DE RNA polymerase II (Fragment).  
 GN RPB2.  
 OS Silene sedoides.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllales; Caryophyllaceae; Silene.  
 OX NCBI\_TaxID=39790;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Popp M., Oxelman B.;  
 RT "Inferring the history of the polyploid Silene aegaea  
 (Caryophyllaceae) using nuclear and chloroplast DNA sequence data.";  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ296112; CAC13035.1; -  
 DR EMBL; AJ296104; CAC13027.1; -  
 DR EMBL; AJ296106; CAC13029.1; -  
 DR EMBL; AJ296107; CAC13030.1; -  
 DR EMBL; AJ296108; CAC13031.1; -  
 DR EMBL; AJ296109; CAC13032.1; -  
 DR EMBL; AJ296110; CAC13033.1; -  
 DR EMBL; AJ296111; CAC13034.1; -  
 FT NON\_TER 1  
 FT NON\_TER 15  
 SQ SEQUENCE 15 AA; 1621 MW; C96B0931E2CF1AB6 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFT 15  
 Db 2 PFT 4

## RESULT 44

Q9FE14 PRELIMINARY; PRT; 15 AA.  
 AC Q9FE14; (Created)  
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)  
 DE RNA polymerase II (Fragment).  
 GN RPB2.  
 OS Silene pentelica.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllales; Caryophyllaceae; Silene.  
 OX NCBI\_TaxID=49735;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Popp M., Oxelman B.;  
 RT "Inferring the history of the polyploid Silene aegaea  
 (Caryophyllaceae) using nuclear and chloroplast DNA sequence data.";  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ296134; CAC13026.1; -  
 DR EMBL; AJ296129; CAC13022.1; -  
 FT NON\_TER 1  
 FT NON\_TER 15  
 SQ SEQUENCE 15 AA; 1621 MW; C96B0931E2CF1AB6 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFT 15

## Db 2 PFT 4

## RESULT 45

Q9FS80 PRELIMINARY; PRT; 15 AA.  
 AC Q9FS80; (Created)  
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)  
 DE RNA polymerase II (Fragment).  
 GN RPB2.  
 OS Silene zawadskii (Zawadskii's campion).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllales; Caryophyllaceae; Silene.  
 OX NCBI\_TaxID=39923;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Popp M., Oxelman B.;  
 RT "Inferring the history of the polyploid Silene aegaea  
 (Caryophyllaceae) using nuclear and chloroplast DNA sequence data.";  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ296141; CAC13039.1; -  
 FT NON\_TER 1  
 FT NON\_TER 15  
 SQ SEQUENCE 15 AA; 1621 MW; C96B0931E2CF1AB6 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFT 15  
 Db 2 PFT 4

## RESULT 46

Q9FSB0 PRELIMINARY; PRT; 15 AA.  
 AC Q9FSB0; (Created)  
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)  
 DE RNA polymerase II (Fragment).  
 GN RPB2.  
 OS Silene aegaea.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllales; Caryophyllaceae; Silene.  
 OX NCBI\_TaxID=49732;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Popp M., Oxelman B.;  
 RT "Inferring the history of the polyploid Silene aegaea  
 (Caryophyllaceae) using nuclear and chloroplast DNA sequence data.";  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ296124; CAC13009.1; -  
 FT NON\_TER 1  
 FT NON\_TER 15  
 SQ SEQUENCE 15 AA; 1616 MW; C96B0931E2CF0AF6 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFT 15  
 Db 2 PFT 4

## RESULT 47

Q9PRM3  
ID Q9PRM3 PRELIMINARY; PRT; 15 AA.  
AC Q9PRM3  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE 17 kDa major immunophilin (Fragment).  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCECB.  
RX MEDLINE=94072550; PubMed=7504525;  
RA Yem A.W., Reardon I.M., Leone J.W., Reinrikson R.L., Deibel M.R.Jr.;  
RT "An active FK506-binding domain of 17,000 daltons is isolated  
following limited proteolysis of chicken thymus hsp56.";  
RL Biochemistry 32:12571-12576(1993)  
SQ SEQUENCE 15 AA; 1606 MW; 6269732398D1B71C CRC64;

Query Match 16.7%; Score 3; DB 13; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17  
Db |||  
7 TES 9

RESULT 48  
Q9RAJ0  
ID Q9RAJ0 PRELIMINARY; PRT; 16 AA.  
AC Q9RAJ0  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
DE LIMONATE dehydrogenase (Fragment).  
OS Arthrobacter globiformis.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Micrococccineae; Micrococccaceae; Arthrobacter.  
OX NCBI\_TaxID=1665;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=96045380; PubMed=7546548;  
RA Subayda C.G., Omura M., Hasegawa S.;  
RT "Limonate dehydrogenase from Arthrobacter globiformis: the native  
enzyme and its N-terminal sequence.";  
RL Phytochemistry 40:17-20(1995).  
SQ SEQUENCE 16 AA; 1759 MW; 514B2DE906FD5984 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MPF 6  
Db |||  
1 MPF 3

RESULT 49  
Q9RAJ4  
ID Q9RAJ4 PRELIMINARY; PRT; 16 AA.  
AC Q9RAJ4  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE Peptidyl-ASP metalloendopeptidase (Fragment).  
OS Pseudomonas fragi.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Pseudomonas.  
OX NCBI\_TaxID=296;  
RN [1]

QY 15 TES 17  
Db |||  
11 TES 13

RESULT 50  
Q44610  
ID Q44610 PRELIMINARY; PRT; 16 AA.  
AC Q44610  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
DE Shikimate dehydrogenase (Fragment).  
GN ARCE.  
OS Buchnera aphidicola.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Buchnera.  
OX NCBI\_TaxID=9;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95212914; PubMed=7535281;  
RA Roubakhan D., Baumann P.;  
RT "Characterization of a putative 23S-5S rRNA operon of Buchnera  
aphidicola (endosymbiont of aphids) unlinked to the 16S rRNA-encoding  
gene.";  
RL Gene 155:107-112(1995).  
DR ENBL: U10499; AAA79128.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 16 AA; 1891 MW; 72A8175598D30DF1 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPK 8  
Db |||  
9 FPK 11

RESULT 51  
Q9R514  
ID Q9R514 PRELIMINARY; PRT; 16 AA.  
AC Q9R514  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE 17 kDa lysine-specific cysteine proteinase (Fragment).  
OS Porphyromonas gingivalis (Bacteroides gingivalis).  
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;  
OC Porphyromonadaceae; Porphyromonas.  
OX NCBI\_TaxID=837;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=94103245; PubMed=8276827;  
RA Pike R., McGraw W., Potempa J., Travis J.;  
RT "Lysine- and arginine-specific proteinases from Porphyromonas  
gingivalis. Isolation, characterization, and evidence for the existence  
of complexes with hemagglutinins.";  
RL J. Biol. Chem. 269:406-411(1994).  
SQ SEQUENCE 16 AA; 1819 MW; D864F9BF367828C6 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 16;

Best Local Similarity 100.0%; Pred. No. 9e+03; Mismatches 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0

Qy 14 FTE 16  
Db 3 FTE 5

RESULT 52

Q8KLP7 ID Q8KLP7 PRELIMINARY; PRT; 16 AA.  
AC Q8KLP7;  
DT 01-OCT-2002 (TREMBlrel. 22, Created)  
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
DE Adenosine phosphotransferase (Fragment).  
GN APT.  
OS Streptomyces griseus.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomycineae; Streptomycetaceae; Streptomycetes.  
OX NCBI\_TaxID=1911;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=N2-3-11;  
RA Wehmeier U.F.;  
RT "Analysis of the secD genes from Streptomyces griseus N2-3-11.";  
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.  
DE EMBL; AF503986; CAD44524.1; -.  
KW Transferase.  
FT NON TER 16 16  
SQ SEQUENCE 16 AA; 1838 MW; 5B369FE66365B45F CRC64;

Query Match

Best Local Similarity 16.7%; Score 3; DB 2; Length 16;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TES 17  
Db 5 TES 7

RESULT 53

P82597 ID P82597 PRELIMINARY; PRT; 16 AA.  
AC P82597;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE The most stable monoacylglycerol lipase (MGLP) (24 kDa) (EC 3.1.1.23) (Fragment).  
OS Bacillus sp.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1409;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=H-257;  
RA MEDLINE=20198254; PubMed=10731713;  
RA Imamura S.; Kitaura S.;  
RT "Purification and characterization of a monoacylglycerol lipase from the moderately thermophilic Bacillus sp. H-257.";  
RL J. Biochem. 127:419-425(2000).  
CC -!- FUNCTION: HYDROLYZES MONOACYLGLYCEROLS, WITH THE HIGHEST ACTIVITY OCCURRING WITH 1-MONOLAUROYLGLYCEROL.  
CC -!- ENZYME REGULATION: NOT INHIBITED BY CHOLATE, BUT SLIGHTLY INHIBITED BY TRITON X-100 AND DEOXYCHOLATE.  
CC -!- SUBUNIT: MONOMER.  
CC -!- MISCELLANEOUS: HAS AN ISOELECTRIC POINT OF 4.66. OPTIMUM TEMPERATURE IS 75 DEGREES CELSIUS AND MAXIMUM ACTIVITY AT PH 6-8.  
CC -!- MISCELLANEOUS: THIS LIPASE IS NOT SECRETED EXTRACELLULARLY AS OTHER BACTERIAL LIPASES.  
KW Hydrolase.  
FT NON TER 16 16  
SQ SEQUENCE 16 AA; 1787 MW; 900CF59289521D8F CRC64;

Query Match

Best Local Similarity 100.0%; Pred. No. 9e+03; Length 16;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 YPV 11  
Db 4 YPV 6

RESULT 54

Q9UBQ9 ID Q9UBQ9 PRELIMINARY; PRT; 16 AA.  
AC Q9UBQ9;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE Apolipoprotein (A) (Fragment).  
GN APOA2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93163698; PubMed=7679504;  
RA Wade D.P.; Clarke J.G.; Lindahl G.E.; Liu A.C.; Zysow B.R.; Meer K.; Schwartz K.; Lawn R.M.;  
RT "5' control regions of the apolipoprotein(a) gene and members of the related plasminogen gene family.";  
RL Proc. Natl. Acad. Sci. U.S.A. 90:1369-1373(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93087573; PubMed=1454851;  
RA Magaretti N.; Acquati P.; Magnaghi P.; Bruno L.; Pontoglio M.; Rocchi M.; Saccone S.; Della Valle G.; D'Urso M.; Lepaslier D.; Ottolenghi S.; Taramelli R.;  
RT "Characterization by yeast artificial chromosome cloning of the linked apolipoprotein(a) and plasminogen genes and identification of the apolipoprotein(a) 5' flanking region.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:11584-11588(1992).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91097523; PubMed=2268308;  
RA Magaretti N.; Bruno L.; Pontoglio M.; Candiani G.; Meroni G.; Ottolenghi S.; Taramelli R.;  
RT "Definition of the transcription initiation site of human plasminogen gene in liver and non hepatic cell lines.";  
RL Biochem. Biophys. Res. Commun. 173:1013-1018(1990).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92207924; PubMed=1554698;  
RA Ichinose A.;  
RT "Multiple members of the plasminogen-apolipoprotein(a) gene family associated with thrombosis.";  
RL Biochemistry 31:3113-3118(1992).  
DR EMBL; L07899; AAB66587.2; -.  
DR EMBL; M90079; AAA35546.1; -.  
DR EMBL; M90078; AAA35547.1; -.  
DR EMBL; M62890; AAA36454.1; -.  
DR EMBL; M86878; AAA51749.1; -.  
DR EMBL; M86877; AAB49909.1; -.  
KW Lipoprotein.  
FT NON TER 16 16  
SQ SEQUENCE 16 AA; 1912 MW; 66BDFBF28EDB1A69 CRC64;

Query Match

Best Local Similarity 16.7%; Score 3; DB 4; Length 16;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKE 3  
Db 3 HKE 5



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RESULT 55
Q95M73 PRELIMINARY; PRT; 16 AA.
AC Q95M73
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Apolipoprotein (Fragment).
GN A.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=211303645; PubMed=11301336;
RA Huby T., Dachtel C., Lawn R.M., Wickings J., Chapman M.J., Thillet J.;
RT "Functional analysis of the chimpanzee and human apo(a) promoter
RT sequences. Identification of sequence variations responsible for
RT elevated transcriptional activity in chimpanzee."
RL J. Biol. Chem. 276:22209-22214(2001).
DR EMBL; AY028467; AAK38764.1; -.
KW Lipoprotein.
FT NON_TER
SQ SEQUENCE 16 AA; 1912 MW; 68BDFEF28EDB1A69 CRC64;

Query Match 16.7%; Score 3; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKE 3
DB 3 HKE 5

RESULT 56
Q9TRK9 PRELIMINARY; PRT; 16 AA.
AC Q9TRK9
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Casein kinase II-24 kDa polypeptide (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RX MEDLINE=93054738; PubMed=1331100;
RA Ou W.J., Thomas D.Y., Bell A.W., Bergeron J.J.;
RT "Casein kinase II phosphorylation of signal sequence receptor alpha
RT and the associated membrane chaperone calnexin."
RL J. Biol. Chem. 267:23789-23796(1992).
FT NON_TER
SQ SEQUENCE 16 AA; 2053 MW; F31011034124F59B CRC64;

Query Match 16.7%; Score 3; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EPF 14
DB 6 EPF 8

RESULT 57
Q8HU42 PRELIMINARY; PRT; 16 AA.
AC Q8HU42
DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DE Lectin (DRL) (Fragment).
RN [1]
RP SEQUENCE FROM N.A.
RX Muschner V.C., Lorenz A.P., Scherer N.M., Souza-Chies T.T.,
RA Cervi A.C., Salzano F.M., Bonatto S.L., Freitas L.B.;
RT "Comparative Phylogenetic Analysis of Nuclear and Plastid Sequences in
RT Eucotyledons; core eudicots; Rosidae;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY032819; AAK69795.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 16 AA; 1676 MW; 4A810A81DD549D80 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFT 15
DB 12 PFT 14

RESULT 58
Q8HU29 PRELIMINARY; PRT; 16 AA.
AC Q8HU29
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE PeBA (Fragment).
OS Passiflora haematostigma.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eurosids I; Malpighiales; Passifloraceae; Passiflora.
OX NCBI_TaxID=159429;
RN [1]
RP SEQUENCE FROM N.A.
RX Muschner V.C., Lorenz A.P., Scherer N.M., Souza-Chies T.T.,
RA Cervi A.C., Salzano F.M., Bonatto S.L., Freitas L.B.;
RT "Comparative Phylogenetic Analysis of Nuclear and Plastid Sequences in
RT Passiflora (Passifloraceae).";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY032819; AAK69795.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 16 AA; 1676 MW; 4A810A81DD549D80 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFT 15
DB 12 PFT 14

RESULT 59
P83511 PRELIMINARY; PRT; 16 AA.
AC P83511
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Lectin (DRL) (Fragment).
RN [1]
RP SEQUENCE FROM N.A.
RX Muschner V.C., Lorenz A.P., Scherer N.M., Souza-Chies T.T.,
RA Cervi A.C., Salzano F.M., Bonatto S.L., Freitas L.B.;
RT "Comparative Phylogenetic Analysis of Nuclear and Plastid Sequences in
RT Passiflora (Passifloraceae).";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY032819; AAK69795.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 16 AA; 1676 MW; 4A810A81DD549D80 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFT 15
DB 12 PFT 14
```

OS	Delonix regia (Royal poinciana).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC	eurosid I; Fabales; Fabaceae; Caesalpinioideae; Caesalpinieae;
OC	Delonix.
OX	NCBI_TaxID=72433;
EN	[1]
RP	SEQUENCE, AND CHARACTERIZATION.
RX	TISSUE=Seed;
RX	PubMed=12168698;
RA	Pando S.C., Macedo M.L.R., Freire M.G.M., Toyama M.H., Novello J.C.,
RA	Marangoni S.;
RT	"Biochemical characterization of a lectin from Delonix regia seeds.";
RL	J. Protein Chem. 21:279-285(2002).
CC	-!- FUNCTION: GLUCOSE-SPECIFIC LECTIN.
CC	-!- SUBUNIT: MONOMER.
CC	-!- MISCELLANEOUS: OPTIMAL PH IS 8.0-9.0. ACTIVE UP TO 60 DEGREES
CC	CELSIUS.
CC	-!- MISCELLANEOUS: REQUIRES MANGANESE BUT NOT CALCIUM IONS FOR CELL-
CC	AGGLUTINATING ACTIVITY.
CC	-!- SIMILARITY: BELONGS TO THE LEGUMINOUS LECTIN FAMILY.
DR	InterPro; IPRO01220; Lectin legB.
DR	PROSITE; PS00307; LECTIN LEGUME_BETA; PARTIAL.
KW	Lectin; Glycoprotein; Manganese.
FT	NON_TER 16
FT	SEQUENCE 16 AA; 1816 MW; D3DA3A36D1C308BE CRC64;
SQ	
Query Match	16.7%; Score 3; DB 10; Length 16;
Best Local Similarity	100.0%; Pred. No. 9e+03;
Matches	3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	6 FPK 8 
Dd	5 FPK 7 
RESULT 60	
ID	QCIS2 PRELIMINARY; PRT; 16 AA.
AC	QCIS2;
DT	01-MAR-2003 (TrEMBLrel. 23, Created)
DT	01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE	Plasminogen (Fragment).
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=129/SVJ; TISSUE=Liver;
RX	PubMed=12149246;
RA	Bannach F.G., Gutierrez A., Fowler B.J., Bugge T.H., Degen J.L.,
RA	Parmer R.J., Miles L.A.;
RT	"Localization of Regulatory Elements Mediating Constitutive and
RT	Cytokine-stimulated Plasminogen Gene Expression.";
RL	J. Biol. Chem. 277:38579-38588(2002).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN=129/SVJ; TISSUE=Liver;
RA	Garcia Bannach F., Fowler B.J., Gutierrez A., Bugge T.H., Degen J.L.,
RA	Parmer R.J., Miles L.A.;
RL	Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AY134430; AAN15805.1; -
FT	NON_TER 16
FT	SEQUENCE 16 AA; 1922 MW; 647558FC6EDB15CC CRC64;
SQ	
Query Match	16.7%; Score 3; DB 11; Length 16;
Best Local Similarity	100.0%; Pred. No. 9e+03;
Matches	3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 HKE 3 

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RESULT 63
Q9UC43
ID Q9UC43 PRELIMINARY; PRT; 17 AA.
AC Q9UC43;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Interferon-alpha-induced protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=96132854; PubMed=8557639;
RA Rich S.A., Bose M., Tempest P., Rudofsky U.H.;
RT "Purification, macrosequencing, and immunolocalization of p36, a new
RT interferon-alpha-induced protein that is associated with human lupus
RT inclusions.";
RL J. Biol. Chem. 271:1118-1126(1996).
SQ SEQUENCE 17 AA; 2027 MW; 762BE7300049ACBC CRC64;

Query Match 16.7%; Score 3; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KYP 10
DB 15 KYP 17

RESULT 64
Q9TRH5
ID Q9TRH5 PRELIMINARY; PRT; 17 AA.
AC Q9TRH5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Alpha-S1-casein homolog (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=93231344; PubMed=1299613;
RA Neuteboom B., Gluffrida M.G., Conti A.;
RT "Isolation of a new ligand-carrying casein fragment from bovine
RT mammary gland microsomes.";
RL FEBS Lett. 305:189-191(1992).
SQ SEQUENCE 17 AA; 1950 MW; 8890EF0685A0537F CRC64;

Query Match 16.7%; Score 3; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PFP 7
DB 4 PFP 6

RESULT 65
Q9SM49
ID Q9SM49 PRELIMINARY; PRT; 17 AA.
AC Q9SM49;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Acetyl-CoA-carboxylase alpha (EC 6.4.1.2) (Fragment).
GN ACC1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

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OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Mao J., Molenaar A., Wheeler T.T., Seyfert H.M.;
RT "STAT5-binding is mandatory for lactational stimulation of the bovine
RT promoter PIII of the Acetyl-Coenzyme A-Carboxylase alpha-encoding gene
RT in the mammary gland but not in other tissues.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBSJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Mao J.;
RL Thesis (2001), Department of Biological Sciences,
RL University of Rostock, Rostock, Germany.
DR EMBL; AJ312201; CAC59690.1; -.
KW Ligase.
FT NON TER 17 17
SQ SEQUENCE 17 AA; 2082 MW; 0B379CCF0A078E55 CRC64;

Query Match 16.7%; Score 3; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KEM 4
DB 9 KEM 11

RESULT 66
Q36741
ID Q36741 PRELIMINARY; PRT; 17 AA.
AC Q36741;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Glutaryl CoA dehydrogenase (Fragment).
GN GCDH.
OS Homo sapiens (Human).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95315953; PubMed=7795610;
RA Greenberg C.R., Reimer D., Singal R., Triggs-Raine B., Chudley A.E.,
RA Dilling L.A., Phillips S., Haworth J.C., Seargeant L.E., Goodman S.I.;
RT "A G-to-T transversion at the +5 position of intron 1 in the glutaryl
RT CoA dehydrogenase gene is associated with the Island Lake variant of
RT glutaric acidemia type I.";
RL Hum. Mol. Genet. 4:493-495(1995).
DR EMBL; S77773; AAB34724.2; -.
KW Mitochondrion.
FT NON TER 1 1
SQ SEQUENCE 17 AA; 1896 MW; 4D77B628C59A9E32 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17
DB 7 TES 9

RESULT 67
Q9S8Y2
ID Q9S8Y2 PRELIMINARY; PRT; 17 AA.
AC Q9S8Y2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
```

DE L-asparaginase isoform A (EC 3.5.1.1) (Fragment).  
OS *Lupinus arboreus* (Tree lupine).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Genisteae; Lupinus.  
OX NCBI\_TaxID=3872;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92344803; PubMed=1368361;  
RA Lough T.J., Chang K.S., Carne A., Monk B.C., Reynolds P.H.,  
RA Farnden K.J.;  
RL Phytochemistry 31:1519-1527(1992).  
FT NON\_TER 1  
FT NON\_TER 17  
SQ SEQUENCE 17 AA; 1877 MW; DB7925924D5F46AF CRC64;  
Query Match 16.7%; Score 3; DB 10; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 4 MPF 6  
Db 3 MEF 5  
RESULT 68  
Q9QVS7 PRELIMINARY; PRT; 17 AA.  
AC Q9QVS7;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Lactate dehydrogenase-A (Fragment).  
OS Mus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10095;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95201434; PubMed=7534515;  
RA Sandulache R., Pretsch W., Chatterjee B., Gimbel W., Graw J.,  
RA FAVOR J.;  
RT "Molecular analysis of four lactate dehydrogenase-A mutants in the  
RT mouse";  
RL Mamm. Genome 5:777-780(1994).  
SQ SEQUENCE 17 AA; 1982 MW; E941E0A3F2477D45 CRC64;  
Query Match 16.7%; Score 3; DB 11; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 HKE 3  
Db 11 HKE 13  
RESULT 69  
Q9IHG7 PRELIMINARY; PRT; 17 AA.  
AC Q9IHG7;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
DE Core protein 2C (Fragment).  
OS Human poliovirus 1.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;  
OC Enterovirus.  
OX NCBI\_TaxID=12080;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=6013TAJ94;  
RL "Evolution of circulating wild poliovirus and of vaccine-derived  
RA poliovirus in an immunodeficient patient: a unifying model.";  
RA J. Virol. 74:7381-7390(2000).  
RA Gavrillin G.V., Cherkasova E.A., Lipskaya G.Y., Kew O.M., Agol V.I.;

RT "Evolution of circulating wild poliovirus and of vaccine-derived  
RT poliovirus in an immunodeficient patient: a unifying model.";  
RL J. Virol. 74:7381-7390(2000).  
DR EMBL; AF233188; AAF35092.1; -.  
FT NON\_TER 1  
FT NON\_TER 17  
SQ SEQUENCE 17 AA; 1840 MW; 004DEB22D713051 CRC64;  
Query Match 16.7%; Score 3; DB 12; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 14 FTE 16  
Db 8 FTE 10  
RESULT 70  
Q9IHH9 PRELIMINARY; PRT; 17 AA.  
AC Q9IHH9;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
DE Core protein 2C (Fragment).  
OS Human poliovirus 1.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;  
OC Enterovirus.  
OX NCBI\_TaxID=12080;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=6427ING95;  
RA MEDLINE=20366294; PubMed=10906191;  
RA Gavrillin G.V., Cherkasova E.A., Lipskaya G.Y., Kew O.M., Agol V.I.;  
RT "Evolution of circulating wild poliovirus and of vaccine-derived  
RT poliovirus in an immunodeficient patient: a unifying model.";  
RL J. Virol. 74:7381-7390(2000).  
DR EMBL; AF233176; AAF35080.1; -.  
FT NON\_TER 1  
FT NON\_TER 17  
SQ SEQUENCE 17 AA; 1826 MW; 6B3DEB22D713050 CRC64;  
Query Match 16.7%; Score 3; DB 12; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 14 FTE 16  
Db 8 FTE 10  
RESULT 71  
Q9IHG4 PRELIMINARY; PRT; 17 AA.  
AC Q9IHG4;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
DE Core protein 2C (Fragment).  
OS Human poliovirus 1.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;  
OC Enterovirus.  
OX NCBI\_TaxID=12080;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=6433PAK95;  
RA MEDLINE=20366294; PubMed=10906191;  
RA Gavrillin G.V., Cherkasova E.A., Lipskaya G.Y., Kew O.M., Agol V.I.;  
RT "Evolution of circulating wild poliovirus and of vaccine-derived  
RT poliovirus in an immunodeficient patient: a unifying model.";  
RL J. Virol. 74:7381-7390(2000).  
DR EMBL; AF233191; AAF35095.1; -.  
FT NON\_TER 1

```
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1826 MW; 6B3DEB222D713050 CRC64;

Query Match 16.7%; Score 3; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FTE 16
DB 8 FTE 10

RESULT 72
Q9IHI7 PRELIMINARY; PRT; 17 AA.
AC Q9IHI7;
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DE Core protein 2C (Fragment).
OS Human poliovirus 1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus.
OX NCBI_TaxID=12080;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3038USA82DI58;
RX MEDLINE=20366294; PubMed=10906191;
RA Gavrilin G.V., Cherkasova E.A., Lipskaya G.Y., Kew O.M., Agol V.I.;
RT "Evolution of circulating wild poliovirus and of vaccine-derived
poliovirus in an immunodeficient patient: a unifying model.";
RL J. Virol. 74:7381-7390(2000).
DR EMBL; AF233168; AAF35072.1; -.
FT NON_TER 1 1
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1826 MW; 6B3DEB222D713050 CRC64;

Query Match 16.7%; Score 3; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FTE 16
DB 8 FTE 10

RESULT 73
Q9IHH4 PRELIMINARY; PRT; 17 AA.
AC Q9IHH4;
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DE Core protein 2C (Fragment).
OS Human poliovirus 1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus.
OX NCBI_TaxID=12080;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=7TAJ91;
RX MEDLINE=20366294; PubMed=10906191;
RA Gavrilin G.V., Cherkasova E.A., Lipskaya G.Y., Kew O.M., Agol V.I.;
RT "Evolution of circulating wild poliovirus and of vaccine-derived
poliovirus in an immunodeficient patient: a unifying model.";
RL J. Virol. 74:7381-7390(2000).
DR EMBL; AF233181; AAF35085.1; -.
FT NON_TER 1 1
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1826 MW; 6B3DEB222D713050 CRC64;

Query Match 16.7%; Score 3; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FTE 16
DB 8 FTE 10

RESULT 74
Q9IHI9 PRELIMINARY; PRT; 17 AA.
AC Q9IHI9;
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DE Core protein 2C (Fragment).
OS Human poliovirus 1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus.
OX NCBI_TaxID=12080;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2677USA81D48;
RX MEDLINE=20366294; PubMed=10906191;
RA Gavrilin G.V., Cherkasova E.A., Lipskaya G.Y., Kew O.M., Agol V.I.;
RT "Evolution of circulating wild poliovirus and of vaccine-derived
poliovirus in an immunodeficient patient: a unifying model.";
RL J. Virol. 74:7381-7390(2000).
DR EMBL; AF233166; AAF35070.1; -.
FT NON_TER 1 1
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1826 MW; 6B3DEB222D713050 CRC64;

Query Match 16.7%; Score 3; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FTE 16
DB 8 FTE 10

RESULT 75
Q9IHI4 PRELIMINARY; PRT; 17 AA.
AC Q9IHI4;
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DE Core protein 2C (Fragment).
OS Human poliovirus 1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus.
OX NCBI_TaxID=12080;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=422RUS91;
RX MEDLINE=20366294; PubMed=10906191;
RA Gavrilin G.V., Cherkasova E.A., Lipskaya G.Y., Kew O.M., Agol V.I.;
RT "Evolution of circulating wild poliovirus and of vaccine-derived
poliovirus in an immunodeficient patient: a unifying model.";
RL J. Virol. 74:7381-7390(2000).
DR EMBL; AF233171; AAF35075.1; -.
FT NON_TER 1 1
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1826 MW; 6B3DEB222D713050 CRC64;

Query Match 16.7%; Score 3; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FTE 16
DB 8 FTE 10
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Search completed: November 25, 2003, 19:34:00  
Job time : 34.8023 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:16:09 ; Search time 45.9419 Seconds  
(without alignments)  
62.189 Million cell updates/sec

Title: US-09-641-801-22

Perfect score: 18

Sequence: 1 HKMPFPKYPVPTESQ 18

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : A\_Geneseq\_19Jun03.\*

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23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	22	Colostrinin derive
2	18	100.0	18	22	Colostrinin peptid
3	18	100.0	18	22	Colostrinin peptid
4	18	100.0	18	22	Ewe colostrinin pe
5	18	100.0	18	23	Colostrinin consti
6	18	100.0	18	23	Colostrinin consti
7	18	100.0	18	23	Neural cell regula
8	11	61.1	14	15	Hypotensive polype
9	10	55.6	11	17	CNS-inhibiting pep

10	10	55.6	13	17	AAW03291	CNS-inhibiting pep
11	7	38.9	7	23	ABG32211	Sheep colostrinin
12	6	33.3	6	17	AAW03289	CNS-inhibiting pep
13	6	33.3	6	23	ABG32212	Sheep colostrinin
14	6	33.3	15	15	AAR58330	Hypotensive polype
15	5	27.8	10	22	AAE07187	Colostrinin peptid
16	5	27.8	10	22	AAE07197	Colostrinin peptid
17	5	27.8	14	22	AAG96055	Modified colostrin
18	5	27.8	15	22	AAE07187	Human SNP associat
19	5	27.8	15	22	AAE07187	Colostrinin deriv
20	5	27.8	15	22	AAE07187	Colostrinin peptid
21	5	27.8	15	22	AAE07187	Colostrinin pe
22	5	27.8	15	23	AAE07187	Colostrinin consti
23	5	27.8	15	23	AAE07187	Colostrinin consti
24	5	27.8	15	23	AAE07187	Neural cell regula
25	5	27.8	16	22	AAE07187	Ewe colostrinin pe
26	4	22.2	5	19	AAE07187	Polypyril inhibit
27	4	22.2	6	20	AAE07187	Cellulase EGIII-11
28	4	22.2	6	21	AAE07187	EGIII-like cellula
29	4	22.2	6	23	AAU77071	Endoglucanase EGII
30	4	22.2	6	23	AAU77071	EGIII-like cellula
31	4	22.2	6	23	AAU77071	Endoglucanase III
32	4	22.2	7	16	AAW21388	Plasminogen activa
33	4	22.2	7	21	AAW21388	Arabidopsis AHAS s
34	4	22.2	8	16	AAE61422	Pr4-related octape
35	4	22.2	8	17	AAW05539	Peptide fragment #
36	4	22.2	8	19	AAW58608	Platelet factor 4
37	4	22.2	9	21	AAW58608	Human B99-1 HLA B*
38	4	22.2	9	21	AAW58608	Human B99-1 HLA B*
39	4	22.2	9	21	AAW58608	Hepatitis B virus
40	4	22.2	9	21	AAW58608	Human MHC class I
41	4	22.2	9	22	AAW44524	Human MHC class I
42	4	22.2	9	22	AAW44524	Human MHC class I
43	4	22.2	9	22	AAW44524	Human MHC molecule
44	4	22.2	9	22	AAW44524	Human MHC molecule
45	4	22.2	9	23	AAU94282	Human novel protei
46	4	22.2	9	23	AAU94282	Human novel protei
47	4	22.2	9	23	AAU94282	Human novel protei
48	4	22.2	9	24	ABU20159	MHC binding peptid
49	4	22.2	10	21	AAU94204	Human cytotoxic T
50	4	22.2	10	22	AAW68075	Antitumour cancer
51	4	22.2	10	22	AAW68075	HLA class I bindin
52	4	22.2	10	22	AAW68075	Human melanoma ass
53	4	22.2	10	22	AAW68075	Human MHC class I
54	4	22.2	10	22	AAW68075	Human MHC class I
55	4	22.2	10	22	AAW68075	Human MHC molecule
56	4	22.2	10	22	AAW68075	Human MHC molecule
57	4	22.2	10	22	AAW68075	Human MHC molecule
58	4	22.2	10	22	AAW68075	Human MHC molecule
59	4	22.2	10	22	AAW68075	Human MHC molecule
60	4	22.2	10	23	AAO17822	Sponge okadaic aci
61	4	22.2	10	23	AAU94390	Human novel protei
62	4	22.2	10	23	AAU94412	Human novel protei
63	4	22.2	10	23	AAU95356	Human novel protei
64	4	22.2	10	23	AAU95384	Human novel protei
65	4	22.2	10	24	ABR47212	Staphylococcus aur
66	4	22.2	10	24	ABR47239	Staphylococcus aur
67	4	22.2	10	24	ABR47292	Staphylococcus aur
68	4	22.2	10	24	ABR47319	Staphylococcus aur
69	4	22.2	11	14	AAE41812	M13TMD1 mutated fr
70	4	22.2	11	15	AAE52835	Streptolysin O pep
71	4	22.2	12	21	AAE23183	Hsp47-binding hydr
72	4	22.2	12	23	AAE57781	Bovine DNaseI pept
73	4	22.2	12	23	AAE57781	Epitopic peptide b
74	4	22.2	12	23	AAE57781	Human ADPI tryptic
75	4	22.2	13	15	ABG67387	Bacillus thuringie
76	4	22.2	13	17	AAE91853	European corn bore
77	4	22.2	13	18	AAW19525	B. thuringiensis p
78	4	22.2	13	19	AAW80325	Bacillus thuringie
79	4	22.2	13	19	AAW80325	N-terminal amino a
80	4	22.2	13	23	AAE26715	Human MIST protein
81	4	22.2	13	23	AAE26715	Human MIST protein
82	4	22.2	14	16	AAE58799	Human phospholip
	4	22.2	14	20	AAE58799	Rheumatoid arthrit

83 4 22.2 14 22 AAM98010 Human peptide #128  
 84 4 22.2 14 22 AAU28525 DPI tryptic digest  
 85 4 22.2 14 22 AAU26171 Depression-Asocia  
 86 4 22.2 14 23 ABG96070 Cysteine-containin  
 87 4 22.2 14 24 ABP57207 Breast cancer asso  
 88 4 22.2 15 16 AAR70027 Hydroxylamin pepti  
 89 4 22.2 15 16 AAR79630 Endocarditis speci  
 90 4 22.2 15 16 AAR79631 Endocarditis speci  
 91 4 22.2 15 21 AAY93322 Antigenic peptide  
 92 4 22.2 15 21 AAY93322 Antigenic peptide  
 93 4 22.2 15 21 AAY76361 Fragment of human  
 94 4 22.2 15 22 ABP24630 HIV DR super motif  
 95 4 22.2 15 22 AAB72253 Colostrinin derive  
 96 4 22.2 15 22 AAB72507 Colostrinin peptid  
 97 4 22.2 15 22 AAB72539 Colostrinin peptid  
 98 4 22.2 15 22 AAB59313 Ewe colostrinin pe  
 99 4 22.2 15 23 ABP58951 Human macroprotein  
 100 4 22.2 15 23 AAC26556 Human macroprotein

## ALIGNMENTS

RESULT 1  
 AAB72267  
 ID AAB72267 standard; peptide; 18 AA.  
 XX  
 AC AAB72267;  
 XX  
 DT 14-MAY-2001 (first entry)  
 XX  
 DE Colostrinin derived cytokine inducing peptide SEQ ID 22.  
 XX  
 KW Colostrinin; immune response; cytokine; blood cell proliferation;  
 KW central nervous system disorder; neurological disorder; mental disorder;  
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;  
 KW neurosis; infection.  
 XX  
 OS Synthetic.  
 XX  
 PN WO20011937-A2.  
 XX  
 XX  
 PD 22-FEB-2001.  
 XX  
 PF 17-AUG-2000; 2000WO-US22818.  
 XX  
 PR 17-AUG-1999; 99US-0149311.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 PA (REGG-) REGEN THERAPEUTICS PLC.  
 XX  
 PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
 XX WPI; 2001-202804/20.  
 XX  
 PT Inducing a cytokine and modulating an immune response, useful for  
 PT treating central nervous system diseases and bacterial and viral  
 PT infections, comprises administering colostrinin as an immunological  
 PT regulator -  
 XX  
 PS Claim 1; Page 34; 50pp; English.  
 XX  
 CC Sequences AAB72246 - AAB72275 represent peptides derived from clostrinin,  
 CC a proline rich polypeptide aggregate contained in colostrum. The  
 CC peptides have immune response modulatory activity, and are capable of  
 CC inducing cytokines. Colostrinin and its derived peptides are useful for  
 CC inducing cytokine production, for modulating an immunological response  
 CC and for inducing blood cell proliferation. The peptides are useful in the  
 CC treatment of disorders of the central nervous system, neurological  
 CC disorders, mental disorders, dementia, neurodegenerative diseases,  
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic  
 CC disorders of the immune system, bacterial and viral infections and  
 CC acquired immunological deficiencies.

XX  
 SQ Sequence 18 AA;  
 Query Match 100.0%; Score 18; DB 22; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-13;  
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 DB 1 HKEMPFPKYPVEPFTESQ 18  
 ||||||||||||||||  
 RESULT 2  
 AAB72520  
 ID AAB72520 standard; Peptide; 18 AA.  
 XX  
 AC AAB72520;  
 XX  
 DT 09-MAY-2001 (first entry)  
 XX  
 DE Colostrinin peptide #21.  
 XX  
 KW Dermatalogical; oxidative stress regulator; colostrinin.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200112650-A2.  
 XX  
 PD 22-FEB-2001.  
 XX  
 PF 17-AUG-2000; 2000WO-US22665.  
 XX  
 PR 17-AUG-1999; 99US-0149310.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Stanton GJ, Hughes TK, Boldogh I;  
 XX WPI; 2001-218342/22.  
 XX  
 PT Modulating oxidative stress level in a cell, involves contacting the  
 PT cell with an oxidative stress regulator selected from colostrinin, its  
 PT constituent peptide, analog or their combinations -  
 XX  
 PS Claim 6; Page 26; 48pp; English.  
 XX  
 CC The present invention relates to a method for modulating the oxidative  
 CC stress level in a cell or a patient, comprising contacting the cell with,  
 CC or administering to the patient, an oxidative stress regulator selected  
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),  
 CC to change the level of an oxidising species in the cell. The method can  
 CC be used to treat oxidative damage to skin, by decreasing or preventing an  
 CC increase in the level of damage to a biomolecule of the patient.  
 XX  
 SQ Sequence 18 AA;  
 Query Match 100.0%; Score 18; DB 22; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-13;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HKEMPFPKYPVEPFTESQ 18  
 ||||||||||||||||  
 DB 1 HKEMPFPKYPVEPFTESQ 18  
 ||||||||||||||||  
 RESULT 3  
 AAB72552  
 ID AAB72552 standard; Peptide; 18 AA.  
 XX  
 AC AAB72552;  
 XX  
 DT 09-MAY-2001 (first entry)  
 XX



DE Colostrinin peptide #21.  
 XX Neuroprotective; neural cell differentiation regulator; colostrinin;  
 KW Colostrum.  
 XX Unidentified.  
 XX OS  
 XX WO200112651-A2.  
 XX PN  
 XX 22-FEB-2001.  
 XX PD  
 XX 17-AUG-2000; 2000WO-US22774.  
 XX PF  
 XX 17-AUG-1999; 99US-0149633.  
 XX PR  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 XX PA  
 XX Boldogh I;  
 XX PI  
 XX WPI; 2001-226545/23.  
 XX DR  
 XX Use of colostrinin, its constituent peptide or analog as a neural cell  
 PT regulator, for promoting neural cell differentiation and treating  
 PT damaged neural cells in a patient -  
 XX  
 XX Claim 6; Page 21; 35pp; English.  
 XX PS  
 XX The present invention relates to a method for promoting neural cell  
 CC differentiation and treating damaged neural cells, using colostrinin and  
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural  
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.  
 XX CC  
 XX Sequence 18 AA;  
 DE Query Match 100.0%; Score 18; DB 22; Length 18;  
 XX Best Local Similarity 100.0%; Pred. No. 1.5e-13;  
 XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 HKEMPPFKYPVEPTESQ 18  
 DB 1 HKEMPPFKYPVEPTESQ 18  
 DE 1 HKEMPPFKYPVEPTESQ 18  
 XX  
 XX RESULT 4  
 XX AAB59330  
 ID AAB59330 standard; Peptide; 18 AA.  
 XX AC  
 XX AAB59330;  
 XX AC  
 XX 21-MAR-2001 (first entry)  
 XX DT  
 XX Ewe colostrinin peptide fragment C-5.  
 DE  
 XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.  
 KW  
 XX Ovis sp.  
 OS  
 XX WO200075173-A2.  
 XX PN  
 XX 14-DEC-2000.  
 XX PD  
 XX 02-JUN-2000; 2000WO-GB02128.  
 XX PF  
 XX 02-JUN-1999; 99GB-0012852.  
 XX PR  
 XX (RBGE-) REGEN THERAPEUTICS PLC.  
 XX PA  
 XX Georgiades JA;  
 XX PI  
 XX WPI; 2001-071058/08.  
 XX DR  
 XX Peptides having an N-terminal amino acid sequence isolated from

PT colostrinin for treating e.g. disorders of the central nervous system  
 PT and immune system, viral and bacterial infections, and diseases  
 PT characterized by amyloid plaques -  
 XX  
 XX Claim 7; Page 27; 63pp; English.  
 XX PS  
 XX The present invention provides the sequences of a number of peptides  
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
 CC fragment of colostrum. These peptides can be used in the treatment of  
 CC central nervous system disorders such as senile dementia, Parkinson's  
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
 CC disorders such as bacterial and viral infections, to improve the  
 CC development of a child's immune system, as a dietary supplement, and to  
 CC promote the dissolution of beta-amyloid plaques.  
 XX CC  
 XX Sequence 18 AA;  
 DE Query Match 100.0%; Score 18; DB 22; Length 18;  
 XX Best Local Similarity 100.0%; Pred. No. 1.5e-13;  
 XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 HKEMPPFKYPVEPTESQ 18  
 DB 1 HKEMPPFKYPVEPTESQ 18  
 DE 1 HKEMPPFKYPVEPTESQ 18  
 XX  
 XX RESULT 5  
 XX AAE20249  
 ID AAE20249 standard; peptide; 18 AA.  
 XX AC  
 XX AAE20249;  
 XX AC  
 XX 18-JUN-2002 (first entry)  
 XX DT  
 XX Colostrinin constituent peptide #21.  
 DE  
 XX Blood cell regulator; colostrinin; constituent peptide; oxidative stress;  
 KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;  
 KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;  
 KW transplantation; implantation; dermatological; vulnerary.  
 XX  
 XX Unidentified.  
 OS  
 XX Key Location/Qualifiers  
 PH Modified-site 18  
 FT /note= "Optionally C-terminal amide"  
 FT  
 XX WO200213850-A1.  
 XX PN  
 XX 21-FEB-2002.  
 XX PD  
 XX 17-AUG-2000; 2000WO-US22776.  
 XX PF  
 XX 17-AUG-2000; 2000WO-US22776.  
 XX PR  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 XX PA  
 XX Stanton GJ, Hughes TK, Boldogh I;  
 XX PI  
 XX WPI; 2002-269151/31.  
 XX DR  
 XX Composition useful for the modulation of blood cell proliferation in a  
 PT patient comprises a blood cell regulator selected from colostrinin, its  
 PT constituent peptide and/or analog -  
 XX  
 XX Claim 6; Page 26; 51pp; English.  
 XX PS  
 XX The invention relates to a composition which comprises a blood cell  
 CC regulator selected from colostrinin, its constituent peptide and/or  
 CC analogue. The invention is used for modulating the oxidative stress  
 CC level in a cell e.g. mammalian or human cell present in a cell culture,  
 CC tissue, organ, or organism; or for treating oxidative damage to the skin  
 CC of a patient e.g. animal or human; to modulate oxidative stress during/

CC after a premature birth or normal birth, preventing/delaying aging in a  
 CC patient, enhancing wound healing, and the reduction of side effects of  
 CC cosmetic procedures. The method changes the level of an oxidising species  
 CC in the cell, such as decreases or prevents increase in the level of  
 CC damage to a biomolecule of the patient selected from DNA, protein and/or  
 CC lipid, compared to the same conditions when the oxidative stress  
 CC regulator is not present. The modulation of oxidative stress results in  
 CC enhanced repair, regeneration, and replacement of cells, tissues and  
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
 CC external organs), as well as enhanced preservation of such organs for  
 CC transplantation, implantation, or scientific research. The present  
 CC sequence is a colostrinin constituent peptide.

XX Sequence 18 AA;

Query Match 100.0%; Score 18; DB 23; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-13;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKMPFPKYPVPPFTESQ 18  
 |||||  
 Db 1 HKMPFPKYPVPPFTESQ 18

# RESULT 6

AAW51056  
 ID AAW51056 standard; Peptide; 18 AA.

AC AAW51056;

DT 30-MAY-2002 (first entry)

DE Colostrinin constituent peptide (casein amino acids 121-138).

DE Colostrinin; colostrum; immunomodulator; cardiovascular;

KW blood cell regulator; cytokine inducer; beta-casein; human.

XX Homo sapiens.

Key Location/Qualifiers

FT Modified-site 18 /note= "optional C-terminal amidation"

FT WO200213849-A1.

PD 21-FEB-2002.

PF 17-AUG-2000; 2000WO-US22775.

PR 17-AUG-2000; 2000WO-US22775.

XX (TEXA ) UNIV TEXAS SYSTEM.

PA (REGE-) REGEN THERAPEUTICS PLC.

PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2002-269150/31.

XX Modulation of blood cell proliferation in a patient involves use of  
 PT blood cell regulator selected from colostrinin, its constituent peptide  
 PT and/or analogue -

PS Claim 1; Page 34; 54pp; English.

XX The present sequence is that of a colostrinin constituent peptide  
 CC that is preferred for use as an immunological regulator and as a  
 CC blood cell regulator in claimed methods of the invention. It is  
 CC classified as having a beta-casein homologue precursor, and  
 CC corresponds to casein amino acids 121-138. Methods are claimed  
 CC for: inducing a cytokine in a cell by contact with an immunological  
 CC regulator, where the cell is present in a cell culture, a tissue,  
 CC an organ or an organism, and the cell is mammalian, including human;  
 CC modulating an immune response in a cell by contact with the

CC immunological regulator under conditions effective to induce a  
 CC cytokine, modulating an immune response in a patient by administering  
 CC an immunological regulator under conditions effective to induce a  
 CC cytokine, where the immunological regulator is administered topically  
 CC or as part of a dietary supplement, and where the immune response is  
 CC specific or non specific, an interferon response or an antibody  
 CC response; modulating blood cell proliferation by contacting blood  
 CC cells with a blood cell regulator, where the blood cells are present  
 CC in a cell culture or an organism, are mammalian or human, and where  
 CC the blood cells are increased in number or differentiated; and a  
 CC method for modulating blood cell proliferation in a patent. A  
 CC claimed cytokine-inducing composition comprises a pharmaceutical  
 CC carrier and an active agent such as the present peptide. Cytokines  
 CC induced by this peptide in human leucocyte cultures include  
 CC interferon-gamma, tumour necrosis factor-alpha and interleukin-10.

XX Sequence 18 AA;

Query Match 100.0%; Score 18; DB 23; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-13;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKMPFPKYPVPPFTESQ 18  
 |||||  
 Db 1 HKMPFPKYPVPPFTESQ 18

# RESULT 7

AAO14598

ID AAO14598 standard; peptide; 18 AA.

AC AAO14598;

XX 27-MAY-2002 (first entry)

DE Neural cell regulatory colostrinin peptide 21.

DE Neural cell differentiation; neural cell regulator; colostrinin peptide;  
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;  
 KW neural cell treatment.

XX Unidentified.

PH Key Location/Qualifiers

FT Modified-site 18 /note= "Optional C-terminal amide"

FT WO200213851-A1.

PN 21-FEB-2002.

PD 17-AUG-2000; 2000WO-US22777.

XX 17-AUG-2000; 2000WO-US22777.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX Boldogh I, Stanton JG, Hughes TK;

XX WPI; 2002-269152/31.

XX Promoting cell differentiation in a patient involves use of blood cell  
 PT regulator selected from colostrinin, its constituent peptide and/or  
 PT analog -

PS Claim 7; Page 21; 37pp; English.

XX The invention comprises a method for promoting cell differentiation (e.g.  
 CC neural cell differentiation). The method involves contacting cells with a  
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the  
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich  
 CC polypeptide aggregate that is present in colostrum. The method of the  
 CC invention is useful for promoting the differentiation of cells and for

CC treating damaged neural cells in a patient. The present amino acid  
 CC sequence represents a specifically claimed colostrin peptide used in  
 CC the method of the invention.

SQ Sequence 18 AA;  
 Query Match 100.0%; Score 18; DB 23; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-13; Indels 0; Gaps 0;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKEMFFPKYPVEPTESQ 18  
 |||||  
 Db 1 HKEMFFPKYPVEPTESQ 18

RESULT 8  
 AAR58339  
 ID AAR58339 standard; peptide; 14 AA.

AC AAR58339;  
 XX  
 DT 22-SEP-1994 (first entry)  
 XX  
 DE Hypotensive polypeptide.  
 XX  
 KW Hypotensive; antioxidative; calcium absorption; salt; food;  
 KW pharmaceuticals; physiologically active agents.

OS Lactobacillus helveticus.  
 XX  
 FN JP06041191-A.  
 XX  
 PD 15-FEB-1994.  
 XX  
 XX 03-MAR-1993; 93JP-0043047.  
 XX  
 PR 04-MAR-1992; 92JP-0047340.  
 XX  
 PA (CALV ) CALPIS SHOKUIN KOGYO KK.  
 XX  
 XX WPI; 1994-089332/11.

PT New polypeptide - used in physiologically active agents having  
 FT e.g. hypotensive antioxidative and calcium absorption promoting  
 PT activity

PS Claim 1-2; Page 10; 10pp; Japanese.  
 XX  
 CC Sequences (AAR58319-341) are used in conjunction with  
 CC physiologically active agents showing a property such as  
 CC hypotensive activity, calcium absorption promoting activity and  
 CC antioxidative activity. The peptides are non-toxic and can be  
 CC used in physiologically active agents.

SQ Sequence 14 AA;  
 Query Match 61.1%; Score 11; DB 15; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-06;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKEMFFPKYPV 11  
 |||||  
 Db 1 HKEMFFPKYPV 11

RESULT 9  
 AAW03290  
 ID AAW03290 standard; peptide; 11 AA.

XX  
 AC AAW03290;  
 XX  
 DT 23-MAR-1997 (first entry)  
 XX

DE CNS-inhibiting peptide from casein.  
 XX  
 KW casein; central nervous system; CNS inhibiting; antitussive;  
 KW analgesic; sedative.  
 XX  
 OS Synthetic.

PN JP08269090-A.  
 PD 15-OCT-1996.

XX 28-MAR-1995; 95JP-0094516.

PR 28-MAR-1995; 95JP-0094516.

XX (SNOW ) SNOW BRAND MILK PROD CO LTD.

PA WPI; 1996-515013/51.

XX New peptide(s) obtd. by digestion of casein - useful as drugs  
 PT displaying e.g. CNS inhibiting, antitussive, analgesic and sedative  
 FT activities

XX Claim 1; Page 2; 11pp; Japanese.

CC Acid casein was prepared from raw milk by acid precipitation, and  
 CC beta casein was formed by the product by the method of Hipp et al.  
 CC This material was digested with porcine pepsin. The digested protein  
 CC was neutralised with NaOH, then heated to inactivate the enzyme. The  
 CC product was further digested with bovine pancreatin, trypsin and porcine  
 CC kidney-derived LAP and then subjected to reverse phase chromatography  
 CC to provide the present peptide.  
 CC The peptide is useful as a drug having CNS inhibiting, antitussive,  
 CC analgesic and sedative activities

SQ Sequence 11 AA;

Query Match 55.6%; Score 10; DB 17; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-05;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 YPVEPFTESQ 18  
 |||||  
 Db 1 YPVEPFTESQ 10

RESULT 10  
 AAW03291  
 ID AAW03291 standard; peptide; 13 AA.

XX  
 AC AAW03291;

XX 23-MAR-1997 (first entry)

XX CNS-inhibiting peptide from casein.

XX casein; central nervous system; CNS inhibiting; antitussive;  
 KW analgesic; sedative.

OS Synthetic.

XX JP08269090-A.

XX 15-OCT-1996.

XX 28-MAR-1995; 95JP-0094516.

PR 28-MAR-1995; 95JP-0094516.

XX (SNOW ) SNOW BRAND MILK PROD CO LTD.

XX WPI; 1996-515013/51.

PT New peptide(s) obtd. by digestion of casein - useful as drugs  
PT displaying e.g. CNS inhibiting, antitussive, analgesic and sedative  
PT activities  
XX Claim 1; Page 2; 1lpp; Japanese.  
XX Acid casein was prepared from raw milk by acid precipitation, and  
CC beta casein was formed by the product by the method of Hipp et al.  
CC This material was digested with porcine pepsin. The digested protein  
CC was neutralised with NaOH, then heated to inactivate the enzyme. The  
CC product was further digested with bovine pancreatin, trypsin and porcine  
CC kidney-derived LAP and then subjected to reverse phase chromatography  
CC to provide the present peptide.  
CC The peptide is useful as a drug having CNS inhibiting, antitussive,  
CC analgesic and sedative activities  
XX Sequence 13 AA;  
SQ Query Match 55.6%; Score 10; DB 17; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.0001;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 9 YPVEPFTSQ 18  
Db 1 YPVEPFTSQ 10  
RESULT 11  
ABG32211  
ID ABG32211 standard; peptide; 7 AA.  
XX AC ABG32211;  
XX DT 05-NOV-2002 (first entry)  
XX DE Sheep colostrinin derived peptide #5.  
XX KW Sheep; colostrinin; colostrum; cytokine inducer; antigen; dementia;  
KW central nervous system disorder; neurological disorder; neurosis;  
KW mental disorder; psychosis; neurodegenerative disorder;  
KW Alzheimer's disease; motor neuron disease; immune system disorder;  
KW acquired immunological deficiency; bacterial infection; viral infection;  
KW amyloid plaque; dietary supplement; cachexia; weight loss;  
KW senile dementia; Parkinson's disease; emotional disturbance; depression;  
KW drug addiction; drug withdrawal.  
XX OS Ovis aries.  
XX PN WO200246211-A2.  
XX PD 13-JUN-2002.  
XX PF 05-DEC-2001; 2001WO-GB05376.  
XX PR 06-DEC-2000; 2000GB-0029777.  
XX (REG- ) REGEN THERAPEUTICS PLC.  
XX PA Georgiades JA;  
XX PI WPI; 2002-619016/66.  
XX DR Novel peptides isolated from colostrinin polypeptide, useful for  
XX PT treating viral and bacterial infections, disorders of immune system and  
XX PT central nervous system e.g., Alzheimer's disease, dementia, and as food  
XX PT additive -  
XX PS Claim 1; Page 8; 16pp; English.  
XX CC The invention relates to a peptide derived from colostrinin (a colostrum  
XX protein known to be a cytokine inducer) substantially entirely consists  
XX CC of the peptide sequences appearing as ABG32207-ABG32223. Also included  
XX CC are a composition comprising two or more of the peptides in combination

CC with a carrier, a dietary supplement comprising an orally ingestible  
CC combination of the peptide in combination with a carrier and an antibody  
CC which binds to the peptide, and which is obtainable by using peptide as  
CC an antigen. The peptide is useful as a medicament for treating chronic  
CC disorders of central nervous system e.g., neurological disorders and/or  
CC mental disorders such as psychosis and/or neurosis, dementia,  
CC neurodegenerative disorders such as Alzheimer's disease, motor  
CC neuron disease, chronic disorders of immune system, diseases  
CC with bacterial and viral infections, acquired immunological deficiencies,  
CC chronic bacterial, viral infections. The peptide is also useful for  
CC treating diseases characterised by presence of amyloid plaque. The  
CC peptide is also useful as a dietary supplement for babies, small  
CC children, adults who have been subjected to chemotherapy and/or  
CC adults who have suffered from cachexia or weight loss due to chronic  
CC disease. The peptide is also useful for treating senile dementia,  
CC Parkinson's disease, emotional disturbances and depression. The peptides  
CC may also be used as an auxiliary withdrawal treatment for drug addicts,  
CC after a period of detoxification, and in persons dependent on stimulants.  
CC The present sequence is a colostrinin derived peptide of the invention.  
XX Sequence 7 AA;  
SQ Query Match 38.9%; Score 7; DB 23; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 EMPFPKY 9  
Db 1 EMPFPKY 7  
RESULT 12  
AAW03289  
ID AAW03289 standard; peptide; 6 AA.  
XX AC AAW03289;  
XX DT 23-MAR-1997 (first entry)  
XX DE CNS-inhibiting peptide from casein.  
XX KW casein; central nervous system; CNS inhibiting; antitussive;  
KW analgesic; sedative.  
XX OS Synthetic.  
XX PN JP08269090-A.  
XX PD 15-OCT-1996.  
XX PF 28-MAR-1995; 95JP-0094516.  
XX PR 28-MAR-1995; 95JP-0094516.  
XX PA (SNOW ) SNOW BRAND MILK PROD CO LTD.  
XX DR WPI; 1996-515013/51.  
XX PT New peptide(s) obtd. by digestion of casein - useful as drugs  
XX PT displaying e.g. CNS inhibiting, antitussive, analgesic and sedative  
XX PT activities  
XX PS Claim 1; Page 2; 1lpp; Japanese.  
XX CC Acid casein was prepared from raw milk by acid precipitation, and  
XX CC beta casein was formed by the product by the method of Hipp et al.  
XX CC This material was digested with porcine pepsin. The digested protein  
XX CC was neutralised with NaOH, then heated to inactivate the enzyme. The  
XX CC product was further digested with bovine pancreatin, trypsin and porcine  
XX CC kidney-derived LAP and then subjected to reverse phase chromatography  
XX CC to provide the present peptide.  
XX CC The peptide is useful as a drug having CNS inhibiting, antitussive,  
XX CC analgesic and sedative activities

XX Sequence 6 AA;  
 SQ Query Match 33.3%; Score 6; DB 17; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPVEPF 14  
 |||||  
 Db 1 YPVEPF 6

RESULT 13  
 ABG32212  
 ID ABG32212 standard; peptide; 6 AA.  
 XX  
 AC ABG32212;  
 XX  
 DT 05-NOV-2002 (first entry)  
 XX  
 DE Sheep colostrinin derived peptide #6.  
 XX  
 KW Sheep; colostrinin; colostrum; cytokine inducer; antigen; dementia;  
 KW central nervous system disorder; neurological disorder; neurosis;  
 KW mental disorder; psychosis; neurodegenerative disorder;  
 KW Alzheimer's disease; motor neuron disease; immune system disorder;  
 KW acquired immunological deficiency; bacterial infection; viral infection;  
 KW amyloid plaque; dietary supplement; cachexia; weight loss;  
 KW senile dementia; Parkinson's disease; emotional disturbance; depression;  
 KW drug addiction; drug withdrawal.  
 XX  
 OS Ovis aries.  
 XX  
 FN WO200246211-A2.  
 XX  
 PD 13-JUN-2002.  
 XX  
 PF 05-DEC-2001; 2001WO-GB053376.  
 XX  
 PR 06-DEC-2000; 2000GB-0029777.  
 XX  
 XX (REGG-) REGEN THERAPEUTICS PLC.  
 DA  
 PI Georgiades JA;  
 XX  
 XX WPI; 2002-619016/66.  
 DR  
 XX Novel peptides isolated from colostrinin polypeptide, useful for  
 PT treating viral and bacterial infections, disorders of immune system and  
 PT central nervous system e.g., Alzheimer's disease, dementia, and as food  
 PT additive -  
 XX  
 PS Claim 1; Page 8; 16pp; English.  
 XX  
 CC The invention relates to a peptide derived from colostrinin (a colostrum  
 CC protein known to be a cytokine inducer) substantially entirely consists  
 CC of the peptide sequences appearing as ABG32207-ABG32223. Also included  
 CC are a composition comprising two or more of the peptides in combination  
 CC with a carrier, a dietary supplement comprising an orally ingestible  
 CC combination of the peptide in combination with a carrier and an antibody  
 CC which binds to the peptide, and which is obtainable by using peptide as  
 CC an antigen. The peptide is useful as a medicament for treating chronic  
 CC disorders of central nervous system e.g., neurological disorders and/or  
 CC mental disorders such as psychosis and/or neurosis, dementia,  
 CC neurodegenerative disorders such as Alzheimer's disease, motor  
 CC neuron disease, chronic disorders of immune system, diseases  
 CC with bacterial and viral etiology, acquired immunological deficiencies,  
 CC chronic bacterial, viral infections. The peptide is also useful for  
 CC treating diseases characterised by presence of amyloid plaque. The  
 CC peptide is also useful as a dietary supplement for babies, small  
 CC children, adults who have been subjected to chemotherapy and/or  
 CC adults who have suffered from cachexia or weight loss due to chronic  
 CC disease. The peptide is also useful for treating senile dementia,

CC Parkinson's disease, emotional disturbances and depression. The peptides  
 CC may also be used as an auxiliary withdrawal treatment for drug addicts,  
 CC after a period of detoxification, and in persons dependent on stimulants.  
 CC The present sequence is a colostrinin derived peptide of the invention.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 33.3%; Score 6; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PVEPFT 15  
 |||||  
 Db 1 PVEPFT 6

RESULT 14  
 AAR58330  
 ID AAR58330 standard; peptide; 15 AA.  
 XX  
 AC AAR58330;  
 XX  
 DT 22-SEP-1994 (first entry)  
 XX  
 DE Hypotensive polypeptide.  
 XX  
 KW Hypotensive; antioxidative; calcium absorption; salt; food;  
 KW pharmaceuticals; physiologically active agents.  
 KW  
 OS Lactobacillus helveticus.  
 XX  
 FN JP06041191-A.  
 XX  
 PD 15-FEB-1994.  
 XX  
 PF 03-MAR-1993; 93JP-0043047.  
 XX  
 PR 04-MAR-1992; 92JP-0047340.  
 XX  
 XX (CALV ) CALPIS SHOKUHIN KOGYO KK.  
 PA  
 XX WPI; 1994-089332/11.  
 DR  
 XX New polypeptide - used in physiologically active agents having  
 PT e.g. hypotensive antioxidative and calcium absorption promoting  
 PT activity  
 PT  
 PS Claim 1-2; Page 8; 10pp; Japanese.  
 XX  
 CC Sequences (AAR58319-341) are used in conjunction with  
 CC physiologically active agents showing a property such as  
 CC hypotensive activity, calcium absorption promoting activity and  
 CC antioxidative activity. The peptides are non-toxic and can be  
 CC used in physiologically active agents.  
 XX  
 SQ Sequence 15 AA;  
 Query Match 33.3%; Score 6; DB 15; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.4;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFTESQ 18  
 |||||  
 Db 6 PFTESQ 11

RESULT 15  
 AAE07187  
 ID AAE07187 standard; peptide; 10 AA.  
 XX  
 AC AAE07187;  
 XX  
 DT 06-NOV-2001 (first entry)

```

XX DE Colostrinin peptide 3.
XX KW Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;
XX KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;
XX KW central nervous system disorder; neurodegenerative disorder; weight loss;
XX KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;
XX KW acquired immunological deficiency; neurological disorder; dementia;
XX KW antiviral.
XX OS Unidentified.
XX OS WO200155199-A1.
XX FT Modified-site 1
XX FT /note= "N-terminal acetyl; this residue forms a cyclic
XX FT linkage with Pro found at the C-terminal end"
XX PD 02-AUG-2001.
XX PF 26-JAN-2001; 2001WO-GB00329.
XX PR 26-JAN-2000; 2000GB-0001825.
XX PA (REG-) REGEN THERAPEUTICS PLC.
XX PI Georgiades JA;
XX PI WPI; 2001-488775/53.
XX PT Peptide useful as an inter alia in the treatment of e.g. disorders of
XX PT the immune system and the central nervous system comprises ten
XX PT amino-terminal amino acid sequence derived from peptides present in
XX PT colostrinin -
XX PS Claim 1; Page 15; 40pp; English.
XX CC The invention relates to colostrinin peptide fragments which are useful,
XX CC inter alia, in the treatment of chronic disorders of the immune system
XX CC and the central nervous system. Colostrinin peptides are used as a
XX CC medicament in the treatment of neurological disorders e.g., dementia,
XX CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron
XX CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and
XX CC neurosis, in acquired immunological deficiencies, chronic bacterial and
XX CC viral infections and diseases characterised by the presence of beta-
XX CC amyloid plaques and as a dietary supplement for babies, small children,
XX CC adults and senile persons, who have been subjected to chemotherapy or
XX CC have suffered from cachexia or weight loss due to the chronic disease.
XX CC Colostrinin peptides are also used as food additives and as an auxiliary
XX CC withdrawal treatment for drug addicts, after a period of detoxification
XX CC and in persons dependent on stimulants. Colostrinin peptides are used to
XX CC prepare antibodies and to treat emotional disturbances, e.g. emotional
XX CC disturbances of psychiatric patients in a state of depression. These
XX CC colostrinin peptides improves the development of immune system in a new
XX CC born child and to correct the immunological deficiencies in a child.
XX CC The present sequence is colostrinin peptide 3 related to the invention.
XX SQ Sequence 10 AA;
XX Query Match 27.8%; Score 5; DB 22; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 32;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 PVEPF 14
Db 4 PVEPF 8
RESULT 16
AAE07197
ID AAE07197 standard; peptide; 10 AA.
XX AC AAE07197;
XX DT 06-NOV-2001 (first entry)
XX DE Modified colostrinin cyclic peptide #3.
XX KW Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;
XX KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;
XX KW central nervous system disorder; neurodegenerative disorder; weight loss;
XX KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;
XX KW acquired immunological deficiency; neurological disorder; dementia;
XX KW antiviral.
XX OS Unidentified.
XX OS WO200155199-A1.
XX FT Modified-site 1
XX FT /note= "N-terminal acetyl; this residue forms a cyclic
XX FT linkage with Pro found at the C-terminal end"
XX PD 02-AUG-2001.
XX PF 26-JAN-2001; 2001WO-GB00329.
XX PR 26-JAN-2000; 2000GB-0001825.
XX PA (REG-) REGEN THERAPEUTICS PLC.
XX PI Georgiades JA;
XX PI WPI; 2001-488775/53.
XX PT Peptide useful as an inter alia in the treatment of e.g. disorders of
XX PT the immune system and the central nervous system comprises ten
XX PT amino-terminal amino acid sequence derived from peptides present in
XX PT colostrinin -
XX PS Claim 1; Page 15; 40pp; English.
XX CC The invention relates to colostrinin peptide fragments which are useful,
XX CC inter alia, in the treatment of chronic disorders of the immune system
XX CC and the central nervous system. Colostrinin peptides are used as a
XX CC medicament in the treatment of neurological disorders e.g., dementia,
XX CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron
XX CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and
XX CC neurosis, in acquired immunological deficiencies, chronic bacterial and
XX CC viral infections and diseases characterised by the presence of beta-
XX CC amyloid plaques and as a dietary supplement for babies, small children,
XX CC adults and senile persons, who have been subjected to chemotherapy or
XX CC have suffered from cachexia or weight loss due to the chronic disease.
XX CC Colostrinin peptides are also used as food additives and as an auxiliary
XX CC withdrawal treatment for drug addicts, after a period of detoxification
XX CC and in persons dependent on stimulants. Colostrinin peptides are used to
XX CC prepare antibodies and to treat emotional disturbances, e.g. emotional
XX CC disturbances of psychiatric patients in a state of depression. These
XX CC colostrinin peptides improves the development of immune system in a new
XX CC born child and to correct the immunological deficiencies in a child.
XX CC The present sequence is colostrinin peptide 3 related to the invention.
XX SQ Sequence 10 AA;
XX Query Match 27.8%; Score 5; DB 22; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 32;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 PVEPF 14
Db 5 PVEPF 9
RESULT 17
AAG98055
ID AAG98055 standard; Peptide; 14 AA.
XX AC AAG98055;

```

XX	19-SEP-2001	(first entry)
XX	Human SNP associated peptide SEQ ID NO. 697.	
XX	Human; single nucleotide polymorphism; SNP; angiotensinogen;	
XX	4-hydroxybutyrate; dehydrogenase; protein therapy;	
KW	adenosine triphosphate-dependent RNA helicase;	
KW	major histocompatibility complex Class I histocompatibility antigen; MHC;	
KW	phosphoglycerate kinase; immunosuppressive; immunostimulatory;	
KW	antirheumatic; antisclerotic; antidiabetic; antiinflammatory; cytostatic;	
KW	antiileukemic; neuroprotective; antimicrobial; gene therapy; vaccine.	
XX		
OS	Homo sapiens.	
XX		
XX	WO200148245-A2.	
XX		
XX	05-JUL-2001.	
XX		
XX	27-DEC-2000; 2000WO-US35346.	
Pf		
XX	27-DEC-1999; 99US-0472688.	
XX		
XX	(CURA-) CURAGEN CORP.	
PA		
XX	Shimkets RA, Leach M;	
PI		
XX	WPI; 2001-418297/44.	
DR		
XX		
PT	Polymorphic nucleic acids encoding e.g. angiotensinogen, dehydrogenase,	
PT	adenosine triphosphate-dependent RNA helicase and/or phosphoglycerate	
PT	kinase, useful for diagnosing and treating, e.g. cancer, autoimmune	
PT	diseases and infections -	
XX		
PS	Disclosure; Page 444; 484pp; English.	
XX		
CC	The invention relates to nucleic acids (AAH9386-AAH80036) encoding	
CC	polymorphic variants of proteins (AAG98010-AAG98238) related to	
CC	angiotensin, 4-hydroxybutyrate, dehydrogenase, adenosine triphosphate	
CC	(ATP)-dependent RNA helicase, major histocompatibility complex (MHC)	
CC	Class I histocompatibility antigen and/or phosphoglycerate kinase. These	
CC	nucleic acid single nucleotide polymorphisms (SNPs) and the encoded	
CC	proteins have potential immunosuppressive, immunostimulatory,	
CC	antirheumatic, antisclerotic, antidiabetic, antiinflammatory, cytostatic,	
CC	antileukemic, neuroprotective and antimicrobial activity and may be	
CC	useful in gene/protein therapy, vaccines modulation of the expression	
CC	and activity of proteins related to angiotensin, 4-hydroxybutyrate,	
CC	dehydrogenase, adenosine triphosphate (ATP)-dependent RNA helicase,	
CC	and/or phosphoglycerate kinase. Disorders that may be prevented,	
CC	diagnosed and/or treated by the above methods include multifactorial	
CC	diseases with a genetic component, such as autoimmune diseases (e.g.	
CC	rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus	
CC	erythematosus and Grave's disease), inflammation, cancer (e.g. cancers	
CC	of the bladder, brain, breast, colon and kidney, leukemia), diseases of	
CC	the nervous system, an infection of pathogenic organisms. They may also	
CC	be used to alter phenotypic traits such as longevity, appearance,	
CC	strength, speed and endurance.	
XX		
SQ	Sequence 14 AA;	
	Query Match 27.8%; Score 5; DB 22; Length 14;	
	Best Local Similarity 100.0%; Pred. No. 43;	
	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	13 PFTES 17	
Dd	9 PFTES 13	
RESULT 18		
AAB72250		
ID	AAB72250 standard; peptide; 15 AA.	

XX	AAB72250;
AC	
XX	14-MAY-2001 (first entry)
DT	
DE	Colostrinin derived cytokine inducing peptide SEQ ID 5.
XX	
KW	Colostrinin; immune response; cytokine; blood cell proliferation;
KW	central nervous system disorder; neurological disorder; mental disorder;
KW	dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
KW	neurosis; infection.
XX	
OS	Synthetic.
XX	
PN	WO200111937-A2.
XX	
XX	22-FEB-2001.
PD	
XX	
Pf	17-AUG-2000; 2000WO-US22918.
XX	
PR	17-AUG-1999; 99US-0149311.
XX	
PA	(TEXA ) UNIV TEXAS SYSTEM.
PA	(REGE-) REGEN THERAPEUTICS PLC.
XX	
PI	Stanton GJ, Hughes TK, Boldogh I, Georgiadis J;
XX	
XX	WPI; 2001-202804/20.
DR	
XX	
PT	Inducing a cytokine and modulating an immune response, useful for
PT	treating central nervous system diseases and bacterial and viral
PT	infections, comprises administering colostrinin as an immunological
PT	regulator -
XX	
PS	Claim 1; Page 34; 50pp; English.
XX	
CC	Sequences AAB72246 - AAB72275 represent peptides derived from clostrinin,
CC	a proline rich polypeptide aggregate contained in colostrum. The
CC	peptides have immune response modulatory activity, and are capable of
CC	inducing cytokines. Colostrinin and its derived peptides are useful for
CC	inducing cytokine production, for modulating an immunological response
CC	and for inducing blood cell proliferation. The peptides are useful in the
CC	treatment of disorders of the central nervous system, neurological
CC	disorders, mental disorders, dementia, neurodegenerative diseases,
CC	Alzheimer's disease, motor neuron disease, psychosis, neurosis, chronic
CC	disorders of the immune system, bacterial and viral infections and
CC	acquired immunological deficiencies.
XX	
SQ	Sequence 15 AA;
	Query Match 27.8%; Score 5; DB 22; Length 15;
	Best Local Similarity 100.0%; Pred. No. 45;
	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Qy	10 PVPEPF 14
Dd	8 PVPEPF 12
RESULT 19	
AAB72504	
ID	AAB72504 standard; Peptide; 15 AA.
XX	
AC	AAB72504;
XX	
DT	09-MAY-2001 (first entry)
XX	
DE	Colostrinin peptide #5.
XX	
KW	Dermatological; oxidative stress regulator; colostrinin.
XX	
OS	Unidentified.
XX	

PN WO200112650-A2.  
 XX 22-FEB-2001.  
 XX 17-AUG-2000; 2000WO-US22665.  
 XX 17-AUG-1999; 99US-0149310.  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 XX Stanton GJ, Hughes TK, Boldogh I;  
 XX WPI; 2001-218342/22.  
 XX Modulating oxidative stress level in a cell, involves contacting the  
 PT cell with an oxidative stress regulator selected from colostrinin, its  
 PT constituent peptide, analog or their combinations -  
 XX  
 XX Claim 6; Page 25; 48pp; English.  
 XX The present invention relates to a method for modulating the oxidative  
 CC stress level in a cell or a patient, comprising contacting the cell with,  
 CC or administering to the patient, an oxidative stress regulator selected  
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),  
 CC to change the level of an oxidising species in the cell. The method can  
 CC be used to treat oxidative damage to skin, by decreasing or preventing an  
 CC increase in the level of damage to a biomolecule of the patient.  
 XX  
 XX Sequence 15 AA;  
 SQ  
 Query Match 27.8%; Score 5; DB 22; Length 15;  
 Best Local Similarity 100.0%; Pred.No. 45;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 10 PVEPF 14  
 Db 8 PVEPF 12  
 |||||  
 RESULT 20  
 AAB72536  
 ID AAB72536 standard; Peptide; 15 AA.  
 XX  
 XX AAB72536;  
 AC  
 XX 09-MAY-2001 (first entry)  
 DT  
 XX Colostrinin peptide #5.  
 DE  
 XX Neuroprotective; neural cell differentiation regulator; colostrinin;  
 KW colostrum.  
 XX  
 XX Unidentified.  
 OS  
 XX WO200112651-A2.  
 PN  
 XX 22-FEB-2001.  
 PD  
 XX 17-AUG-2000; 2000WO-US22774.  
 PF  
 XX 17-AUG-1999; 99US-0149633.  
 PR  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA  
 XX Boldogh I;  
 PI  
 XX WPI; 2001-226545/23.  
 DR  
 XX Use of colostrinin, its constituent peptide or analog as a neural cell  
 PT regulator, for promoting neural cell differentiation and treating  
 PT damaged neural cells in a patient -  
 XX  
 XX Claim 6; Page 21; 35pp; English.

XX The present invention relates to a method for promoting neural cell  
 CC differentiation and treating damaged neural cells, using colostrinin and  
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural  
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.  
 XX  
 XX Sequence 15 AA;  
 SQ  
 Query Match 27.8%; Score 5; DB 22; Length 15;  
 Best Local Similarity 100.0%; Pred.No. 45;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 10 PVEPF 14  
 Db 8 PVEPF 12  
 |||||  
 RESULT 21  
 AAB59322  
 ID AAB59322 standard; Peptide; 15 AA.  
 XX  
 XX AAB59322;  
 AC  
 XX 21-MAR-2001 (first entry)  
 DT  
 XX Ewe colostrinin peptide fragment B-7.  
 DE  
 XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.  
 XX  
 XX Ovis sp.  
 OS  
 XX WO200075173-A2.  
 PN  
 XX 14-DEC-2000.  
 PD  
 XX 02-JUN-2000; 2000WO-GB02128.  
 PF  
 XX 02-JUN-1999; 99GB-0012852.  
 PR  
 XX (REGE-) REGEN THERAPEUTICS PLC.  
 PA  
 XX Georgiades JA;  
 PI  
 XX WPI; 2001-071058/08.  
 DR  
 XX Peptides having an N-terminal amino acid sequence isolated from  
 PT colostrinin for treating e.g. disorders of the central nervous system  
 PT and immune system, viral and bacterial infections, and diseases  
 PT characterized by amyloid plaques -  
 XX  
 XX Claim 7; Page 27; 63pp; English.  
 PS  
 XX The present invention provides the sequences of a number of peptides  
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
 CC fragment of colostrum. These peptides can be used in the treatment of  
 CC central nervous system disorders such as senile dementia, Parkinson's  
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
 CC disorders such as bacterial and viral infections, to improve the  
 CC development of a child's immune system, as a dietary supplement, and to  
 CC promote the dissolution of beta-amyloid plaques.  
 XX  
 XX Sequence 15 AA;  
 SQ  
 Query Match 27.8%; Score 5; DB 22; Length 15;  
 Best Local Similarity 100.0%; Pred.No. 45;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 10 PVEPF 14  
 Db 8 PVEPF 12  
 |||||



## RESULT 22

AAE20232  
ID AAE20232 standard; peptide; 15 AA.

XX AC AAE20232;

XX DT 18-JUN-2002 (first entry)

XX DE Colostrinin constituent peptide #5.

XX KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;

XX KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;

XX KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;

XX KW transplantation; implantation; dermatological; vulnary.

XX OS Unidentified.

XX FT Key

XX FT Modified-site 15

XX FT /note= "Optionally C-terminal amide"

XX PN WO200213850-A1.

XX PD 21-FEB-2002.

XX PF 17-AUG-2000; 2000WO-US22776.

XX PR 17-AUG-2000; 2000WO-US22776.

XX PA (TEXA ) UNIV TEXAS SYSTEM.

XX PI Stanton GJ, Hughes TK, Boldogh I;

XX DR WPI; 2002-269151/31.

XX PT Composition useful for the modulation of blood cell proliferation in a

XX PT patient comprises a blood cell regulator selected from colostrinin, its

XX PT constituent peptide and/or analog

XX PS Claim 6; Page 25; 5lpp; English.

XX CC The invention relates to a composition which comprises a blood cell

XX CC regulator selected from colostrinin, its constituent peptide and/or

XX CC analogue. The invention is used for modulating the oxidative stress

XX CC level in a cell e.g. mammalian or human cell present in a cell culture,

XX CC tissue, organ, or organism; or for treating oxidative damage to the skin

XX CC of a patient e.g. animal or human; to modulate oxidative stress during/

XX CC after a premature birth or normal birth, preventing/delaying aging in a

XX CC patient, enhancing wound healing, and the reduction of side effects of

XX CC cosmetic procedures. The method changes the level of an oxidising species

XX CC in the cell, such as decreases or prevents increase in the level of

XX CC damage to a biomolecule of the patient selected from DNA, protein and/or

XX CC lipid, compared to the same conditions when the oxidative stress

XX CC regulator is not present. The modulation of oxidative stress results in

XX CC enhanced repair, regeneration, and replacement of cells, tissues and

XX CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and

XX CC external organs), as well as enhanced preservation of such organs for

XX CC transplantation, implantation, or scientific research. The present

XX CC sequence is a colostrinin constituent peptide.

XX SQ Sequence 15 AA;

Query Match 27.8%; Score 5; DB 23; Length 15;

Best Local Similarity 100.0%; Pred. No. 45;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PVEPFF 14

DB 8 PVEPFF 12

## RESULT 23

AAE51040

ID

XX AAE51040 standard; Peptide; 15 AA.

XX AC AAE51040;

XX DT 30-MAY-2002 (first entry)

XX DE Colostrinin constituent peptide.

XX KW Colostrinin; colostrum; immunomodulator; cardiovascular;

XX KW blood cell regulator; cytokine inducer; beta-casein; human.

XX OS Homo sapiens.

XX FT Key

XX FT Modified-site 15

XX FT /note= "optional C-terminal amidation"

XX PN WO200213849-A1.

XX PD 21-FEB-2002.

XX PF 17-AUG-2000; 2000WO-US22775.

XX PR 17-AUG-2000; 2000WO-US22775.

XX PA (TEXA ) UNIV TEXAS SYSTEM.

XX PR (REG- ) REGEN THERAPEUTICS PLC.

XX XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX PI WPI; 2002-269150/31.

XX DR Modulation of blood cell proliferation in a patient involves use of

XX XX blood cell regulator selected from colostrinin, its constituent peptide

XX PT and/or analogue

XX PS Claim 1; Page 34; 54pp; English.

XX CC The present sequence is that of a colostrinin constituent peptide

XX CC that is preferred for use as an immunological regulator and as a

XX CC blood cell regulator in claimed methods of the invention. It is

XX CC classified as having a beta-casein homologue precursor. Methods

XX CC are claimed for: inducing a cytokine in a cell by contact with an

XX CC immunological regulator, where the cell is present in a cell

XX CC culture, a tissue, an organ or an organism, and the cell is

XX CC by contact with the immunological regulator under conditions

XX CC effective to induce a cytokine; modulating an immune response in a

XX CC patient by administering an immunological regulator under conditions

XX CC effective to induce a cytokine, where the immunological regulator

XX CC is administered topically or as part of a dietary supplement, and

XX CC where the immune response is specific or non specific, an interferon

XX CC response or an antibody response; modulating blood cell proliferation

XX CC by contacting blood cells with a blood cell regulator, where the

XX CC blood cells are present in a cell culture or an organism, are

XX CC mammalian or human, and where the blood cells are increased in

XX CC number or differentiated; and a method for modulating blood cell

XX CC proliferation in a patent. A claimed cytokine-inducing composition

XX CC comprises a pharmaceutical carrier and an active agent such as the

XX CC present peptide. Cytokines induced by this peptide in human

XX CC leucocyte cultures include interferon-gamma, tumour necrosis

XX CC factor-alpha, interleukin-6 and interleukin-10.

XX SQ Sequence 15 AA;

Query Match 27.8%; Score 5; DB 23; Length 15;

Best Local Similarity 100.0%; Pred. No. 45;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PVEPFF 14

DB 8 PVEPFF 12

```

RESULT 24
AAO14581
ID AAO14581 standard; peptide; 15 AA.
XX
XX AC AAO14581;
XX
DT 27-MAY-2002 (first entry)
XX
DE Neural cell regulatory colostrinin peptide 5.
XX
KW Neural cell differentiation; neural cell regulator; colostrinin peptide;
KW neural cell formation; proline-rich polypeptide aggregate; colostrum;
XX neural cell treatment.
XX
XX OS Unidentified.
XX
FH Key Location/Qualifiers
FT Modified-site 15 /note= "Optional C-terminal amide"
XX
XX PN WO200213851-A1.
XX
XX PD 21-FEB-2002.
XX
XX PF 17-AUG-2000; 2000WO-US22777.
XX
XX PR 17-AUG-2000; 2000WO-US22777.
XX
XX PA (TEXA ) UNIV TEXAS SYSTEM.
XX
XX PI Boldogh I, Stanton JG, Hughes TK;
XX
XX DR WPI; 2002-269152/31.
XX
XX PT Promoting cell differentiation in a patient involves use of blood cell
XX regulator selected from colostrinin, its constituent peptide and/or
XX analog -
XX
XX PS Claim 7; Page 21; 37pp; English.
XX
CC The invention comprises a method for promoting cell differentiation (e.g.
CC neural cell differentiation). The method involves contacting cells with a
CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
CC cells in morphology to form neural cells. Colostrinin is a proline-rich
CC polypeptide aggregate that is present in colostrum. The method of the
CC invention is useful for promoting the differentiation of cells and for
CC treating damaged neural cells in a patient. The present amino acid
CC sequence represents a specifically claimed colostrinin peptide used in
CC the method of the invention.
XX
XX SQ Sequence 15 AA;
XX
XX Query Match 27.8%; Score 5; DB 23; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 45;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 10 PVEPF 14
XX |||||
XX Db 8 PVEPF 12
XX
XX RESULT 25
XX AAB59352
XX ID AAB59352 standard; Peptide; 16 AA.
XX
XX AC AAB59352;
XX
XX DT 21-MAR-2001 (first entry)
XX
XX DE Ewe colostrinin peptide fragment derived sequence #12.
XX
XX KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
XX

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KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
XX
XX OS Ovis sp.
XX
XX PN WO200075173-A2.
XX
XX PD 14-DEC-2000.
XX
XX PF 02-JUN-2000; 2000WO-GB02128.
XX
XX PR 02-JUN-1999; 99GB-0012852.
XX
XX PA (REGG-) REGEN THERAPEUTICS PLC.
XX
XX PI Georgiades JA;
XX
XX DR WPI; 2001-071058/08.
XX
XX PT Peptides having an N-terminal amino acid sequence isolated from
XX colostrinin for treating e.g. disorders of the central nervous system
XX and immune system, viral and bacterial infections, and diseases
XX characterized by amyloid plaques -
XX
XX PS Claim 8; Page 27; 63pp; English.
XX
XX CC The present invention provides the sequences of a number of peptides
XX found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
XX fragment of colostrum. These peptides can be used in the treatment of
XX central nervous system disorders such as senile dementia, Parkinson's
XX disease, Alzheimer's disease, psychosis and neurosis, immune system
XX disorders such as bacterial and viral infections, to improve the
XX development of a child's immune system, as a dietary supplement, and to
XX promote the dissolution of beta-amyloid plaques.
XX
XX SQ Sequence 16 AA;
XX
XX Query Match 27.8%; Score 5; DB 22; Length 16;
XX Best Local Similarity 100.0%; Pred. No. 48;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 10 PVEPF 14
XX |||||
XX Db 9 PVEPF 13
XX
XX RESULT 26
XX AAW65794
XX ID AAW65794 standard; peptide; 5 AA.
XX
XX AC AAW65794;
XX
XX DT 19-OCT-1998 (first entry)
XX
XX DE Polypyrrol inhibitor of cyclophilin.
XX
XX KW polypyrrol; cyclophilin; inhibitor; neurotrophic compound; PPI;
XX ptiptydyl-prolyl isomerase; rotamase; immunophilin protein; degeneration;
XX neuronal damage.
XX
XX OS Synthetic.
XX
XX PN WO9825950-A1.
XX
XX PD 18-JUN-1998.
XX
XX PF 08-DEC-1997; 97WO-US23102.
XX
XX PR 09-DEC-1996; 96US-0761902.
XX
XX PA (GUIL-) GUILFORD PHARM INC.
XX
XX PI Hamilton GS, Steiner JP, Wei L;
XX

```

DR WPI; 1998-348444/30.

XX Effecting neuronal activity in mammals - by administering tetra-

PT and penta- peptide inhibitors of cyclophilin and rotamase enzyme,

PT useful in treatment of neuronal damage or degeneration disorders

XX

PS Claim 11; Page 41; 70pp; English.

XX The invention relates to a method of effecting a neuronal activity. It

CC comprises administering a neurotrophic compound with an affinity for a

CC cyclophilin type immunophilin. The immunophilin shows peptidyl-prolyl

CC isomerase (rotamase) activity. The neurotrophic compound achieves the

CC stimulation of damaged neurons, promotion of neuronal regeneration or

CC prevention of neurodegeneration, and treatment of neurological disorder.

CC The neurotrophic compounds are potent peptidyl-proline isomerase

CC (rotamase) inhibitors. They are of use in disorders which include

CC peripheral neuropathy caused by physical injury or disease state, i.e.

CC physical injury to the brain or spinal cord, stroke, or neurological

CC disorder leading to neurodegeneration, notably Alzheimer's and

CC Parkinson's diseases, or amyotrophic lateral sclerosis. The neurotrophic

CC compounds avoid the side effects of immunosuppressant drugs, including

CC nephrotoxicity, impaired glomerular filtration, interstitial fibrosis,

CC involuntary tremors, headaches, and hypertension. They are also free from

CC the difficulties in delivery and bioavailability of large molecular

CC weight proteins. The present sequence represents a specifically claimed

CC neurotrophic compound.

XX

XX Sequence 5 AA;

SQ

Query Match 22.2%; Score 4; DB 19; Length 5;

Best Local Similarity 100.0%; Pred. No. 9.3e+05; Length 5;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PFPK 8

Db 2 PFPK 5

|||||

RESULT 27

AA06327

ID AAY06327 standard; Peptide; 6 AA.

XX

AC AAY06327;

XX

XX 06-SEP-1999 (first entry)

DT

DE Cellulase EGIII-like enzyme conserved motif.

XX

XX Cellulase; endoglucanase; EGIII; textile; feed additive; baking;

KW food processing; grain wet milling; pulp; paper.

KW

OS Synthetic.

OS

XX WO9931255-A2.

PN

XX 24-JUN-1999.

PD

XX 14-DEC-1998; 98WO-US26552.

XX

XX 16-DEC-1997; 97US-0991720.

PR

XX (GEMV ) GENENCOR INT INC.

PA

XX Bower BS, Fowler T, Phillips JI;

PI

XX WPI; 1999-395187/33.

DR

XX EGIII like cellulase

PT

XX Claim 1c; Page 34; 47pp; English.

PS

XX The invention relates to novel enzymes which share certain

CC conserved sequences (see AAY06325-29), including the present

CC sequence, with EGIII cellulase from *Trichoderma reesei* (see

CC AA06330). These novel EGIII-like enzymes contain one or more of

CC the conserved motifs. PCR primers (see AAX59180-91) based on the

CC conserved motifs can be used to detect novel EGIII-like enzymes

CC (see AAY06331-70) in fungal and bacterial sources. The invention

CC also provides a vector comprising DNA encoding an EGIII-like

CC enzyme, host cells and a method of producing a cellulase by

CC culturing the host cell. The EGIII-like cellulases can be used in

CC the treatment of a cellulose-containing textile, as a feed

CC additive, in the treatment of wood pulp, in the reduction of

CC biomass to glucose, in the stone washing of indigo dyed denim, or

CC as a laundry detergent component (all claimed).

XX

XX Sequence 6 AA;

SQ

Query Match 22.2%; Score 4; DB 20; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 EPPT 15

Db 3 EPPT 6

|||||

RESULT 28

AA06330

ID AAB14886 standard; peptide; 6 AA.

XX

AC AAB14886;

XX

XX 21-NOV-2000 (first entry)

DT

XX EGIII-like cellulase amino acid string #3.

DE

XX Endoglucanase III; EGIII; cellulase; mutant; *Trichoderma reesei*;

KW enzyme stability; textile treatment; wood pulp treatment; feed additive;

KW detergent.

KW

XX Acromonium brachyphenium.

OS

OS Chaetomium brasiliense.

OS Chaetomium vitellium.

OS Emericella desertoru.

OS Fusarium equiseti.

OS Gliocladium roseum.

OS Humicola grisea.

OS Myceliophthora thermophila.

OS Penicillium notatum.

OS Phanerochaete chrysosporium.

OS Trichoderma reesei.

OS

XX WO200037614-A2.

PN

XX 29-JUN-2000.

XX

PD 12-NOV-1999; 99WO-US26704.

XX

PF 18-DEC-1998; 98US-0216295.

PR

XX (GEMV ) GENENCOR INT INC.

PA

XX Mitchinson C, Wendt DJ;

PI

XX WPI; 2000-482483/42.

XX

XX Novel endoglucanase III or endoglucanase III-like cellulase useful for

PT treating textiles and wood pulp comprises a substitution or deletion at

PT specified positions in the wild form of endoglucanase III -

XX

XX Disclosure; Page 8; 52pp; English.

PS

XX The present sequence is an amino acid string found in all cellulases

CC related to endoglucanase III (EGIII) from *Trichoderma reesei*. The

CC sequence was used to design primers to amplify EGIII-like genes from

CC genomic DNA libraries constructed from various microorganisms. The  
 CC isolated genes were found to share significant homology with EGIII from  
 CC Trichoderma reesei. Certain substitution and deletion mutations have  
 CC been incorporated into EGIII and EGIII-like cellulases to produce  
 CC variant enzymes with improved stability, e.g. increased resistance to  
 CC temperature stress. The mutants may be used in textile and wood pulp  
 CC treatment, as a feed additive, and for reducing biomass to glucose.  
 CC They are also useful for stonewashing or indigo dyed denim and as an  
 CC agent in laundry and dish detergents.

XX SQ Sequence 6 AA;  
 Query Match 22.2%; Score 4; DB 21; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05; Indels 0;  
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

Qy 12 EPFT 15  
 |||||  
 Db 3 EPFT 6

RESULT 29  
 AAU77071  
 ID AAU77071 standard; peptide; 6 AA.  
 XX AC AAU77071;  
 XX DT 05-JUN-2002 (first entry)  
 XX DE Endoglucanase EGIII-like cellulase BOX3 motif #1.  
 XX KW EGIII; cellulase; BOX3; endoglucanase III; detergent;  
 KW cellulose treatment; stonewashing; indigo dyed denim; feed additive;  
 KW wood pulp treatment; biomass reduction; laundry; dish detergent;  
 KW milling; depilling; softening; surface fibre removal; anti-greying.

XX OS Acremonium chrysogenum.  
 OS Chaetomium brasiliense.  
 OS Chaetomium vitellium.  
 OS Emericella desertoru.  
 OS Fusarium equiseti.  
 OS Gliocladium roseum.  
 OS Humicola grisea var thermoida.  
 OS Myceliophthora thermophila.  
 OS Penicillium notatum.  
 OS Phanerochaete chrysosporium.

XX WO200212466-A2.  
 XX PD 14-FEB-2002.  
 XX PF 31-JUL-2001; 2001WO-US23991.  
 XX PR 04-AUG-2000; 2000US-0633085.  
 XX PA (GEMV) GENENCOR INT INC.  
 XX PI Day AG, Gualfetti P, Mitchinson C, Shaw A;  
 XX WPI; 2002-241752/29.  
 XX Novel variant of endoglucanase III or endoglucanase III-like cellulase  
 PT for treating cellulose containing textile, has performance sensitive  
 PT residues replaced to residue having modified stability -  
 XX Disclosure; Page 6; 47pp; English.

XX The invention relates to a variant of endoglucanase III (EGIII) or  
 CC EGIII-like cellulase comprising a substitution or deletion at a position  
 CC corresponding to one or more of residues W7, G31, A35, T145, Y147, Q162  
 CC and/or Y168 in EGIII from Trichoderma reesei. Also included are a  
 CC DNA encoding the variant, a vector comprising the DNA, a host cell  
 CC transformed with the vector and a detergent composition comprising a

CC surfactant and the variant. The variant is useful in the treatment of a  
 CC cellulose containing textile, stonewashing or indigo dyed denim or as a  
 CC feed additive or in the treatment of wood pulp, in reduction of biomass  
 CC to glucose. The detergent composition is useful as the main component of  
 CC a laundry or dish detergent and is further useful as pre-wash  
 CC composition, pre-soak composition or for cleaning during the regular wash  
 CC or clean cycle. The variant increases value of animal feed, improves the  
 CC drainability of food pulp, enhances food products and reduces fibre in  
 CC grain during grain wet (or dry) milling process. Further cellulase  
 CC improves the feel e.g. smoothness and/or appearance e.g. removing pills  
 CC and fibrils which tend to reduce the sharpness in appearance of a  
 CC fabric, of cellulose containing fabric, and imparts desirable effects  
 CC such as depilling, softening, anti-pilling, surface fiber removal,  
 CC anti-greying and cleaning. The present sequence is a BOX motif found  
 CC in the EGIII-like cellulases, used to construct degenerate primers  
 CC for isolation of the genes encoding the EGIII-like cellulases.

XX SQ Sequence 6 AA;  
 Query Match 22.2%; Score 4; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 EPFT 15  
 |||||  
 Db 3 EPFT 6

RESULT 30  
 AAU77438  
 ID AAU77438 standard; peptide; 6 AA.  
 XX AC AAU77438;  
 XX DT 05-JUN-2002 (first entry)  
 XX DE EGIII-like cellulase consensus peptide #3.  
 XX KW Endoglucanase III-like cellulase; EGIII-like; fungus;  
 KW cellulose containing textile.  
 XX OS Synthetic.  
 XX PN WO200212464-A2.  
 XX PD 14-FEB-2002.  
 XX PF 31-JUL-2001; 2001WO-US23989.  
 XX PR 04-AUG-2000; 2000US-0632426.  
 XX PA (GEMV) GENENCOR INT INC.  
 XX PI Mitchinson C, Ropp TH, Swanson BA;  
 XX WPI; 2002-241750/29.  
 XX Novel endoglucanase III (EGIII)-like cellulase variant comprising  
 PT substitution/deletion at positions corresponding to specific residues  
 PT in EGIII from Trichoderma reesei, useful for treating cellulose  
 PT containing textile -  
 XX Disclosure; Page 5; 41pp; English.

XX The present invention relates to novel endoglucanase III (EGIII)-like  
 CC cellulase variants which comprise a substitution or deletion at a  
 CC position corresponding to one or more of residues M79, M154 and/or  
 CC M118 in mature EGIII from the fungus, Trichoderma reesei. The variants  
 CC are useful in the treatment of a cellulose containing textile. By  
 CC substituting other amino acids for the native methionines at  
 CC positions 79, 118 and 154 (sites where oxidation of the enzyme takes  
 CC place) in EGIII from T. reesei, oxidatively more stable enzymes are  
 CC obtained. The present sequence represents an EGIII-like cellulase

CC consensus peptide used to construct degenerate primers for the  
 CC isolation of EGIII-like cellulases from different organisms.

SQ Sequence 6 AA;

Query Match 22.2%; Score 4; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EPFT 15  
 ||||  
 Db 3 EPFT 6

## RESULT 31

ID AAU87807 standard; Peptide; 6 AA.

XX AC AAU87807;

DT 05-JUN-2002 (first entry)

XX Endoglucanase III (EGIII)-like cellulase peptide #3.

DE Endoglucanase III cellulase; EGIII; textile; stonewash;

KW indigo dyed denim; wood pulp; feed additive; grain wet milling;

KW grain dry milling; detergent; pre-wash composition;

KW pre-soak composition; paper processing; surfactant mediated stress;

KW thermal mediated stress.

XX OS Synthetic.

XX PN WO200212462-A2.

XX PD 14-FEB-2002.

XX PF 31-JUL-2001; 2001WO-US23946.

XX PR 04-AUG-2000; 2000US-0632570.

XX PA (GEMV ) GENENCOR INT INC.

XX PI Mitchinson C, Gualfetti P, Phillips JI;

XX WPI; 2002-241748/29.

XX Variant endoglucanase-III, useful in treatment of cellulose containing  
 PT textile and wood pulp, in treatment of biomass to glucose and as a feed  
 PT additive, is a variant of EGIII from *Trichoderma reesei* -  
 XX Disclosure; Page 6; 44pp; English.

XX The invention describes a variant endoglucanase (EG)-III or EGIII-like  
 CC cellulase (I), comprising a substitution or deletion at a position  
 CC corresponding to residues P201, G170 and/or V210 in EGIII from  
 CC *Trichoderma reesei*. (I) is useful in the treatment of a cellulose  
 CC containing textile such as stonewashing or indigo dyed denim, in the  
 CC treatment of wood pulp, in the reduction of biomass to glucose and as a  
 CC feed additive. (I) is also useful in the treatment of starch during grain  
 CC wet milling or dry milling to facilitate the production of glucose, high  
 CC fructose corn syrup and/or alcohol. A detergent composition containing  
 CC (I) is useful as pre-wash compositions, pre-soak compositions, and for  
 CC cleaning during the regular wash or rinse cycle. (I) is useful in the  
 CC processing of pulp and paper. (I) confers improved performance, including  
 CC stability in the presence of thermal and/or surfactant mediated stress.  
 CC This sequence represents a peptide encoded by a degenerate primer that  
 CC can be used as a probe to identify EGIII-like cellulases in fungal  
 CC genomic DNA.

XX SQ Sequence 6 AA;

Query Match 22.2%; Score 4; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 12 EPFT 15  
 ||||  
 Db 3 EPFT 6

## RESULT 32

AAW21388 standard; peptide; 7 AA.

XX AC AAW21388;

XX DT 29-JUL-1997 (first entry)

XX Plasminogen activator inhibitor 1 derived signal oligopeptide #16.

DE Hydrophilic; signal oligopeptide; hydrophilicity maxima; vaccine; SIV;

XX competitive inhibitor; feedback regulator; synthesis; gastrin precursor;

KW charge; polarity; farnesyl synthetase; plasminogen activator inhibitor 1;

KW hydroxymethylglutaryl coenzyme A reductase; glucagon precursor; rhesus;

KW gonadoliberin precursor; plasminogen activator inhibitor 2; prerenin;

KW Alzheimer amyloid A4; corticotropin releasing factor binding protein;

KW apolipoprotein E; herpes virus 1 glycoprotein B; HSV1; human; OMVVS;

KW herpes virus 2 glycoprotein B; HSV2; collagenase; apolipoprotein A;

KW Treponema pallidum membrane protein; TWPA; islet amyloid polypeptide;

KW fibroblast MMP; schistosoma elastase precursor; schistosomin;

KW hepatitis delta antigen; rev protein; HIV; VILV; angiotensinogen.

XX OS Homo sapiens.

XX PN WO9519568-A1.

XX PD 20-JUL-1995.

XX PF 12-JAN-1995; 95WO-US000575.

XX PR 14-JAN-1994; 94US-0182248.

XX PA (RATH/) RATH M.

XX PI Rath M;

XX WPI; 1995-263953/34.

XX Identifying signal oligopeptide(s) in protein sequence(s) - shown as  
 PT regions of max. hydrophilicity, used in modulating communication  
 PT between protein(s)  
 XX Claim 5; Page 54; 88pp; English.

XX The sequences given in AAW21201-560 represent hydrophilic signal oligo-  
 CC peptides. These signal oligopeptides are localised on the surface  
 CC of the protein and are represented by the hydrophilicity maxima of  
 CC the protein. These peptides are enriched in charged amino acids  
 CC arranged with neutral spacer amino acids. The specific signal  
 CC character of these oligopeptides is determined by a characteristic  
 CC combination of conformation and charge within the signal sequence.  
 CC These oligopeptides may be used as vaccines in the treatment of  
 CC human disease, as competitive inhibitors to prevent or reduce the  
 CC metabolic action or interaction of a selected protein by blocking  
 CC its specific signal sequences, or as therapeutic agents to function  
 CC as feedback regulators to reduce synthesis rate of a selected protein.  
 CC These peptides may be modified by omitting one or more amino acids at  
 CC the N- and/or C-terminal, by substituting one or more amino acids  
 CC without consideration of charge and polarity, by substituting one or  
 CC more amino acids with amino acid residues with similar charge and/or  
 CC polarity, by omitting one or more amino acids or a combination of these.

XX SQ Sequence 7 AA;

Query Match 22.2%; Score 4; DB 16; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MPFP 7  
Db 2 MPFP 5

RESULT 33  
AAY96209  
ID AAY96209 standard; Peptide; 7 AA.

XX AC AAY96209;  
XX DT 11-AUG-2000 (first entry)

XX DE Arabidopsis AHAS small subunit F3 gene fragment N-terminal sequence.

XX KW Herbicide-resistance; acetohydroxy-acid synthase; AHAS;  
XX KW acetolactate synthase; imidazolinone; sulfonyleurea;  
XX KW triazolopyrimidine sulfonamide; sulfamoylurea; enzyme;  
XX KW pyrimidyl-oxy-benzoic acid; sulfonyleurea; transgenic plant;  
XX KW branched-chain amino acid synthesis.

XX OS Arabidopsis.

XX PN WO200026390-A2.

XX PD 11-MAY-2000.

XX PF 28-OCT-1999; 99WO-US25452.

XX PR 29-OCT-1998; 98US-0106239.

XX XX (AMCY ) AMERICAN CYANAMID CO.

XX PI Kakefuda G, Costello C, Sun M, Hu W;

XX DR WPI; 2000-365633/31.

XX PT New polynucleotide encoding eukaryotic acetohydroxy-acid synthetase  
XX PT small subunit protein for producing transgenic herbicide resistant  
XX PT plants and identifying mutations affecting enzymatic activity of the  
XX PT synthetase -

XX PS Disclosure; Page 25; 57pp; English.

XX CC Arabidopsis acetohydroxy-acid synthase (AHAS) small subunit is needed  
XX CC for branched-chain amino acid synthesis and so is essential for life.  
XX CC AHAS is also known as acetolactate synthase. Inhibition of this enzyme  
XX CC in plants would lead to plant death and therefore inhibitors would be  
XX CC potential herbicides. Certain herbicides are known to inhibit AHAS:  
XX CC imidazolinones, sulfonyleureas, triazolopyrimidine sulfonamides,  
XX CC pyrimidyl-oxy-benzoic acids, sulfamoylureas and sulfonyleureas.  
XX CC Mutant AHAS may be resistant to these herbicides and may be used to  
XX CC create herbicide resistant transgenic plants e.g. dicot and monocot crop  
XX CC plants. A thrombin cleavage site was incorporated into an AHAS small  
XX CC subunit gene. The AHAS small subunit gene fragments were cloned into  
XX CC plasmid expression vectors, and were expressed as glutathione  
XX CC transferase/ AHAS small subunit fusion proteins. The glutathione  
XX CC transferase was then cleaved via the thrombin cleavage site. Cleavage  
XX CC however modifies the N-terminal sequence of the AHAS small subunit gene  
XX CC fragments, in that the glycine and serine residues of the cleavage site  
XX CC are maintained on the AHAS protein. The present sequence details the  
XX CC N-terminal sequence of one such AHAS small subunit gene fragment,  
XX CC F3, which is a near full length AHAS small subunit gene, with the  
XX CC modification due to cleavage.

XX SQ Sequence 7 AA;

Query Match 22.2%; Score 4; DB 21; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VEPF 14  
Db 3 VEPF 6

RESULT 34  
AAR61422  
ID AAR61422 standard; peptide; 8 AA.

XX AC AAR61422;

XX DT 25-MAR-2003 (updated)  
XX DT 25-AUG-1995 (first entry)

XX DE PF4-related octapeptide.

XX KW antiinflammatory; platelet factor 4; PF-4 autoimmune disease;  
XX KW graft-versus-host; reperfusion injury; atherosclerosis; asthma.  
XX OS Synthetic.

XX PN WO9500543-A1.

XX PD 05-JAN-1995.

XX PF 17-JUN-1994; 94WO-US06888.

XX PR 18-JUN-1993; 93US-0080371.

XX PA (COUN/) COUNTS D F.  
XX PA (DUFF/) DUFF R G.

XX PI Counts DF, Duff RG;

XX DR WPI; 1995-052005/07.

XX PT New peptide(s) and derivs. based on platelet factor 4 - used for  
XX PT inhibiting an immune response, including an inflammatory response  
XX PT in e.g. autoimmune diseases.

XX PS Disclosure; Page 44; 99pp; English.

XX CC New peptides are disclosed which include any peptide, peptide  
XX CC derivative or peptide analogue which comprises either (i) at least a  
XX CC 4 amino acid portion of PF-4 (see AAR61401) or a functionally equivalent  
XX CC sequence, or (ii) at least a 6 amino acid sequence which is at least  
XX CC 66% homologous to a portion of the PF-4 sequence, or a functionally  
XX CC equivalent sequence. Pref. the peptide contains the sequence  
XX CC Thr-Ser-Gln and/or Val-Arg-Pro, and more preferably Thr-Thr-Ser-Gln  
XX CC and/or Val-Arg-Pro-Arg. The most preferred peptide is  
XX CC Thr-Thr-Ser-Gln-Val-Arg-Pro-Arg (see AAR61493), designated CT-112.  
XX CC The peptide may be derivatised at the N- and/or C-terminal, or may be  
XX CC cyclised, substituted, truncated or contain D-amino acid residues.  
XX CC The present sequence is an analogue CT-112 containing Glu substitution.  
XX CC The peptides exhibit antiinflammatory activity and may be used to treat  
XX CC autoimmune diseases (such as insulin-dependent diabetes, ulcerative  
XX CC colitis, rheumatoid arthritis, scleroderma, mixed connective tissue  
XX CC disease and SLE), reperfusion tissue damage, inflammatory lung disease,  
XX CC graft-versus-host disease, atherosclerosis and asthma.  
XX CC When tested for antiinflammatory activity by a single 6 mg/kg  
XX CC subcutaneous dose using the mouse ear acute inflammation model,  
XX CC peptide CT-112 gave an inhibition value of 64.9%. In comparison,  
XX CC the present sequence gave a value of 43.2%.  
XX CC (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 8 AA;

Query Match 22.2%; Score 4; DB 16; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 YESQ 18  
|||||

Db 1 TESQ 4

RESULT 35  
AAW05539  
ID AAW05539 standard; peptide; 8 AA.  
XX  
AC AAW05539;  
XX  
DT 17-JUN-1997 (first entry)  
XX  
DE Peptide fragment #1 of aminopeptidase of the invention.  
XX  
KW Aminopeptidase; aspergillus oryzae; enzyme; protein hydrolysate; gluten;  
KW protease; N-terminus.  
XX  
OS Aspergillus oryzae.  
XX  
FN WO9628542-A1.  
XX  
PD 19-SEP-1996.  
XX  
PF 15-MAR-1996; 96WO-DK00104.  
XX  
PR 16-MAR-1995; 95DK-0000262.  
XX  
PA (NOVO ) NOVO-NORDISK AS.  
XX  
PI Dammann C, Halkier T, Kauppinen S, Ostergaard PR;  
PI Si JQ, Spandler T;  
XX  
XX WPI; 1996-464617/46.  
XX  
XX Enzyme with aminopeptidase activity - used in bread or  
PT dough-improving compsns., and to reduce the bitter taste of proteins  
PT or protein hydrolysates for foodstuffs, partic. cheese or cocoa  
XX  
XX Claim 7; Page 56; 75pp; English.  
XX  
XX AAW05538-W05543 represent fragments of the Aspergillus oryzae  
CC aminopeptidase (see AAW05589) of the invention. Aminopeptidases are  
CC capable of removing one or more amino terminal residues from  
CC polypeptides. The enzyme is used in a preparation to reduce the bitter  
CC taste of proteins or protein hydrolysates for foodstuffs, particularly  
CC cheese or cocoa, so improving their flavour. It is also useful in a bread  
CC or dough-improving composition, and in the preparation of baked products  
CC from a flour dough or frozen dough. The enzyme is also useful to improve  
CC dough stickiness, crumb structure or crust colour of a baked product. The  
CC enzyme preparation can also be used to clean contact lenses and in  
CC brewing. The enzyme does not degrade the network of the gluten normally  
CC seen when proteases are used in the preparation of baked products. Thus,  
CC the dough characteristics and crumb structure are unaffected.  
XX  
SQ Sequence 8 AA;  
Query Match 22.2%; Score 4; DB 17; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 11 VEPF 14  
| | | |  
Db 4 VEPF 7

RESULT 36  
AAW58608  
ID AAW58608 standard; peptide; 8 AA.  
XX  
AC AAW58608;  
XX  
DT 25-MAR-2003 (updated)  
DT 08-SEP-1998 (first entry)  
XX

DE Platelet factor 4 derived peptide SEQ ID NO:30.  
XX  
KW Platelet factor 4; PF4; anti-inflammatory; inhibition; inflammation;  
KW autoimmune disease; graft versus host disease; reperfusion injury;  
XX atherosclerosis; asthma.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FN US5776892-A.  
XX  
PD 07-JUL-1998.  
XX  
PF 16-JUN-1994; 94US-0259550.  
XX  
PR 16-JUN-1994; 94US-0259550.  
PR 21-DEC-1990; 90US-0631823.  
PR 24-MAR-1993; 93US-0037486.  
PR 18-JUN-1993; 93US-0080371.  
XX  
PA (CURA-) CURATIVE HEALTH SERVICES INC.  
XX  
PI Counts DF, Duff RG;  
XX  
XX WPI; 1998-398086/34.  
XX  
PT New antiinflammatory peptide(s) based on platelet factor 4 sequences  
PT - used for treating e.g. auto:immune diseases, graft versus host  
PT disease, reperfusion injury, atherosclerosis or asthma  
XX  
PS Claim 2; Column 75; 55pp; English.  
XX  
XX The present sequence represents a peptide which is related to platelet  
CC factor 4 (PF4) and can be used to inhibit an inflammatory response.  
CC Peptides, peptide analogues and peptide derivatives of PF4 can be used  
CC for treating e.g. autoimmune diseases such as insulin dependent  
CC diabetes, Goodpasture's syndrome, pemphigus and pemphigoid, primary  
CC biliary cirrhosis, ulcerative colitis, rheumatoid arthritis,  
CC scleroderma, mixed connective tissue disease and lupus erythematosus,  
CC graft versus host disease, septic shock, reperfusion injury (including  
CC injury subsequent to myocardial or cerebral infarction),  
CC atherosclerosis, asthma and inflammatory lung disease. The peptides  
CC give a new and effective method of inhibiting the inflammatory response  
CC by acting on cytokines rather than the prior art arachidonic acid.  
CC (Updated on 25-MAR-2003 to correct PF field.)  
XX  
SQ Sequence 8 AA;  
Query Match 22.2%; Score 4; DB 19; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 15 TESQ 18  
| | | |  
Db 1 TESQ 4

RESULT 37  
AAB45558  
ID AAB45558 standard; Protein; 9 AA.  
XX  
AC AAB45558;  
XX  
DT 02-MAR-2001 (first entry)  
XX  
DE Human B99-1 HLA B\*4403 immunogenic peptide SEQ ID NO 95.  
XX  
KW Tumor-associated antigen; B99; immunogenic; humoral immune response;  
KW cellular immune response; immunotherapy; cancer; kidney; lung; colon;  
KW pancreas; breast; stomach; vaccine; diagnosis; treatment.  
XX  
OS Homo sapiens.  
XX

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PN WO200066727-A1.
XX
PD 09-NOV-2000.
XX
PF 19-APR-2000; 2000WO-EP03552.
XX
PR 28-APR-1999; 99DE-1019225.
XX
XX (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
XX
PI Adolf G, Heider K, Sommergruber W;
XX
DR WPI; 2000-679759/66.
XX
PT New tumor-associated antigen B99, useful in immunotherapy of cancer,
PT and related nucleic acid and antibodies -
XX
PS Example 7; Page 46; 75pp; German.
XX
CC This invention describes a novel tumor-associated antigen, designated
CC B99 which has anticancer activity. B99, or its immunogenic fragments or
CC peptides, induces a humoral and/or cellular immune response against
CC tumor cells that express B99. B99 (or its immunogenic fragments or
CC peptides) and also the nucleic acid that encodes them, are useful for
CC immunotherapy of cancer, in vivo or in vitro, especially cancers of
CC kidney, lung, colon, pancreas, breast or stomach. Cells that express B99
CC are useful in cancer vaccines and antibodies (Ab) directed against B99
CC are used for diagnosis and treatment of cancers that express B99,
CC optionally when coupled to a cytotoxin or radioisotope. Peptides from
CC B99 can also be used diagnostically to monitor a patient's response to
CC treatment and B99, or its DNA, are used to identify specific modulators,
CC particularly inhibitors, of B99 activity.
XX
SQ Sequence 9 AA;
Query Match 22.2%; Score 4; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 EPPT 15
Db 1 EPPT 4
|||||
RESULT 39
AAY73039
ID AAY73039 standard; Peptide; 9 AA.
XX
AC AAY73039;
XX
DT 28-FEB-2000 (first entry)
XX
DE Hepatitis B virus (HBV)-derived MHC class I (CTL) epitope, #197.
XX
KW Chimeric; pan DR epitope; expression vector;
KW promoter; major histocompatibility complex; MHC; targeting; peptide;
KW epitope; antigen; presentation; class I; cytosolic pathway;
KW endoplasmic reticulum; class II; extracellular antigen;
KW endocytic pathway; helper T lymphocyte; HTL; universal epitope;
KW cytotoxic T lymphocyte; CTL; immune response; immunogenicity; assay;
KW vaccine; immunity; infection; pathogen; virus; HIV; HBV; HCV;
KW hepatitis B; hepatitis C; bacterium; protozoan; tumour cell;
KW autoimmune disease; activation; antiviral; antimalarial;
KW immunoprotective.
XX
OS Synthetic.
OS Hepatitis b virus.
XX
PN WO9558558-A2.
XX
PD 18-NOV-1999.
XX
PF 13-MAY-1999; 99WO-US10646.
XX
PR 13-MAY-1998; 98US-0078904.
PR 15-MAY-1998; 98US-0085751.
XX
XX (EPTM-) EPIMUNE INC.
XX
PI Fikes JD, Hermanson GG, Sette A, Ishioka GY, Livingston B;
PI Chesnut RW;
XX
DR WPI; 2000-039103/03.
XX
PT Expression vectors encoding major histocompatibility targeting
PT sequence, used as, e.g. tumor vaccines -

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PN WO200066727-A1.
XX
PD 09-NOV-2000.
XX
PF 19-APR-2000; 2000WO-EP03552.
XX
PR 28-APR-1999; 99DE-1019225.
XX
XX (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
XX
PI Adolf G, Heider K, Sommergruber W;
XX
DR WPI; 2000-679759/66.
XX
PT New tumor-associated antigen B99, useful in immunotherapy of cancer,
PT and related nucleic acid and antibodies -
XX
PS Example 7; Page 46; 75pp; German.
XX
CC This invention describes a novel tumor-associated antigen, designated
CC B99 which has anticancer activity. B99, or its immunogenic fragments or
CC peptides, induces a humoral and/or cellular immune response against
CC tumor cells that express B99. B99 (or its immunogenic fragments or
CC peptides) and also the nucleic acid that encodes them, are useful for
CC immunotherapy of cancer, in vivo or in vitro, especially cancers of
CC kidney, lung, colon, pancreas, breast or stomach. Cells that express B99
CC are useful in cancer vaccines and antibodies (Ab) directed against B99
CC are used for diagnosis and treatment of cancers that express B99,
CC optionally when coupled to a cytotoxin or radioisotope. Peptides from
CC B99 can also be used diagnostically to monitor a patient's response to
CC treatment and B99, or its DNA, are used to identify specific modulators,
CC particularly inhibitors, of B99 activity.
XX
SQ Sequence 9 AA;
Query Match 22.2%; Score 4; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 EPPT 15
Db 2 EPPT 5
|||||
RESULT 38
AAB45559
ID AAB45559 standard; Protein; 9 AA.
XX
AC AAB45559;
XX
DT 02-MAR-2001 (first entry)
XX
DE Human B99-1 HLA B7 immunogenic peptide SEQ ID NO 96.
XX
KW Tumor-associated antigen; B99; immunogenic; humoral immune response;
KW cellular immune response; immunotherapy; cancer; kidney; lung; colon;
KW pancreas; breast; stomach; vaccine; diagnosis; treatment.
XX
OS Homo sapiens.
XX
PN WO200066727-A1.
XX
PD 09-NOV-2000.
XX
PF 19-APR-2000; 2000WO-EP03552.
XX
PR 28-APR-1999; 99DE-1019225.
XX
XX (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
XX
PI Adolf G, Heider K, Sommergruber W;
XX
DR WPI; 2000-679759/66.

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XX Claim 11; Page 65; 130pp; English.

PS Sequences AAY72998-Y73086 represent hepatitis B virus (HBV)-derived MHC

XX Class I (CTL) epitopes which are claimed for use in the present

CC invention. The invention relates to a novel expression vector comprising

CC a promoter operably linked to a fusion gene encoding a major

CC histocompatibility complex (MHC) targeting sequence, and two or more

CC heterologous peptide epitopes. The MHC targeting sequence may be a

CC class I targeting sequence, which directs an MHC class I epitope to

CC a cytosolic pathway or to the endoplasmic reticulum, or an MHC class

CC II targeting sequence, which directs extracellular antigens to

CC enter the endocytic pathway to be processed into antigen peptides

CC for presentation on MHC class II molecules. The heterologous

CC epitopes may comprise either helper T lymphocyte (HTL) epitopes,

CC or a cytotoxic T lymphocyte (CTL) epitope and a universal HTL

CC epitope such as a pan DR epitope (PADRE). The vectors are useful

CC for stimulating an immune response in vivo, as well as for use in

CC assaying the human immunogenicity of a human T cell peptide epitope in

CC vivo in a non-human mammal. They provide a nucleic acid vaccine for

CC enhancing immunity against infectious pathogens, such as viruses (e.g.,

CC HIV, hepatitis B (HBV) and hepatitis C (HCV)), bacteria, protozoa (e.g.,

CC Plasmodium falciparum, the cause of malaria) and also tumour cells and

CC autoimmune diseases. Universal MHC class II epitopes are advantageously

CC combined with other MHC class I and class II epitopes to increase the

CC number of cells that are activated in response to a given antigen and

CC provide a broader population coverage of MHC-reactive alleles.

XX SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 21; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 FTES 17

Db 2 FTES 5

RESULT 40

AAM24524

ID AAM24524 standard; Peptide; 9 AA.

XX AAM24524;

AC AAM24524;

XX 04-DEC-2001 (first entry)

DT Human MHC class I molecule HLA-A1 binding 83P5G4 peptide #1.

DE

XX 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;

XX tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;

XX cytostatic; gene therapy; antibody therapy; ribozyme; blood; cervix;

XX single chain monoclonal antibody; urine; uterus; rectum; stomach; human;

XX chromosome 1q31-q32.

XX Homo sapiens.

OS

XX W0200159115-A2.

PN 16-AUG-2001.

PD 09-FEB-2001; 2001WO-US04426.

PF

XX (UROG-) UROGENESYS INC.

XX Hubert RS, Afar DEH, Challita-eid PM, Faris M, Levin E;

XX Mitchell SC, Jakobovits A;

XX WPI; 2001-514669/56.

XX An isolated 83P5G4-related protein useful as a diagnostic and/or

PT

PT therapeutic agent in multiple cancers such as prostate, bladder and

PT bone cancer -

XX Example 15; Page 74; 112pp; English.

PS

XX The polypeptide sequences represent the 83P5G4-related protein and

CC peptide fragments of the protein. 83P5G4 exhibits prostate specific

CC expression in normal adult tissue, but it is also aberrantly expressed in

CC many cancers including tumours of the prostate, testis, bladder, kidney,

CC brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum,

CC liver, colon and lung. The 83P5G4 polynucleotide, its related protein and

CC peptide fragments and specific PCR primers are therefore useful for

CC diagnosing and treating cancer. A vector comprising a polynucleotide

CC which encodes a single chain monoclonal antibody that immunospecifically

CC binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a

CC polynucleotide having the 83P5G4 coding sequence, are both useful in the

CC preparation of a composition for treating a patient with a cancer that

CC expresses 83P5G4. The sequences can be used in diagnostic methods to

CC monitor the level of 83P5G4 gene products in serum, blood, urine and

CC tissue and to thereby detect the presence of cancerous cells.

XX SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 22; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TESQ 18

Db 2 TESQ 5

RESULT 41

AAM24745

ID AAM24745 standard; Peptide; 9 AA.

XX AAM24745;

AC AAM24745;

XX 04-DEC-2001 (first entry)

DT Human MHC class I molecule HLA-A3 binding 83P5G4 peptide #22.

DE

XX 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;

XX tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;

XX cytostatic; gene therapy; antibody therapy; ribozyme; blood; cervix;

XX single chain monoclonal antibody; urine; uterus; rectum; stomach; human;

XX chromosome 1q31-q32.

XX Homo sapiens.

OS

XX W0200159115-A2.

PN 16-AUG-2001.

PD 09-FEB-2001; 2001WO-US04426.

PF

XX (UROG-) UROGENESYS INC.

XX Hubert RS, Afar DEH, Challita-eid PM, Faris M, Levin E;

XX Mitchell SC, Jakobovits A;

XX WPI; 2001-514669/56.

XX An isolated 83P5G4-related protein useful as a diagnostic and/or

PT therapeutic agent in multiple cancers such as prostate, bladder and

PT bone cancer -

XX Example 15; Page 79; 112pp; English.

PS

XX The polypeptide sequences represent the 83P5G4-related protein and

CC peptide fragments of the protein. 83P5G4 exhibits prostate specific

CC expression in normal adult tissue, but it is also aberrantly expressed in  
 CC many cancers including tumours of the prostate, testis, bladder, kidney,  
 CC brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum,  
 CC liver, colon and lung. The 83P5G4 polynucleotide, its related protein and  
 CC peptide fragments and specific PCR primers are therefore useful for  
 CC diagnosing and treating cancer. A vector comprising a polynucleotide  
 CC which encodes a single chain monoclonal antibody, that immunospecifically  
 CC binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a  
 CC polynucleotide having the 83P5G4 coding sequence, are both useful in the  
 CC preparation of a composition for treating a patient with a cancer that  
 CC expresses 83P5G4. The sequences can be used in diagnostic methods to  
 CC monitor the level of 83P5G4 gene products in serum, blood, urine and  
 CC tissue and to thereby detect the presence of cancerous cells.

XX  
 XX  
 SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TESQ 18  
 |||||  
 Db 2 TESQ 5

RESULT 42  
 AAM24826  
 ID AAM24826 standard; Peptide; 9 AA.  
 AC AAM24826;  
 XX  
 DT 04-DEC-2001 (first entry)  
 XX  
 DE Human MHC molecule HLA-A11 binding 83P5G4 peptide #3.  
 XX  
 KW 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;  
 KW tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;  
 KW cytostatic; gene therapy; antibody therapy; ribozyme; blood; cervix;  
 KW single chain monoclonal antibody; urine; uterus; rectum; stomach; human;  
 KW chromosome 1q31-q32.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200159115-A2.  
 XX  
 PD 16-AUG-2001.  
 XX  
 PF 09-FEB-2001; 2001WO-US04426.  
 XX  
 PR 09-FEB-2000; 2000US-0181261.  
 XX  
 PA (UROG-) UROGENESYS INC.  
 XX  
 PI Hubert RS, Afar DEH, Challita-eid PM, Faris M, Levin E;  
 PI Mitchell SC, Jakobovits A;  
 XX  
 WPI; 2001-514669/56.

XX An isolated 83P5G4-related protein useful as a diagnostic and/or  
 PT therapeutic agent in multiple cancers such as prostate, bladder and  
 PT bone cancer -  
 XX  
 PS Example 15; Page 81; 112pp; English.

XX The polypeptide sequences represent the 83P5G4-related protein and  
 CC peptide fragments of the protein. 83P5G4 exhibits prostate specific  
 CC expression in normal adult tissue, but it is also aberrantly expressed in  
 CC many cancers including tumours of the prostate, testis, bladder, kidney,  
 CC brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum,  
 CC liver, colon and lung. The 83P5G4 polynucleotide, its related protein and  
 CC peptide fragments and specific PCR primers are therefore useful for  
 CC diagnosing and treating cancer. A vector comprising a polynucleotide  
 CC which encodes a single chain monoclonal antibody, that immunospecifically

CC binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a  
 CC polynucleotide having the 83P5G4 coding sequence, are both useful in the  
 CC preparation of a composition for treating a patient with a cancer that  
 CC expresses 83P5G4. The sequences can be used in diagnostic methods to  
 CC monitor the level of 83P5G4 gene products in serum, blood, urine and  
 CC tissue and to thereby detect the presence of cancerous cells.

XX Sequence 9 AA;

Query Match 22.2%; Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TESQ 18  
 |||||  
 Db 2 TESQ 5

RESULT 43  
 AAM24925  
 ID AAM24925 standard; Peptide; 9 AA.  
 XX  
 AC AAM24925;  
 XX  
 DT 04-DEC-2001 (first entry)  
 XX  
 DE Human MHC class I molecule HLA-A24 binding 83P5G4 peptide #2.  
 XX  
 KW 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;  
 KW tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;  
 KW cytostatic; gene therapy; antibody therapy; ribozyme; blood; cervix;  
 KW single chain monoclonal antibody; urine; uterus; rectum; stomach; human;  
 KW chromosome 1q31-q32.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200159115-A2.  
 XX  
 PD 16-AUG-2001.  
 XX  
 PF 09-FEB-2001; 2001WO-US04426.  
 XX  
 PR 09-FEB-2000; 2000US-0181261.  
 XX  
 PA (UROG-) UROGENESYS INC.  
 XX  
 PI Hubert RS, Afar DEH, Challita-eid PM, Faris M, Levin E;  
 PI Mitchell SC, Jakobovits A;  
 XX  
 WPI; 2001-514669/56.

XX An isolated 83P5G4-related protein useful as a diagnostic and/or  
 PT therapeutic agent in multiple cancers such as prostate, bladder and  
 PT bone cancer -  
 XX  
 PS Example 15; Page 84; 112pp; English.

XX The polypeptide sequences represent the 83P5G4-related protein and  
 CC peptide fragments of the protein. 83P5G4 exhibits prostate specific  
 CC expression in normal adult tissue, but it is also aberrantly expressed in  
 CC many cancers including tumours of the prostate, testis, bladder, kidney,  
 CC brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum,  
 CC liver, colon and lung. The 83P5G4 polynucleotide, its related protein and  
 CC peptide fragments and specific PCR primers are therefore useful for  
 CC diagnosing and treating cancer. A vector comprising a polynucleotide  
 CC which encodes a single chain monoclonal antibody, that immunospecifically  
 CC binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a  
 CC polynucleotide having the 83P5G4 coding sequence, are both useful in the  
 CC preparation of a composition for treating a patient with a cancer that  
 CC expresses 83P5G4. The sequences can be used in diagnostic methods to  
 CC monitor the level of 83P5G4 gene products in serum, blood, urine and  
 CC tissue and to thereby detect the presence of cancerous cells.

SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 22; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TESQ 18  
|||||

Db 4 TESQ 7  
|||||

RESULT 44  
AAU94282  
ID AAU94282 standard; Peptide; 9 AA.  
XX  
AC AAU94282;  
XX  
XX  
DT 02-JUL-2002 (first entry)  
XX  
XX Human novel protein CaTrF2E11 HLA binding peptide #115.  
DE  
XX  
XX Human; human leukocyte antigen; HLA; immunogen; 83P2H3; CaTrF2E11;  
KW calcium transport protein; cancer; prostate cancer; cytostatic;  
KW chromosome 7q34; chromosome 12q24.1; T cell; B cell.  
XX  
XX Homo sapiens.  
XX  
XX WO200214361-A2.  
FN  
XX  
PD 21-FEB-2002.  
XX  
XX 17-AUG-2001; 2001WO-US25782.  
PF  
XX  
XX 17-AUG-2000; 2000US-226329P.  
PR  
XX  
XX (AGEN-) AGENSYS INC.  
PA  
PI Raitano AB, Challita-Eid PM, Paris M, Saffran DC, Afar DEH;  
PI Levin E, Hubert RS, Ge W, Jakobovits A;  
XX  
XX WPI; 2002-269179/31.  
DR  
XX  
XX Monitoring 83P2H3 gene products for monitoring the presence of cancer  
PT in a subject, comprises determining the status of 83P2H3 gene products  
PT in a tissue sample from the subject and comparing it to a normal sample  
PT -  
XX  
XX Example 11; Page 172; 270pp; English.  
PS  
XX  
XX The invention relates to monitoring 83P2H3 (a calcium transport  
CC protein whose gene is located on chromosome 7q34) gene products in a  
CC biological sample from a patient who has or is suspected of having  
CC cancer (especially prostate cancer), comprises: (a) determining the  
CC status of 83P2H3 gene products expressed by cells in a tissue sample from  
CC an individual and (b) comparing the status to the status of 83P2H3 gene  
CC products in a normal sample. Also included are modulators of 83P2H3  
CC function or status, generating antibodies/immune response against  
CC 83P2H3 (or related protein CaTrF2E11 whose gene is located on chromosome  
CC 12q24.1) using identified HLA (human leukocyte antigen) binding  
CC peptides derived from the protein, delivering a cytotoxic agent to  
CC a cell expressing 83P2H3 by conjugating the agent to an anti-83P2H3  
CC antibody, a recombinant protein comprising an antigen-binding region of  
CC the antibody, a non-human transgenic animal that produces the recombinant  
CC protein, a hybridoma that produces the recombinant protein, a single-  
CC chain monoclonal antibody that comprises the variable domains of the  
CC heavy and light chains of the anti-83P2H3 antibody, a vector comprising a  
CC polynucleotide that encodes the monoclonal antibody and inducing an  
CC immune response to a 83P2H3 protein, by providing a 83P2H3-related  
CC epitope that comprises a T cell or B cell epitope, and contacting the  
CC protein with an immune system T cell or B cell, respectively. The method  
CC is useful for monitoring 83P2H3 gene products in a biological sample for  
CC monitoring the presence of cancer in an individual. The modulator is  
CC useful for inhibiting the growth of cancer cells that express 83P2H3, for

CC treating cancer and the vector is useful for treating a patient with a  
CC cancer that expresses 83P2H3. The immunological methods are useful for  
CC generating an immune response against 83P2H3, and for detecting the  
CC presence of 83P2H3-related protein or polynucleotide in a biological  
CC sample from a patient who has or is suspected of having cancer. The  
CC antibody is useful in prostate cancer diagnosis, prognosis, imaging  
CC methodologies and treatment, to detect and quantify 83P2H3 and mutant  
CC 83P2H3-related proteins, for purifying a 83P2H3-related protein, for  
CC isolating 83P2H3 homologues/related molecules, and for generating anti-  
CC idiotypic antibodies that mimic the 83P2H3 protein. The present sequence  
CC is an HLA binding peptide motif from 83P2H3 or its related protein  
CC CaTrF2E11.  
XX  
SQ Sequence 9 AA;  
Query Match 22.2%; Score 4; DB 23; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KYPV 11  
|||||

Db 6 KYPV 9  
|||||

RESULT 45  
AAU94868  
ID AAU94868 standard; Peptide; 9 AA.  
XX  
AC AAU94868;  
XX  
XX  
DT 02-JUL-2002 (first entry)  
XX  
XX Human novel protein CaTrF2E11 HLA binding peptide #401.  
DE  
XX  
XX Human; human leukocyte antigen; HLA; immunogen; 83P2H3; CaTrF2E11;  
KW calcium transport protein; cancer; prostate cancer; cytostatic;  
KW chromosome 7q34; chromosome 12q24.1; T cell; B cell.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200214361-A2.  
FN  
XX  
PD 21-FEB-2002.  
XX  
XX 17-AUG-2001; 2001WO-US25782.  
PF  
XX  
XX 17-AUG-2000; 2000US-226329P.  
PR  
XX  
XX (AGEN-) AGENSYS INC.  
PA  
PI Raitano AB, Challita-Eid PM, Paris M, Saffran DC, Afar DEH;  
PI Levin E, Hubert RS, Ge W, Jakobovits A;  
XX  
XX WPI; 2002-269179/31.  
DR  
XX  
XX Monitoring 83P2H3 gene products for monitoring the presence of cancer  
PT in a subject, comprises determining the status of 83P2H3 gene products  
PT in a tissue sample from the subject and comparing it to a normal sample  
PT -  
XX  
XX Example 11; Page 193; 270pp; English.  
PS  
XX  
XX The invention relates to monitoring 83P2H3 (a calcium transport  
CC protein whose gene is located on chromosome 7q34) gene products in a  
CC biological sample from a patient who has or is suspected of having  
CC cancer (especially prostate cancer), comprises: (a) determining the  
CC status of 83P2H3 gene products expressed by cells in a tissue sample from  
CC an individual and (b) comparing the status to the status of 83P2H3 gene  
CC products in a normal sample. Also included are modulators of 83P2H3  
CC function or status, generating antibodies/immune response against  
CC 83P2H3 (or related protein CaTrF2E11 whose gene is located on chromosome  
CC 12q24.1) using identified HLA (human leukocyte antigen) binding  
CC peptides derived from the protein, delivering a cytotoxic agent to  
CC a cell expressing 83P2H3 by conjugating the agent to an anti-83P2H3  
CC antibody, a recombinant protein comprising an antigen-binding region of  
CC the antibody, a non-human transgenic animal that produces the recombinant  
CC protein, a hybridoma that produces the recombinant protein, a single-  
CC chain monoclonal antibody that comprises the variable domains of the  
CC heavy and light chains of the anti-83P2H3 antibody, a vector comprising a  
CC polynucleotide that encodes the monoclonal antibody and inducing an  
CC immune response to a 83P2H3 protein, by providing a 83P2H3-related  
CC epitope that comprises a T cell or B cell epitope, and contacting the  
CC protein with an immune system T cell or B cell, respectively. The method  
CC is useful for monitoring 83P2H3 gene products in a biological sample for  
CC monitoring the presence of cancer in an individual. The modulator is  
CC useful for inhibiting the growth of cancer cells that express 83P2H3, for

CC a cell expressing 83P2H3 by conjugating the agent to an anti-83P2H3  
 CC antibody, a recombinant protein comprising an antigen-binding region of  
 CC the antibody, a non-human transgenic animal that produces the recombinant  
 CC protein, a hybridoma that produces the recombinant protein, a single-  
 CC chain monoclonal antibody that comprises the variable domains of the  
 CC heavy and light chains of the anti-83P2H3 antibody, a vector comprising a  
 CC polynucleotide that encodes the monoclonal antibody, and inducing an  
 CC immune response to a 83P2H3 protein, by providing a 83P2H3-related  
 CC protein that comprises a T cell or B cell epitope, and contacting the  
 CC epitope with an immune system T cell or B cell, respectively. The method  
 CC is useful for monitoring 83P2H3 gene products in a biological sample for  
 CC monitoring the presence of cancer in an individual. The modulator is  
 CC useful for inhibiting the growth of cancer cells that express 83P2H3, for  
 CC treating cancer and the vector is useful for treating a patient with a  
 CC cancer that expresses 83P2H3. The immunological methods are useful for  
 CC generating an immune response against 83P2H3, and for detecting the  
 CC presence of 83P2H3-related protein or polynucleotide in a biological  
 CC sample from a patient who has or who is suspected of having cancer. The  
 CC antibody is useful in prostate cancer diagnosis, prognosis, imaging  
 CC methodologies and treatment, to detect and quantify 83P2H3 and mutant  
 CC 83P2H3-related proteins, for purifying a 83P2H3-related protein, for  
 CC isolating 83P2H3 homologues/related molecules, and for generating anti-  
 CC idiotypic antibodies that mimic the 83P2H3 protein. The present sequence  
 CC is an HLA binding peptide motif from 83P2H3 or its related protein  
 CC CaTrF2E11.

XX Sequence 9 AA;

Query Match 22.2%; Score 4; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KYPV 11  
 ||||  
 Db 1 KYPV 4

RESULT 46

AAU95255  
 ID AAU95255 standard; Peptide; 9 AA.

XX AAU95255;

AC 02-JUL-2002 (first entry)

DE Human novel protein CaTrF2E11 HLA binding peptide #588.

XX Human; human leukocyte antigen; HLA; immunogen: 83P2H3; CaTrF2E11;  
 KW calcium transport protein; cancer; prostate cancer; cytostatic;  
 KW chromosome 7q34; chromosome 12q24.1; T cell; B cell.

XX Homo sapiens.

XX WO200214361-A2.

XX 21-FEB-2002.

XX 17-AUG-2001; 2001WO-US25782.

XX 17-AUG-2000; 2000US-226329P.

XX (AGEN-) AGENSYS INC.

XX Raitano AB, Challita-Eid PM, Faris M, Saffran DC, Afar DBH;  
 PI Levin E, Hubert RS, Ge W, Jakobovits A;

XX WPI; 2002-269179/31.

XX Monitoring 83P2H3 gene products for monitoring the presence of cancer  
 PT in a subject, comprises determining the status of 83P2H3 gene products  
 PT in a tissue sample from the subject and comparing it to a normal sample

XX

XX Example 11; Page 208; 270pp; English.

XX The invention relates to monitoring 83P2H3 (a calcium transport  
 CC protein whose gene is located on chromosome 7q34) gene products in a  
 CC biological sample from a patient who has or is suspected of having  
 CC cancer (especially prostate cancer), comprises: (a) determining the  
 CC status of 83P2H3 gene products expressed by cells in a tissue sample from  
 CC an individual and (b) comparing the status to the status of 83P2H3 gene  
 CC products in a normal sample. Also included are modulators of 83P2H3  
 CC function or status, generating antibodies/immune response against  
 CC 83P2H3 (or related protein CaTrF2E11 whose gene is located on chromosome  
 CC 12q24.1) using identified HLA (human leukocyte antigen) binding  
 CC peptides derived from the protein, delivering a cytotoxic agent to  
 CC a cell expressing 83P2H3 by conjugating the agent to an anti-83P2H3  
 CC antibody, a recombinant protein comprising an antigen-binding region of  
 CC the antibody, a non-human transgenic animal that produces the recombinant  
 CC protein, a hybridoma that produces the recombinant protein, a single-  
 CC chain monoclonal antibody that comprises the variable domains of the  
 CC heavy and light chains of the anti-83P2H3 antibody, a vector comprising a  
 CC polynucleotide that encodes the monoclonal antibody and inducing an  
 CC immune response to a 83P2H3 protein, by providing a 83P2H3-related  
 CC protein that comprises a T cell or B cell epitope, and contacting the  
 CC epitope with an immune system T cell or B cell, respectively. The method  
 CC is useful for monitoring 83P2H3 gene products in a biological sample for  
 CC monitoring the presence of cancer in an individual. The modulator is  
 CC useful for inhibiting the growth of cancer cells that express 83P2H3, for  
 CC treating cancer and the vector is useful for treating a patient with a  
 CC cancer that expresses 83P2H3. The immunological methods are useful for  
 CC generating an immune response against 83P2H3, and for detecting the  
 CC presence of 83P2H3-related protein or polynucleotide in a biological  
 CC sample from a patient who has or who is suspected of having cancer. The  
 CC antibody is useful in prostate cancer diagnosis, prognosis, imaging  
 CC methodologies and treatment, to detect and quantify 83P2H3 and mutant  
 CC 83P2H3-related proteins, for purifying a 83P2H3-related protein, for  
 CC isolating 83P2H3 homologues/related molecules, and for generating anti-  
 CC idiotypic antibodies that mimic the 83P2H3 protein. The present sequence  
 CC is an HLA binding peptide motif from 83P2H3 or its related protein  
 CC CaTrF2E11.

XX Sequence 9 AA;

Query Match 22.2%; Score 4; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KYPV 11  
 ||||  
 Db 4 KYPV 7

RESULT 47

ABU20159  
 ID ABU20159 standard; Peptide; 9 AA.

XX ABU20159;

XX 10-APR-2003 (first entry)

DE MHC binding peptide SEQ ID No 324.

XX Antirheumatic; antiallergic; antiarthritic; nootropic; neuroprotective;  
 KW antiinflammatory; major histocompatibility complex; MHC;  
 KW autoimmune disease; T cell; B cell; allergic disease; multiple sclerosis;  
 KW rheumatoid arthritis; neurodegenerative disorder; Alzheimer's disease;  
 XX inflammation; gene therapy; MHC binding peptide.

XX Synthetic.

XX WO200294981-A2.

XX 28-NOV-2002.

XX 16-MAY-2002; 2002WO-IL00383.



Qy	3 EMPF 6 	22.2%; Score 4; DB 22; Length 10; Best Local Similarity 100.0%; Pred. No. 4.2e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	5 EMPF 8 	
XX	Result 50	
AC	AAB75678 standard; Peptide; 10 AA.	
XX	AAB75678;	
DT	10-APR-2001 (first entry)	
XX	HLA class I binding motif in HOM-TES-84 SEQ ID NO:81.	
XX	Human; cancer associated antigen precursor; cancer associated antigen;	
KW	seminoma; HLA; human leukocyte antigen; cytostatic; gene therapy;	
KW	vaccine; cancer.	
XX	Homo sapiens.	
OS	WO200100874-A2.	
XX	04-JAN-2001.	
XX	23-JUN-2000; 2000WO-US17207.	
PF	30-JUN-1999; 99US-0346498.	
XX	(LUDW-) LUDWIG INST CANCER RES.	
PA	Sahin U, Tureci O, Pfreundschuh M;	
PI	WPI; 2001-112465/12.	
XX	Diagnosing a disorder characterized by expression of a human cancer	
DR	associated antigen precursor, comprises detecting interaction of an	
XX	agent with a nucleic acid molecule encoding the antigen precursor -	
PT	Example 10; Page 63; 126pp; English.	
PT	The present invention describes a method for diagnosing a disorder	
XX	characterised by expression of a human cancer associated antigen (CAA)	
CC	precursor (I) coded by a NA Group 1 nucleic acid molecule (N1)	
CC	comprising contacting the biological sample with an agent (A) that	
CC	specifically binds to N1, (I) or its fragment, complexed with an human	
CC	leukocyte antigen (HLA) molecule and determining the interaction between	
CC	the agent and N1 or (I). (I) has cytostatic activity and can be used in	
CC	gene therapy and vaccine production. The method can be used for treating	
CC	a subject with a condition characterised by expression of (I) in cells	
CC	of a subject. AAB75607 and AAB75608 represent proteins from human cancer	
CC	associated antigen precursors, and AAB75609 to AAB75802 represent HLA	
CC	class I binding motifs in human cancer associated antigen precursors	
CC	given in the exemplification of the present invention.	
XX	Sequence 10 AA;	
SQ	Query Match 22.2%; Score 4; DB 22; Length 10; Best Local Similarity 100.0%; Pred. No. 4.2e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	10 PVEP 13 	
Db	5 PVEP 8 	
XX	Result 51	
AC	AAB49971 standard; peptide; 10 AA.	
ID	AAB49971	

XX	AAB49971;	
AC	08-MAR-2001 (first entry)	
DT	Human melanoma associated antigen WAGE-12 peptide.	
XX	Human; melanoma associated antigen; vaccine; cancer; immunogen.	
XX	Homo sapiens.	
OS	WO200071573-A2.	
XX	30-NOV-2000.	
XX	17-MAY-2000; 2000WO-EP04465.	
PF	21-MAY-1999; 99IT-M101121.	
PR	(GENE-) GENERA SPA.	
XX	Traversari C, Tanzarella S, Bordignon C;	
PI	WPI; 2001-032020/04.	
XX	Novel peptides that bind to allele HLA-B (asterisk)3701, useful for	
DR	preparing anti-tumour medicament, and as a cancer vaccine -	
XX	Claim 1; Page 23; 33pp; English.	
XX	The present invention provides novel peptides based on the melanoma	
CC	associated antigens WAGE-1, WAGE-2, WAGE-3, WAGE-4, WAGE-6 and WAGE-12.	
CC	These peptides can be used in vaccines to treat cancer, particularly	
CC	melanoma.	
XX	Sequence 10 AA;	
SQ	Query Match 22.2%; Score 4; DB 22; Length 10; Best Local Similarity 100.0%; Pred. No. 4.2e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	12 EPFT 15 	
Db	2 EPFT 5 	
XX	Result 52	
AC	AAM24575 standard; Peptide; 10 AA.	
ID	AAM24575	
XX	AAM24575;	
XX	04-DEC-2001 (first entry)	
DT	Human MHC class I molecule HLA-A1 binding 83P5G4 peptide #52.	
XX	83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;	
KW	tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;	
KW	cytostatic; gene therapy; antibody therapy; ribozyme; blood; cervix;	
KW	single chain monoclonal antibody; urine; uterus; rectum; stomach; human;	
KW	chromosome 1q31-q32.	
XX	Homo sapiens.	
OS	WO200159115-A2.	
XX	16-AUG-2001.	
PD	09-FEB-2001; 2001WO-US04426.	
XX	09-FEB-2000; 2000US-0181261.	
XX	(UOG-) UROGENESYS INC.	

XX	Hubert RS, Afar DEH, Challita-eid PM, Paris M, Levin E;	therapeutic agent in multiple cancers such as prostate, bladder and
PI	Mitchell SC, Jakobovits A;	bone cancer -
XX	WPI; 2001-514669/56.	
DR		Example 15; Page 75; 112pp; English.
XX	An isolated 83P5G4-related protein useful as a diagnostic and/or	
PT	therapeutic agent in multiple cancers such as prostate, bladder and	
PT	bone cancer -	
XX		
PS	Example 15; Page 75; 112pp; English.	
XX	The polypeptide sequences represent the 83P5G4-related protein and	
CC	peptide fragments of the protein. 83P5G4 exhibits prostate specific	
CC	expression in normal adult tissue, but it is also aberrantly expressed in	
CC	many cancers including tumours of the prostate, testis, bladder, kidney,	
CC	brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum,	
CC	liver, colon and lung. The 83P5G4 polynucleotide, its related protein and	
CC	peptide fragments and specific PCR primers are therefore useful for	
CC	diagnosing and treating cancer. A vector comprising a polynucleotide	
CC	which encodes a single chain monoclonal antibody, that immunospecifically	
CC	binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a	
CC	polynucleotide having the 83P5G4 coding sequence, are both useful in the	
CC	preparation of a composition for treating a patient with a cancer that	
CC	expresses 83P5G4. The sequences can be used in diagnostic methods to	
CC	monitor the level of 83P5G4 gene products in serum, blood, urine and	
CC	tissue and to thereby detect the presence of cancerous cells.	
XX		
SQ	Sequence 10 AA;	
	Query Match 22.2%; Score 4; DB 22; Length 10;	
	Best Local Similarity 100.0%; Pred. No. 4.2e+02;	
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	15 TESQ 18	
Db	2 TESQ 5	
RESULT 53		
AAM24783		
ID	AAM24783 standard; Peptide; 10 AA.	
XX		
AC	AAM24783;	
XX		
DT	04-DEC-2001 (first entry)	
XX		
DE	Human MHC class I molecule HLA-A3 binding 83P5G4 peptide #60.	
XX		
KW	83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;	
KW	tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;	
KW	cytostatic; gene therapy; antibody therapy; ribozyme; blood; cervix;	
KW	single chain monoclonal antibody; urine; uterus; rectum; stomach; human;	
KW	chromosome 1q31-q32.	
XX		
OS	Homo sapiens.	
XX		
PN	W0200159115-A2.	
XX		
PD	16-AUG-2001.	
XX		
PF	09-FEB-2001; 2001WO-US04426.	
XX		
PR	09-FEB-2000; 2000US-0181261.	
XX		
PA	(UROG-) UROGENESYS INC.	
XX		
PI	Hubert RS, Afar DEH, Challita-eid PM, Paris M, Levin E;	
PI	Mitchell SC, Jakobovits A;	
XX	WPI; 2001-514669/56.	
XX		
PT	An isolated 83P5G4-related protein useful as a diagnostic and/or	

PT	therapeutic agent in multiple cancers such as prostate, bladder and	
XX	bone cancer -	
XX		
PS	Example 15; Page 80; 112pp; English.	
XX	The polypeptide sequences represent the 83P5G4-related protein and	
CC	peptide fragments of the protein. 83P5G4 exhibits prostate specific	
CC	expression in normal adult tissue, but it is also aberrantly expressed in	
CC	many cancers including tumours of the prostate, testis, bladder, kidney,	
CC	brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum,	
CC	liver, colon and lung. The 83P5G4 polynucleotide, its related protein and	
CC	peptide fragments and specific PCR primers are therefore useful for	
CC	diagnosing and treating cancer. A vector comprising a polynucleotide	
CC	which encodes a single chain monoclonal antibody, that immunospecifically	
CC	binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a	
CC	polynucleotide having the 83P5G4 coding sequence, are both useful in the	
CC	preparation of a composition for treating a patient with a cancer that	
CC	expresses 83P5G4. The sequences can be used in diagnostic methods to	
CC	monitor the level of 83P5G4 gene products in serum, blood, urine and	
CC	tissue and to thereby detect the presence of cancerous cells.	
XX		
SQ	Sequence 10 AA;	
	Query Match 22.2%; Score 4; DB 22; Length 10;	
	Best Local Similarity 100.0%; Pred. No. 4.2e+02;	
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	15 TESQ 18	
Db	5 TESQ 8	
RESULT 54		
AAM24905		
ID	AAM24905 standard; Peptide; 10 AA.	
XX		
AC	AAM24905;	
XX		
DT	04-DEC-2001 (first entry)	
XX		
DE	Human MHC molecule HLA-A11 binding 83P5G4 peptide #82.	
XX		
KW	83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;	
KW	tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;	
KW	cytostatic; gene therapy; antibody therapy; ribozyme; blood; cervix;	
KW	single chain monoclonal antibody; urine; uterus; rectum; stomach; human;	
KW	chromosome 1q31-q32.	
XX		
OS	Homo sapiens.	
XX		
PN	W0200159115-A2.	
XX		
PD	16-AUG-2001.	
XX		
PF	09-FEB-2001; 2001WO-US04426.	
XX		
PR	09-FEB-2000; 2000US-0181261.	
XX		
PA	(UROG-) UROGENESYS INC.	
XX		
PI	Hubert RS, Afar DEH, Challita-eid PM, Paris M, Levin E;	
PI	Mitchell SC, Jakobovits A;	
XX	WPI; 2001-514669/56.	
XX		
PT	An isolated 83P5G4-related protein useful as a diagnostic and/or	

PT	therapeutic agent in multiple cancers such as prostate, bladder and	
XX	bone cancer -	
XX		
PS	Example 15; Page 83; 112pp; English.	
XX	The polypeptide sequences represent the 83P5G4-related protein and	
CC	peptide fragments of the protein. 83P5G4 exhibits prostate specific	

CC expression in normal adult tissue, but it is also aberrantly expressed in  
 CC many cancers including tumours of the prostate, testis, bladder, kidney,  
 CC brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum,  
 CC liver, colon and lung. The 83P5G4 polynucleotide, its related protein and  
 CC peptide fragments and specific PCR primers are therefore useful for  
 CC diagnosing and treating cancer. A vector comprising a polynucleotide  
 CC which encodes a single chain monoclonal antibody, that immunospecifically  
 CC binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a  
 CC polynucleotide having the 83P5G4 coding sequence, are both useful in the  
 CC preparation of a composition for treating a patient with a cancer that  
 CC expresses 83P5G4. The sequences can be used in diagnostic methods to  
 CC monitor the level of 83P5G4 gene products in serum, blood, urine and  
 CC tissue and to thereby detect the presence of cancerous cells.

XX Sequence 10 AA;

Query Match 22.2%; Score 4; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TESQ 18  
 ||||  
 Db 3 TESQ 6

RESULT 55  
 AAM24911  
 ID AAM24911 standard; Peptide; 10 AA.

AC AAM24911;

DT 04-DEC-2001 (first entry)

DE Human MHC molecule HLA-A11 binding 83P5G4 peptide #88.

XX 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;  
 KW tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;  
 KW cytostatic; gene therapy; antibody therapy; ribozyme; blood; cervix;  
 KW single chain monoclonal antibody; urine; uterus; rectum; stomach; human;  
 KW chromosome lq31-q32.

XX Homo sapiens.

XX WO200159115-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US04426.

XX 09-FEB-2000; 2000US-0181261.

XX (UROG-) UROGENESYS INC.

XX Hubert RS, Afar DEH, Challita-eid PM, Faris M, Levin E;

PI Mitchell SC, Jakobovits A;

XX WPI; 2001-514669/56.

XX An isolated 83P5G4-related protein useful as a diagnostic and/or  
 PT therapeutic agent in multiple cancers such as prostate, bladder and  
 PT bone cancer -

XX Example 15; Page 84; 112pp; English.

XX The polypeptide sequences represent the 83P5G4-related protein and  
 CC peptide fragments of the protein. 83P5G4 exhibits prostate specific  
 CC expression in normal adult tissue, but it is also aberrantly expressed in  
 CC many cancers including tumours of the prostate, testis, bladder, kidney,  
 CC brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum,  
 CC liver, colon and lung. The 83P5G4 polynucleotide, its related protein and  
 CC peptide fragments and specific PCR primers are therefore useful for  
 CC diagnosing and treating cancer. A vector comprising a polynucleotide  
 CC which encodes a single chain monoclonal antibody, that immunospecifically

CC binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a  
 CC polynucleotide having the 83P5G4 coding sequence, are both useful in the  
 CC preparation of a composition for treating a patient with a cancer that  
 CC expresses 83P5G4. The sequences can be used in diagnostic methods to  
 CC monitor the level of 83P5G4 gene products in serum, blood, urine and  
 CC tissue and to thereby detect the presence of cancerous cells.

XX Sequence 10 AA;

Query Match 22.2%; Score 4; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TESQ 18  
 ||||  
 Db 2 TESQ 5

RESULT 56

AAM24914

ID AAM24914 standard; Peptide; 10 AA.

XX AC AAM24914;

XX 04-DEC-2001 (first entry)

XX Human MHC molecule HLA-A11 binding 83P5G4 peptide #91.

XX 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;  
 KW tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;  
 KW cytostatic; gene therapy; antibody therapy; ribozyme; blood; cervix;  
 KW single chain monoclonal antibody; urine; uterus; rectum; stomach; human;  
 KW chromosome lq31-q32.

XX Homo sapiens.

XX WO200159115-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US04426.

XX 09-FEB-2000; 2000US-0181261.

XX (UROG-) UROGENESYS INC.

XX Hubert RS, Afar DEH, Challita-eid PM, Faris M, Levin E;

PI Mitchell SC, Jakobovits A;

XX WPI; 2001-514669/56.

XX An isolated 83P5G4-related protein useful as a diagnostic and/or  
 PT therapeutic agent in multiple cancers such as prostate, bladder and  
 PT bone cancer -

XX Example 15; Page 84; 112pp; English.

XX The polypeptide sequences represent the 83P5G4-related protein and  
 CC peptide fragments of the protein. 83P5G4 exhibits prostate specific  
 CC expression in normal adult tissue, but it is also aberrantly expressed in  
 CC many cancers including tumours of the prostate, testis, bladder, kidney,  
 CC brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum,  
 CC liver, colon and lung. The 83P5G4 polynucleotide, its related protein and  
 CC peptide fragments and specific PCR primers are therefore useful for  
 CC diagnosing and treating cancer. A vector comprising a polynucleotide  
 CC which encodes a single chain monoclonal antibody, that immunospecifically  
 CC binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a  
 CC polynucleotide having the 83P5G4 coding sequence, are both useful in the  
 CC preparation of a composition for treating a patient with a cancer that  
 CC expresses 83P5G4. The sequences can be used in diagnostic methods to  
 CC monitor the level of 83P5G4 gene products in serum, blood, urine and  
 CC tissue and to thereby detect the presence of cancerous cells.

XX



```

SQ Sequence 10 AA;
Query Match 22.2%; Score 4; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TESQ 18
Db ||||
4 TESQ 7

RESULT 57
AAM25003
ID AAM25003 standard; Peptide; 10 AA.
XX
AC AAM25003;
XX
DT 04-DEC-2001 (first entry)
XX
DE Human MHC class I molecule HLA-A24 binding 83P5G4 peptide #80.
XX
KW 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;
KW tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;
KW cytostatic; gene therapy; antibody therapy; ribozyme; blood; cervix;
KW single chain monoclonal antibody; urine; uterus; rectum; stomach; human;
KW chromosome 1q31-q32.
XX
OS Homo sapiens.
XX
PN W0200159115-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US04426.
XX
PR 09-FEB-2000; 2000US-0181261.
XX
PS (UROG-) UROGENESYS INC.
XX
PI Hubert RS, Afar DEH, Challita-eid PM, Faris M, Levin E;
PI Mitchell SC, Jakobovits A;
XX
DR WPI; 2001-514669/56.
XX
XX An isolated 83P5G4-related protein useful as a diagnostic and/or
PT therapeutic agent in multiple cancers such as prostate, bladder and
PT bone cancer -
PS Example 15; Page 86; 112pp; English.
XX
CC The polypeptide sequences represent the 83P5G4-related protein and
CC peptide fragments of the protein. 83P5G4 exhibits prostate specific
CC expression in normal adult tissue, but it is also aberrantly expressed in
CC many cancers including tumours of the prostate, testis, bladder, kidney,
CC brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum,
CC liver, colon and lung. The 83P5G4 polynucleotide, its related protein and
CC peptide fragments and specific PCR primers are therefore useful for
CC diagnosing and treating cancer. A vector comprising a polynucleotide
CC which encodes a single chain monoclonal antibody, that immunospecifically
CC binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a
CC polynucleotide having the 83P5G4 coding sequence, are both useful in the
CC preparation of a composition for treating a patient with a cancer that
CC expresses 83P5G4. The sequences can be used in diagnostic methods to
CC monitor the level of 83P5G4 gene products in serum, blood, urine and
CC tissue and to thereby detect the presence of cancerous cells.
XX
SQ Sequence 10 AA;
Query Match 22.2%; Score 4; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TESQ 18
Db ||||
4 TESQ 7

RESULT 58
AAM25222
ID AAM25222 standard; Peptide; 10 AA.
XX
AC AAM25222;
XX
DT 04-DEC-2001 (first entry)
XX
DE Human MHC molecule HLA-B35 binding 83P5G4 peptide #99.
XX
KW 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;
KW tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;
KW cytostatic; gene therapy; antibody therapy; ribozyme; blood; cervix;
KW single chain monoclonal antibody; urine; uterus; rectum; stomach; human;
KW chromosome 1q31-q32.
XX
OS Homo sapiens.
XX
PN W0200159115-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US04426.
XX
PR 09-FEB-2000; 2000US-0181261.
XX
PS (UROG-) UROGENESYS INC.
XX
PI Hubert RS, Afar DEH, Challita-eid PM, Faris M, Levin E;
PI Mitchell SC, Jakobovits A;
XX
DR WPI; 2001-514669/56.
XX
XX An isolated 83P5G4-related protein useful as a diagnostic and/or
PT therapeutic agent in multiple cancers such as prostate, bladder and
PT bone cancer -
PS Example 15; Page 92; 112pp; English.
XX
CC The polypeptide sequences represent the 83P5G4-related protein and
CC peptide fragments of the protein. 83P5G4 exhibits prostate specific
CC expression in normal adult tissue, but it is also aberrantly expressed in
CC many cancers including tumours of the prostate, testis, bladder, kidney,
CC brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum,
CC liver, colon and lung. The 83P5G4 polynucleotide, its related protein and
CC peptide fragments and specific PCR primers are therefore useful for
CC diagnosing and treating cancer. A vector comprising a polynucleotide
CC which encodes a single chain monoclonal antibody, that immunospecifically
CC binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a
CC polynucleotide having the 83P5G4 coding sequence, are both useful in the
CC preparation of a composition for treating a patient with a cancer that
CC expresses 83P5G4. The sequences can be used in diagnostic methods to
CC monitor the level of 83P5G4 gene products in serum, blood, urine and
CC tissue and to thereby detect the presence of cancerous cells.
XX
SQ Sequence 10 AA;
Query Match 22.2%; Score 4; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TESQ 18
Db ||||
5 TESQ 8

RESULT 59
AAO17822
ID AAO17822 standard; peptide; 10 AA.

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XX	AAO17822;	PI	Raitano AB, Challita-Eid PM, Paris M, Saffran DC, Afar DEH;
XX		PI	Levin E, Hubert RS, Ge W, Jakobovits A;
DT	15-AUG-2002 (first entry)	DR	WPI; 2002-269179/31.
XX	Sponge okadaic acid combining protein related peptide #3.	XX	
DE		PT	Monitoring 83p2H3 gene products for monitoring the presence of cancer
XX		PT	in a subject, comprises determining the status of 83p2H3 gene products
KW	Sponge; okadaic acid combining protein; protein dephosphorylase 1;	PT	in a tissue sample from the subject and comparing it to a normal sample
KW	protein dephosphorylase 2A; okadaic acid; cytotoxicity inactivation.	PT	-
XX		XX	
XX	Unidentified.	PS	Example 11; Page 176; 270pp; English.
OS		XX	
XX		XX	The invention relates to monitoring 83p2H3 (a calcium transport
PN	JP2002101886-A.	CC	protein whose gene is located on chromosome 7q34) gene products in a
XX		CC	biological sample from a patient who has or is suspected of having
PD	09-APR-2002.	CC	cancer (especially prostate cancer), comprises: (a) determining the
XX		CC	status of 83p2H3 gene products expressed by cells in a tissue sample from
PP	28-SEP-2000; 2000JP-0297436.	CC	an individual and (b) comparing the status to the status of 83p2H3 gene
XX		CC	products in a normal sample. Also included are modulators of 83p2H3
PR	28-SEP-2000; 2000JP-0297436.	CC	function or status, generating antibodies/immune response against
XX	(KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.	CC	83p2H3 (or related protein CaTrF2E11 whose gene is located on chromosome
PA		CC	12q24.1) using identified HLA (human leukocyte antigen) binding
XX		CC	peptides derived from the protein, delivering a cytotoxic agent to
DR	WPI; 2002-440456/47.	CC	a cell expressing 83p2H3 by conjugating the agent to an anti-83p2H3
XX		CC	antibody, a recombinant protein comprising an antigen-binding region of
XX		CC	the antibody, a non-human transgenic animal that produces the recombinant
PT	A new protein combining with Okadaic acid and its gene, has no	CC	protein, a hybridoma that produces the recombinant protein, a single-
PT	enzymatic activity of protein dephosphorylase 1 and 2A -	CC	chain monoclonal antibody that comprises the variable domains of the
XX		CC	heavy and light chains of the anti-83p2H3 antibody, a vector comprising a
PS	Example 3; Page 5; 12pp; Japanese.	CC	polynucleotide that encodes the monoclonal antibody and inducing an
XX		CC	immune response to a 83p2H3 protein, by providing a 83p2H3-related
CC	The present invention relates to a protein having combinability to	CC	protein that comprises a T cell or B cell epitope, and contacting the
CC	Okadaic acid and having substantially no enzymatic activity of protein	CC	epitope with an immune system T cell or B cell, respectively. The method
CC	dephosphorylase 1 and 2A. The protein is useful as a drug for	CC	is useful for monitoring 83p2H3 gene products in a biological sample for
CC	inactivating cytotoxicity of a substance enzymatic activity-inhibiting	CC	monitoring the presence of cancer in an individual. The modulator is
CC	activity such as Okadaic acid. The present sequence is a peptide	CC	useful for inhibiting the growth of cancer cells that express 83p2H3, for
CC	described in the exemplification of the invention.	CC	treating cancer and the vector is useful for treating a patient with a
XX		CC	cancer that expresses 83p2H3. The immunological methods are useful for
SQ	Sequence 10 AA;	CC	generating an immune response against 83p2H3, and for detecting the
	Query Match 22.2%; Score 4; DB 23; Length 10;	CC	presence of 83p2H3-related protein or polynucleotide in a biological
	Best Local Similarity 100.0%; Pred. No. 4.2e+02;	CC	sample from a patient who has or who is suspected of having cancer. The
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	CC	antibody is useful in prostate cancer diagnosis, prognosis, imaging
QY	15 TESQ 18	CC	methodologies and treatment, to detect and quantify 83p2H3 and mutant
		CC	83p2H3-related proteins, for purifying a 83p2H3-related protein, for
Db	2 TESQ 5	CC	isolating 83p2H3 homologues/related molecules, and for generating anti-
		CC	idiotypic antibodies that mimic the 83p2H3 protein. The present sequence
		CC	is an HLA binding peptide motif from 83p2H3 or its related protein
		CC	CaTrF2E11.
XX		XX	
SQ	Sequence 10 AA;	SQ	Sequence 10 AA;
	Query Match 22.2%; Score 4; DB 23; Length 10;		Query Match 22.2%; Score 4; DB 23; Length 10;
	Best Local Similarity 100.0%; Pred. No. 4.2e+02;		Best Local Similarity 100.0%; Pred. No. 4.2e+02;
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	8 KYPV 11	QY	8 KYPV 11
Db	6 KYPV 9	Db	6 KYPV 9
XX		XX	
SQ	Sequence 10 AA;	SQ	Sequence 10 AA;
	Query Match 22.2%; Score 4; DB 23; Length 10;		Query Match 22.2%; Score 4; DB 23; Length 10;
	Best Local Similarity 100.0%; Pred. No. 4.2e+02;		Best Local Similarity 100.0%; Pred. No. 4.2e+02;
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	8 KYPV 11	QY	8 KYPV 11
Db	6 KYPV 9	Db	6 KYPV 9
XX		XX	
SQ	Sequence 10 AA;	SQ	Sequence 10 AA;
	Query Match 22.2%; Score 4; DB 23; Length 10;		Query Match 22.2%; Score 4; DB 23; Length 10;
	Best Local Similarity 100.0%; Pred. No. 4.2e+02;		Best Local Similarity 100.0%; Pred. No. 4.2e+02;
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	8 KYPV 11	QY	8 KYPV 11
Db	6 KYPV 9	Db	6 KYPV 9
XX		XX	
SQ	Sequence 10 AA;	SQ	Sequence 10 AA;
	Query Match 22.2%; Score 4; DB 23; Length 10;		Query Match 22.2%; Score 4; DB 23; Length 10;
	Best Local Similarity 100.0%; Pred. No. 4.2e+02;		Best Local Similarity 100.0%; Pred. No. 4.2e+02;
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	8 KYPV 11	QY	8 KYPV 11
Db	6 KYPV 9	Db	6 KYPV 9
XX		XX	
SQ	Sequence 10 AA;	SQ	Sequence 10 AA;
	Query Match 22.2%; Score 4; DB 23; Length 10;		Query Match 22.2%; Score 4; DB 23; Length 10;
	Best Local Similarity 100.0%; Pred. No. 4.2e+02;		Best Local Similarity 100.0%; Pred. No. 4.2e+02;
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	8 KYPV 11	QY	8 KYPV 11
Db	6 KYPV 9	Db	6 KYPV 9
XX		XX	
SQ	Sequence 10 AA;	SQ	Sequence 10 AA;
	Query Match 22.2%; Score 4; DB 23; Length 10;		Query Match 22.2%; Score 4; DB 23; Length 10;
	Best Local Similarity 100.0%; Pred. No. 4.2e+02;		Best Local Similarity 100.0%; Pred. No. 4.2e+02;
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	8 KYPV 11	QY	8 KYPV 11
Db	6 KYPV 9	Db	6 KYPV 9
XX		XX	
SQ	Sequence 10 AA;	SQ	Sequence 10 AA;
	Query Match 22.2%; Score 4; DB 23; Length 10;		Query Match 22.2%; Score 4; DB 23; Length 10;
	Best Local Similarity 100.0%; Pred. No. 4.2e+02;		Best Local Similarity 100.0%; Pred. No. 4.2e+02;
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	8 KYPV 11	QY	8 KYPV 11
Db	6 KYPV 9	Db	6 KYPV 9
XX		XX	
SQ	Sequence 10 AA;	SQ	Sequence 10 AA;
	Query Match 22.2%; Score 4; DB 23; Length 10;		Query Match 22.2%; Score 4; DB 23; Length 10;
	Best Local Similarity 100.0%; Pred. No. 4.2e+02;		Best Local Similarity 100.0%; Pred. No. 4.2e+02;
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	8 KYPV 11	QY	8 KYPV 11
Db	6 KYPV 9	Db	6 KYPV 9
XX		XX	
SQ	Sequence 10 AA;	SQ	Sequence 10 AA;
	Query Match 22.2%; Score 4; DB 23; Length 10;		Query Match 22.2%; Score 4; DB 23; Length 10;
	Best Local Similarity 100.0%; Pred. No. 4.2e+02;		Best Local Similarity 100.0%; Pred. No. 4.2e+02;
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	8 KYPV 11	QY	8 KYPV 11
Db	6 KYPV 9	Db	6 KYPV 9
XX		XX	
SQ	Sequence 10 AA;	SQ	Sequence 10 AA;
	Query Match 22.2%; Score 4; DB 23; Length 10;		Query Match 22.2%; Score 4; DB 23; Length 10;
	Best Local Similarity 100.0%; Pred. No. 4.2e+02;		Best Local Similarity 100.0%; Pred. No. 4.2e+02;
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	8 KYPV 11	QY	8 KYPV 11
Db	6 KYPV 9	Db	6 KYPV 9
XX		XX	
SQ	Sequence 10 AA;	SQ	Sequence 10 AA;
	Query Match 22.2%; Score 4; DB 23; Length 10;		Query Match 22.2%; Score 4; DB 23; Length 10;
	Best Local Similarity 100.0%; Pred. No. 4.2e+02;		Best Local Similarity 100.0%; Pred. No. 4.2e+02;
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	8 KYPV 11	QY	8 KYPV 11
Db	6 KYPV 9	Db	6 KYPV 9
XX		XX	
SQ	Sequence 10 AA;	SQ	Sequence 10 AA;
	Query Match 22.2%; Score 4; DB 23; Length 10;		Query Match 22.2%; Score 4; DB 23; Length 10;
	Best Local Similarity 100.0%; Pred. No. 4.2e+02;		Best Local Similarity 100.0%; Pred. No. 4.2e+02;
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	8 KYPV 11	QY	8 KYPV 11
Db	6 KYPV 9	Db	6 KYPV 9
XX		XX	
SQ	Sequence 10 AA;	SQ	Sequence 10 AA;
	Query Match 22.2%; Score 4; DB 23; Length 10;		Query Match 22.2%; Score 4; DB 23; Length 10;
	Best Local Similarity 100.0%; Pred. No. 4.2e+02;		Best Local Similarity 100.0%; Pred. No. 4.2e+02;
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	8 KYPV 11	QY	8 KYPV 11
Db	6 KYPV 9	Db	6 KYPV 9
XX		XX	
SQ	Sequence 10 AA;	SQ	Sequence 10 AA;
	Query Match 22.2%; Score 4; DB 23; Length 10;		Query Match 22.2%; Score 4; DB 23; Length 10;
	Best Local Similarity 100.0%; Pred. No. 4.2e+02;		Best Local Similarity 100.0%; Pred. No. 4.2e+02;
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	8 KYPV 11	QY	8 KYPV 11
Db	6 KYPV 9	Db	6 KYPV 9
XX		XX	
SQ	Sequence 10 AA;	SQ	Sequence 10 AA;
	Query Match 22.2%; Score 4; DB 23; Length 10;		Query Match 22.2%; Score 4; DB 23; Length 10;
	Best Local Similarity 100.0%; Pred. No. 4.2e+02;		Best Local Similarity 100.0%; Pred. No. 4.2e+02;
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	8 KYPV 11	QY	8 KYPV 11
Db	6 KYPV 9	Db	6 KYPV 9
XX		XX	
SQ	Sequence 10 AA;	SQ	Sequence 10 AA;
	Query Match 22.2%; Score 4; DB 23; Length 10;		Query Match 22.2%; Score 4; DB 23; Length 10;
	Best Local Similarity 100.0%; Pred. No. 4.2e+02;		Best Local Similarity 100.0%; Pred. No. 4.2e+02;
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	8 KYPV 11	QY	8 KYPV 11
Db	6 KYPV 9	Db	6 KYPV 9
XX		XX	
SQ	Sequence 10 AA;	SQ	Sequence 10 AA;
	Query Match 22.2%; Score 4; DB 23; Length 10;		Query Match 22.2%; Score 4; DB 23; Length 10;
	Best Local Similarity 100.0%; Pred. No. 4.2e+02;		Best Local Similarity 100.0%; Pred. No. 4.2e+02;
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	8 KYPV 11	QY	8 KYPV 11
Db	6 KYPV 9	Db	6 KYPV 9
XX		XX	
SQ	Sequence 10 AA;	SQ	Sequence 10 AA;
	Query Match 22.2%; Score 4; DB 23; Length 10;		Query Match 22.2%; Score 4; DB 23; Length 10;
	Best Local Similarity 100.0%; Pred. No. 4.2e+02;		Best Local Similarity 100.0%; Pred. No. 4.2e+02;
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	8 KYPV 11	QY	8 KYPV 11
Db	6 KYPV 9	Db	6 KYPV 9
XX		XX	
SQ	Sequence 10 AA;	SQ	Sequence 10 AA;
	Query Match 22.2%; Score 4; DB 23; Length 10;		Query Match 22.2%; Score 4; DB 23; Length 10;
	Best Local Similarity 100.0%; Pred. No. 4.2e+02;		Best Local Similarity 100.0%; Pred. No. 4.2e+02;
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	8 KYPV 11	QY	8 KYPV 11
Db	6 KYPV 9	Db	6 KYPV 9
XX		XX	
SQ	Sequence 10 AA;	SQ	Sequence 10 AA;
	Query Match 22.2%; Score 4; DB 23; Length 10;		Query Match 22.2%; Score 4; DB 23; Length 10;
	Best Local Similarity 100.0%; Pred. No. 4.2e+02;		Best Local Similarity 100.0%; Pred. No. 4.2e+02;
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	8 KYPV 11	QY	8 KYPV 11
Db	6 KYPV 9	Db	6 KYPV 9
XX		XX	
SQ	Sequence 10 AA;	SQ	Sequence 10 AA;
	Query Match 22.2%; Score 4; DB 23; Length 10;		Query Match 22.2%; Score 4; DB 23; Length 10;
	Best Local Similarity 100.0%; Pred. No. 4.2e+02;		Best Local Similarity 100.0%; Pred. No. 4.2e+02;
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	8 KYPV 11	QY	8 KYPV 11
Db	6 KYPV 9	Db	6 KYPV 9
XX		XX	
SQ	Sequence 10 AA;	SQ	Sequence 10 AA;
	Query Match 22.2%; Score 4; DB 23; Length 10;		Query Match 22.2%; Score 4; DB 23; Length 10;
	Best Local Similarity 100.0%; Pred. No. 4.2e+02;		Best Local Similarity 100.0%; Pred. No. 4.2e+02;
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	8 KYPV 11	QY	8 KYPV 11
Db	6 KYPV 9	Db	6 KYPV 9
XX		XX	
SQ	Sequence 10 AA;	SQ	Sequence 10 AA;
	Query Match 22.2%; Score 4; DB 23; Length 10;		Query Match 22.2%; Score 4; DB 23; Length 10;
	Best Local Similarity 100.0%; Pred. No. 4.2e+02;		Best Local Similarity 100.0%; Pred. No. 4.2e+02;
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	8 KYPV 11	QY	8 KYPV 11
Db	6 KYPV 9	Db	6 KYPV 9
XX		XX	
SQ	Sequence 10 AA;	SQ	Sequence 10 AA;
	Query Match 22.2%; Score 4; DB 23; Length 10;		Query Match 22.2%; Score 4; DB 23; Length 10;
	Best Local Similarity 100.0%; Pred. No. 4.2e+02;		Best Local Similarity 100.0%; Pred. No. 4.2e+02;
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	8 KYPV 11	QY	8 KYPV 11
Db	6 KYPV 9	Db	6 KYPV 9
XX		XX	
SQ	Sequence 10 AA;	SQ	Sequence 10 AA;
	Query Match 22.2%; Score 4; DB 23; Length 10;		Query Match 22.2%; Score 4; DB 23; Length 10;
	Best Local Similarity 100.0%; Pred. No. 4.2e+02;		Best Local Similarity 100.0%; Pred. No. 4.2e+02;
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	8 KYPV 11	QY	8 KYPV 11
Db	6 KYPV 9	Db	6 KYPV 9
XX		XX	
SQ	Sequence 10 AA;	SQ	Sequence 10 AA;
	Query Match 22.2%; Score 4; DB 23; Length 10;		Query Match 22.2%; Score 4; DB 23; Length 10;
	Best Local Similarity 100.0%; Pred. No. 4.2e+02;		Best Local Similarity 100.0%; Pred. No. 4.2e+02;
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps

XX OS Homo sapiens.  
XX PN WO200214361-A2.  
XX PD 21-FEB-2002.  
XX XX 17-AUG-2001; 2001WO-US25782.  
XX PF 17-AUG-2000; 2000US-226329P.  
XX PR (AGEN-) AGENSYS INC.  
XX PA Raitano AB, Challita-Eid PM, Paris M, Saffran DC, Afar DEH;  
XX PI Levin E, Hubert RS, Ge W, Jakobovits A;  
XX XX WPI; 2002-269179/31.  
XX DR Monitoring 83P2H3 gene products for monitoring the presence of cancer  
XX PT in a subject, comprises determining the status of 83P2H3 gene products  
XX PT in a tissue sample from the subject and comparing it to a normal sample  
XX PT -  
XX PS Example 11; Page 177; 270pp; English.  
XX XX The invention relates to monitoring 83P2H3 (a calcium transport  
CC protein whose gene is located on chromosome 7q34) gene products in a  
CC biological sample from a patient who has or is suspected of having  
CC cancer (especially prostate cancer), comprises: (a) determining the  
CC status of 83P2H3 gene products expressed by cells in a tissue sample from  
CC an individual and (b) comparing the status to the status of 83P2H3 gene  
CC products in a normal sample. Also included are modulators of 83P2H3  
CC function or status, generating antibodies/immune response against  
CC 83P2H3 (or related protein CaTrF2E11 whose gene is located on chromosome  
CC 12q24.1) using identified HLA (human leukocyte antigen) binding  
CC peptides derived from the protein, delivering a cytotoxic agent to  
CC a cell expressing 83P2H3 by conjugating the agent to an anti-83P2H3  
CC antibody, a recombinant protein comprising an antigen-binding region of  
CC the antibody, a non-human transgenic animal that produces the recombinant  
CC protein, a hybridoma that produces the recombinant protein, a single-  
CC chain monoclonal antibody that comprises the variable domains of the  
CC heavy and light chains of the anti-83P2H3 antibody, a vector comprising a  
CC polynucleotide that encodes the monoclonal antibody and inducing an  
CC immune response to a 83P2H3 protein, by providing a 83P2H3-related  
CC protein that comprises a T cell or B cell epitope, and contacting the  
CC epitope with an immune system T cell or B cell, respectively. The method  
CC is useful for monitoring 83P2H3 gene products in a biological sample for  
CC monitoring the presence of cancer in an individual. The modulator is  
CC useful for inhibiting the growth of cancer cells that express 83P2H3, for  
CC treating cancer and the vector is useful for treating a patient with a  
CC cancer that expresses 83P2H3. The immunological methods are useful for  
CC generating an immune response against 83P2H3, and for detecting the  
CC presence of 83P2H3-related protein or polynucleotide in a biological  
CC sample from a patient who has or who is suspected of having cancer. The  
CC antibody is useful in prostate cancer diagnosis, prognosis, imaging  
CC methodologies and treatment, to detect and quantify 83P2H3 and mutant  
CC 83P2H3-related proteins, for purifying a 83P2H3-related protein, for  
CC isolating 83P2H3 homologues/related molecules, and for generating anti-  
CC idiotypic antibodies that mimic the 83P2H3 protein. The present sequence  
CC is an HLA binding peptide motif from 83P2H3 or its related protein  
CC CaTrF2E11.  
XX SQ Sequence 10 AA;  
XX  
XX Query Match 22.2%; Score 4; DB 23; Length 10;  
XX Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX 8 KYPV 11  
XX ||||  
XX 7 KYPV 10

## RESULT 62

AAU95356  
ID AAU95356 standard; Peptide; 10 AA.XX AC AAU95356;  
XX DT 02-JUL-2002 (first entry)XX DE Human novel protein CaTrF2E11 HLA binding peptide #639.  
XX KW Human; human leukocyte antigen; HLA; immunogen; 83P2H3; CaTrF2E11;  
XX KW calcium transport protein; cancer; prostate cancer; cytostatic;  
XX KW chromosome 7q34; chromosome 12q24.1; T cell; B cell.  
XX OS Homo sapiens.XX PN WO200214361-A2.  
XX PD 21-FEB-2002.XX PF 17-AUG-2001; 2001WO-US25782.  
XX PR 17-AUG-2000; 2000US-226329P.XX PA (AGEN-) AGENSYS INC.  
XX PI Raitano AB, Challita-Eid PM, Paris M, Saffran DC, Afar DEH;  
XX PI Levin E, Hubert RS, Ge W, Jakobovits A;  
XX XX WPI; 2002-269179/31.

XX PT Monitoring 83P2H3 gene products for monitoring the presence of cancer  
XX PT in a subject, comprises determining the status of 83P2H3 gene products  
XX PT in a tissue sample from the subject and comparing it to a normal sample  
XX PT -  
XX PS Example 11; Page 212; 270pp; English.  
XX XX The invention relates to monitoring 83P2H3 (a calcium transport  
CC protein whose gene is located on chromosome 7q34) gene products in a  
CC biological sample from a patient who has or is suspected of having  
CC cancer (especially prostate cancer), comprises: (a) determining the  
CC status of 83P2H3 gene products expressed by cells in a tissue sample from  
CC an individual and (b) comparing the status to the status of 83P2H3 gene  
CC products in a normal sample. Also included are modulators of 83P2H3  
CC function or status, generating antibodies/immune response against  
CC 83P2H3 (or related protein CaTrF2E11 whose gene is located on chromosome  
CC 12q24.1) using identified HLA (human leukocyte antigen) binding  
CC peptides derived from the protein, delivering a cytotoxic agent to  
CC a cell expressing 83P2H3 by conjugating the agent to an anti-83P2H3  
CC antibody, a recombinant protein comprising an antigen-binding region of  
CC the antibody, a non-human transgenic animal that produces the recombinant  
CC protein, a hybridoma that produces the recombinant protein, a single-  
CC chain monoclonal antibody that comprises the variable domains of the  
CC heavy and light chains of the anti-83P2H3 antibody, a vector comprising a  
CC polynucleotide that encodes the monoclonal antibody and inducing an  
CC immune response to a 83P2H3 protein, by providing a 83P2H3-related  
CC protein that comprises a T cell or B cell epitope, and contacting the  
CC epitope with an immune system T cell or B cell, respectively. The method  
CC is useful for monitoring 83P2H3 gene products in a biological sample for  
CC monitoring the presence of cancer in an individual. The modulator is  
CC useful for inhibiting the growth of cancer cells that express 83P2H3, for  
CC treating cancer and the vector is useful for treating a patient with a  
CC cancer that expresses 83P2H3. The immunological methods are useful for  
CC generating an immune response against 83P2H3, and for detecting the  
CC presence of 83P2H3-related protein or polynucleotide in a biological  
CC sample from a patient who has or who is suspected of having cancer. The  
CC antibody is useful in prostate cancer diagnosis, prognosis, imaging  
CC methodologies and treatment, to detect and quantify 83P2H3 and mutant  
CC 83P2H3-related proteins, for purifying a 83P2H3-related protein, for  
CC isolating 83P2H3 homologues/related molecules, and for generating anti-  
CC idiotypic antibodies that mimic the 83P2H3 protein. The present sequence  
CC is an HLA binding peptide motif from 83P2H3 or its related protein  
CC CaTrF2E11.

```

CC  CaTrF2E11.
XX
SQ  Sequence 10 AA;
      22.2%; Score 4; DB 23; Length 10;
Query Match 100.0%; Pred. No. 4.2e+02;
Best Local Similarity 0; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0;

Qy  8 KYPV 11
    ||||
Db  5 KYPV 8

RESULT 63
AAU95384
ID  AAU95384 standard; Peptide; 10 AA.
XX
AC  AAU95384;
XX
DT  02-JUL-2002 (first entry)
XX
DE  Human novel protein CaTrF2E11 HLA binding peptide #651.
XX
KW  Human; human leukocyte antigen; HLA; immunogen; 83p2H3; CaTrF2E11;
KW  calcium transport protein; cancer; prostate cancer; cytostatic;
KW  chromosome 7q34; chromosome 12q24.1; T cell; B cell.
XX
OS  Homo sapiens.
XX
PN  WO200214361-A2.
XX
PD  21-FEB-2002.
XX
PF  17-AUG-2001; 2001WO-US25782.
XX
PR  17-AUG-2000; 2000US-226329P.
XX
PA  (AGEN-) AGENSYS INC.
XX
PI  Raitano AB, Challita-Eid PM, Faris M, Saffran DC, Afar DEH;
PI  Levin E, Hubert RS, Ge W, Jakobovits A;
XX
XX  WPI; 2002-269179/31.
XX
PT  Monitoring 83p2H3 gene products for monitoring the presence of cancer
PT  in a subject, comprises determining the status of 83p2H3 gene products
PT  in a tissue sample from the subject and comparing it to a normal sample
XX
XX
PS  Example 11; Page 196; 270pp; English.
XX
CC  The invention relates to monitoring 83p2H3 (a calcium transport
CC  protein whose gene is located on chromosome 7q34) gene products in a
CC  biological sample from a patient who has or is suspected of having
CC  cancer (especially prostate cancer), comprises: (a) determining the
CC  status of 83p2H3 gene products expressed by cells in a tissue sample from
CC  an individual and (b) comparing the status to the status of 83p2H3 gene
CC  products in a normal sample. Also included are modulators of 83p2H3
CC  function or status, generating antibodies/immune response against
CC  83p2H3 (or related protein CaTrF2E11 whose gene is located on chromosome
CC  12q24.1) using identified HLA (human leukocyte antigen) binding
CC  peptides derived from the protein, delivering a cytotoxic agent to
CC  a cell expressing 83p2H3 by conjugating the agent to an anti-83p2H3
CC  antibody, a recombinant protein comprising an antigen-binding region of
CC  the antibody, a non-human transgenic animal that produces the recombinant
CC  protein, a hybridoma that produces the recombinant protein, a single-
CC  chain monoclonal antibody that comprises the variable domains of the
CC  heavy and light chains of the anti-83p2H3 antibody, a vector comprising a
CC  polynucleotide that encodes the monoclonal antibody and inducing an
CC  immune response to a 83p2H3 protein, by providing a 83p2H3-related
CC  protein that comprises a T cell or B cell epitope, and contacting the
CC  epitope with an immune system T cell or B cell, respectively. The method
CC  is useful for monitoring 83p2H3 gene products in a biological sample for

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CC  monitoring the presence of cancer in an individual. The modulator is
CC  useful for inhibiting the growth of cancer cells that express 83p2H3, for
CC  treating cancer and the vector is useful for treating a patient with a
CC  cancer that expresses 83p2H3. The immunological methods are useful for
CC  generating an immune response against 83p2H3, and for detecting the
CC  presence of 83p2H3-related protein or polynucleotide in a biological
CC  sample from a patient who has or who is suspected of having cancer. The
CC  antibody is useful in prostate cancer diagnosis, prognosis, imaging
CC  methodologies and treatment, to detect and quantify 83p2H3 and mutant
CC  83p2H3-related proteins, for purifying a 83p2H3-related protein, for
CC  isolating 83p2H3 homologues/related molecules, and for generating anti-
CC  idiotypic antibodies that mimic the 83p2H3 protein. The present sequence
CC  is an HLA binding peptide motif from 83p2H3 or its related protein
CC  CaTrF2E11.
XX
SQ  Sequence 10 AA;
      22.2%; Score 4; DB 23; Length 10;
Query Match 100.0%; Pred. No. 4.2e+02;
Best Local Similarity 0; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0;

Qy  8 KYPV 11
    ||||
Db  1 KYPV 4

RESULT 64
ABR47212
ID  ABR47212 standard; Peptide; 10 AA.
XX
AC  ABR47212;
XX
DT  10-JUN-2003 (first entry)
XX
DE  Staphylococcus aureus CHIPS-related peptide #2401.
XX
KW  CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5ar;
KW  formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
KW  inflammation; cardiovascular disease; central nervous system disease;
KW  gastrointestinal disease; skin disease; genitourinary disease;
KW  joint disease; respiratory disease; HIV infection; antiinflammatory;
KW  cardiac; cerebroprotective; neuroprotective; nootropic; dermatological;
KW  gynecological; immunosuppressive; anti-HIV.
XX
OS  Staphylococcus aureus.
OS  Synthetic.
XX
PN  WO2003006048-A1.
XX
PD  23-JAN-2003.
XX
PF  11-JUL-2001; 2001WO-EP080004.
XX
PR  11-JUL-2001; 2001WO-EP080004.
XX
PA  (JARI-) JARI PHARM BV.
XX
PI  Van Kessel CPM, Gosselaar-de Haas CUC, Kruijtzer JAW;
PI  Van Strijp JAG;
XX
XX  WPI; 2003-247783/25.
XX
CC  Combination of peptides derived from chemotaxis inhibiting protein from
CC  Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
CC  prophylaxis and treatment of inflammation, cardiovascular, skin and
CC  kidney diseases
XX
PS  Example 1; Page 55; 89pp; English.
XX
CC  The present invention relates to peptides (ABR44811-ABR47162 and
CC  ABR47164-ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS)
CC  from Staphylococcus aureus. The peptide fragments are useful in the
CC  prophylaxis or treatment of diseases or disorders involving the

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CC C5a-receptor (C5aR) and/or formylated peptide receptor (FPR) or  
 CC neutrophils, monocytes and endothelial cells or involving acute or  
 CC chronic inflammation reactions. The diseases or disorders include  
 CC cardiovascular diseases, disease of the central nervous system,  
 CC gastrointestinal diseases, skin diseases, genitourinary diseases, joint  
 CC diseases, respiratory diseases and HIV infection.  
 XX Sequence 10 AA;  
 SQ

Query Match 22.2%; Score 4; DB 24; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 PFPK 8  
 DB 5 PFPK 8  
 |||||

RESULT 65  
 ABR47239 standard; Peptide; 10 AA.  
 ID ABR47239  
 XX  
 AC ABR47239;  
 XX  
 DT 10-JUN-2003 (first entry)  
 XX  
 DE Staphylococcus aureus CHIPS-related peptide #2428.  
 XX  
 KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;  
 KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;  
 KW inflammation; cardiovascular disease; central nervous system disease;  
 KW gastrointestinal disease; skin disease; genitourinary disease;  
 KW joint disease; respiratory disease; HIV infection; antiinflammatory;  
 KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;  
 KW gynecological; immunosuppressive; anti-HIV.  
 XX  
 OS Staphylococcus aureus.  
 OS Synthetic.  
 OS  
 XX WO2003006048-A1.  
 XX  
 PN 23-JAN-2003.  
 XX  
 PD 11-JUL-2001; 2001WO-EP080004.  
 XX  
 PF 11-JUL-2001; 2001WO-EP080004.  
 XX  
 PR (JARI-) JARI PHARM BV.  
 XX  
 PA Van Kessel CPM, Gosselaar-de Haas CJC, Kruijtzer JAW;  
 PI Van Strijp JAG;  
 XX  
 DR WPI; 2003-247783/25.  
 XX  
 CC Combination of peptides derived from chemotaxis inhibiting protein from  
 CC Staphylococcus aureus (CHIPS) having CHIPS activity, useful in  
 CC prophylaxis and treatment of inflammation, cardiovascular, skin and  
 CC kidney diseases -  
 XX  
 PS Example 1; Page 55; 89pp; English.  
 XX  
 CC The present invention relates to peptides (ABR44811-ABR47162 and  
 CC ABR47164-ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS)  
 CC from Staphylococcus aureus. The peptide fragments are useful in the  
 CC prophylaxis or treatment of diseases or disorders involving the  
 CC C5a-receptor (C5aR) and/or formylated peptide receptor (FPR) or  
 CC neutrophils, monocytes and endothelial cells or involving acute or  
 CC chronic inflammation reactions. The diseases or disorders include  
 CC cardiovascular diseases, disease of the central nervous system,  
 CC gastrointestinal diseases, skin diseases, genitourinary diseases, joint  
 CC diseases, respiratory diseases and HIV infection.  
 XX  
 SQ Sequence 10 AA;

Query Match 22.2%; Score 4; DB 24; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 12 EPFT 15  
 DB 4 EPFT 7  
 |||||

RESULT 66  
 ABR47292 standard; Peptide; 10 AA.  
 ID ABR47292  
 XX  
 AC ABR47292;  
 XX  
 DT 10-JUN-2003 (first entry)  
 XX  
 DE Staphylococcus aureus CHIPS-related peptide #2481.  
 XX  
 KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;  
 KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;  
 KW inflammation; cardiovascular disease; central nervous system disease;  
 KW gastrointestinal disease; skin disease; genitourinary disease;  
 KW joint disease; respiratory disease; HIV infection; antiinflammatory;  
 KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;  
 KW gynecological; immunosuppressive; anti-HIV.  
 XX  
 OS Staphylococcus aureus.  
 OS Synthetic.  
 OS  
 XX WO2003006048-A1.  
 XX  
 PN 23-JAN-2003.  
 XX  
 PD 11-JUL-2001; 2001WO-EP080004.  
 XX  
 PF 11-JUL-2001; 2001WO-EP080004.  
 XX  
 PR 11-JUL-2001; 2001WO-EP080004.  
 XX  
 PA (JARI-) JARI PHARM BV.  
 XX  
 PI Van Kessel CPM, Gosselaar-de Haas CJC, Kruijtzer JAW;  
 PI Van Strijp JAG;  
 XX  
 DR WPI; 2003-247783/25.  
 XX  
 CC Combination of peptides derived from chemotaxis inhibiting protein from  
 CC Staphylococcus aureus (CHIPS) having CHIPS activity, useful in  
 CC prophylaxis and treatment of inflammation, cardiovascular, skin and  
 CC kidney diseases -  
 XX  
 PS Example 1; Page 56; 89pp; English.  
 XX  
 CC The present invention relates to peptides (ABR44811-ABR47162 and  
 CC ABR47164-ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS)  
 CC from Staphylococcus aureus. The peptide fragments are useful in the  
 CC prophylaxis or treatment of diseases or disorders involving the  
 CC C5a-receptor (C5aR) and/or formylated peptide receptor (FPR) or  
 CC neutrophils, monocytes and endothelial cells or involving acute or  
 CC chronic inflammation reactions. The diseases or disorders include  
 CC cardiovascular diseases, disease of the central nervous system,  
 CC gastrointestinal diseases, skin diseases, genitourinary diseases, joint  
 CC diseases, respiratory diseases and HIV infection.  
 XX  
 SQ Sequence 10 AA;

Query Match 22.2%; Score 4; DB 24; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 MPFP 7  
 DB 4 MPFP 7  
 |||||

AC XX

XX EP600326-A2.  
 XX  
 PD 08-JUN-1994.  
 XX  
 XX 20-NOV-1993; 93EP-0118697.  
 XX  
 XX 28-NOV-1992; 92DE-4240056.  
 XX  
 PA (BOEF ) BOEHRINGER MANNHEIM GMBH.  
 PA (HOFF ) ROCHE DIAGNOSTICS GMBH.  
 XX  
 PI Burns G, Engel W, Seidel C;  
 XX  
 DR WPI; 1994-177677/22.  
 XX  
 PT New streptolysin O-peptide antigen - for detecting specific  
 PT antibodies and is immunogens e.g. in vaccines, for diagnosis of,  
 PT and protection against, streptococcal infections  
 XX  
 XX Claim 1; Page 10; 11pp; German.  
 XX  
 CC Synthetic peptides having this sequence or at least a 4 (pref. less  
 CC than 7) amino acid fragment of it are streptolysin O peptide  
 CC antigens. The antigens are useful in immunoassays to determine  
 CC specific antibodies, e.g. to differentiate between rheumatism and  
 CC rheumatoid arthritis.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 XX  
 XX Sequence 11 AA;  
 SQ  
 Query Match 22.2%; Score 4; DB 15; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 2 KEMP 5  
 DB 6 KEMP 9  
 RESULT 70  
 AAB23183  
 ID AAB23183 standard; peptide; 12 AA.  
 AC  
 AC AAB23183;  
 XX  
 DT 29-JAN-2001 (first entry)  
 XX  
 DE Hsp47-binding hydrophobic phage display dodecapeptide, SEQ ID NO:5.  
 XX  
 KW Hsp47-binding hydrophobic dodecapeptide; phage display library;  
 KW Hsp47 external domain; carcinoma; cancer; targeting molecule;  
 KW therapy; diagnosis; detection; imaging; drug delivery; invasion;  
 KW migration; metastasis; modulation; tumour; skin; basal cells; colon;  
 KW large intestine; lung; breast; bladder; oral cancer;  
 KW head and neck cancer; larynx; nasopharynx; adrenal cortex;  
 KW apocrine gland; kidney; liver; pancreas; prostate.  
 XX  
 OS Synthetic.  
 XX  
 XX WO200054805-A1.  
 PN  
 PD 21-SEP-2000.  
 XX  
 XX 15-MAR-2000; 2000WO-US06588.  
 PF  
 XX 15-MAR-1999; 99US-0124481.  
 PR  
 XX (UYMA-) UNIV MARYLAND BALTIMORE.  
 PA  
 XX Sauk JJ;  
 PI  
 XX

DR WPI; 2000-655997/63.  
 XX  
 PT Treating, diagnosing or modulating a carcinoma cell, which expresses  
 PT Heat shock protein 47 on its surface, involves administering an agent  
 PT comprising targeting moiety which binds to Hsp47 external domain -  
 XX  
 PS Claim 6; Page 8; 87pp; English.  
 XX  
 CC The invention relates to methods of treating and diagnosing carcinomas  
 CC in which heat shock protein 47 (Hsp47) is expressed on the surface  
 CC of the carcinoma cells, involving administering an agent comprising a  
 CC targeting moiety which specifically binds to the external domain of  
 CC Hsp47. The invention also relates to peptides (AAB23181-B23203) which  
 CC specifically bind to external domains of such surface-localised Hsp47  
 CC molecules and have sequences encompassed by the generic sequences  
 CC XHYYXXHYYXXHYY or HYYXXHYYXXHYYXX where X, independently, can be  
 CC any amino acid and HY, independently, can be any hydrophobic amino acid.  
 CC The invention also encompasses methods of screening for agents which  
 CC bind Hsp47 external domains. Hsp47-binding agents can be used to  
 CC treat Hsp47-expressing carcinomas, and for modulating the activity of a  
 CC tumour cell with respect to invasion, migration, motility or metastasis,  
 CC or to its interaction with the extracellular matrix. The targeting  
 CC moiety (such as an Hsp47-binding peptide, a toxin or an antibody) may be  
 CC coupled with a therapeutic moiety (such as a cytotoxic agent or a  
 CC therapeutic gene) for cancer treatment, or with a detectable moiety for  
 CC imaging. Carcinomas which may be treated or diagnosed according to  
 CC methods of the invention include those of the skin, basal cells, large  
 CC intestine, lung, colon, breast, bladder, oral, head and neck, larynx,  
 CC nasopharynx, adrenal cortex, apocrine glands, kidney, liver, pancreas, or  
 CC prostate. Targeting carcinoma cells with Hsp47-binding agents results in  
 CC efficient delivery of therapeutic agents, reduced doses, reduced side  
 CC effects and sensitive detection or imaging of carcinoma cells. Sequences  
 CC AAB23181-B23191 represent predominantly hydrophobic phage display library  
 CC dodecapeptides identified as being able to bind Hsp47 in an  
 CC exemplification of the invention.  
 XX  
 XX Sequence 12 AA;  
 SQ  
 Query Match 22.2%; Score 4; DB 21; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 8 KYPV 11  
 DB 7 KYPV 10  
 RESULT 71  
 AAB57781  
 ID AAB57781 standard; Peptide; 12 AA.  
 XX  
 AC AAB57781;  
 XX  
 DT 09-MAR-2001 (first entry)  
 XX  
 DE Bovine DNaseI peptide #5.  
 XX  
 KW Retrotransposon; Genetic defect; cystic fibrosis.  
 XX  
 OS Bos taurus.  
 XX  
 XX US6150160-A.  
 PN  
 PD 21-NOV-2000.  
 XX  
 XX 28-APR-1997; 97US-0847844.  
 PF  
 XX 16-NOV-1995; 95US-0006831.  
 PR 15-NOV-1996; 96US-0749805.  
 XX  
 XX (UYJO ) UNIV JOHNS HOPKINS.  
 PA (UYPE-) UNIV PENNSYLVANIA.  
 PA  
 XX

PI Moran JV, Dombroski BA, Kazazian HH, Boeke JD;  
XX WPI; 2001-060015/07.  
XX  
XX DNAC comprising a promoter P and an L1 cassette sequence having a core  
PT retrotransposon element, useful for random insertion of a heterologous  
PT or homologous DNA sequence into a cell genome and for correcting  
PT genetic defects -  
XX  
XX Disclosure; Fig 7; 87pp; English.  
XX  
XX The present invention relates to DNA for a promoter and an L1  
CC cassette sequence having a core retrotransposon element. The invention  
CC is useful for random insertion of a heterologous or homologous DNA  
CC sequence into a cell genome, and for correction of a genetic defect  
CC in the cell into which the insertion is made. Genetic defects which  
CC may be corrected includes cystic fibrosis, mutations in the  
CC dystrophin gene, genetic defects associated with blood clotting and  
CC other genetic defects.  
XX  
XX Sequence 12 AA;  
SQ

Query Match 22.2%; Score 4; DB 22; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 9 YPVE 12  
Db 5 YPVE 8

RESULT 72  
ABB82324  
ID ABB82324 standard; peptide; 12 AA.  
XX  
XX ABB82324;  
XX  
XX 08-JAN-2003 (first entry)  
XX  
XX Epitopic peptide binding to a human antibody against C. trachomatis.  
XX  
XX Epitope; immunostimulant; antibacterial; vaccine; gene therapy.  
XX  
XX Chlamydia trachomatis.  
XX  
XX WO200272622-A2.  
XX  
XX 19-SEP-2002.  
XX  
XX 12-FEB-2002; 2002WO-GB00597.  
XX  
XX 12-FEB-2001; 2001GB-0003387.  
XX  
XX (YABA-) YABA LTD.  
XX  
XX Jones GE;  
XX  
XX WPI; 2002-740797/80.  
XX  
XX New epitopic peptide derived from Chlamydia trachomatis, useful as a  
PT vaccine for the induction of protection against Chlamydia trachomatis  
PT infections -  
XX  
XX Claim 1; Page 33; 37pp; English.  
XX  
XX Sequences ABB82301-340 represent epitopic peptides that bind specifically  
CC to a human antibody against Chlamydia trachomatis. The peptides are  
CC useful in vaccine preparations for the induction of protection against  
CC infection by C. trachomatis. The epitopic sequences or a compound  
CC comprising them can be used in medicine, such as in diagnosing,  
CC prognosing or treating infections caused by C. trachomatis.  
XX  
XX Sequence 12 AA;  
SQ

Query Match 22.2%; Score 4; DB 23; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 9 YPVE 12  
Db 5 YPVE 8

RESULT 73  
ABG67387  
ID ABG67387 standard; Peptide; 12 AA.  
XX  
XX ABG67387;  
XX  
XX 07-OCT-2002 (first entry)  
XX  
XX Human ADPI tryptic digest peptide #96.  
XX  
XX Human; Alzheimer's disease; AD; brain tissue; ADPI; ADPI;  
KW Alzheimer's disease-associated feature; neuroprotective;  
KW Alzheimer's disease-associated protein isoform; nootropic;  
KW ADPI tryptic digest peptide.  
XX  
XX Homo sapiens.  
XX  
XX WO200246767-A2.  
XX  
XX 13-JUN-2002.  
XX  
XX 29-NOV-2001; 2001WO-GB05289.  
XX  
XX 08-DEC-2000; 2000US-254431P.  
XX  
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
XX  
XX Herath HMAC, Parekh RB, Rohlf C;  
XX  
XX WPI; 2002-508575/54.  
XX  
XX Screening, diagnosis or prognosis of Alzheimer's disease in subject,  
PT comprises detecting Alzheimer's disease-associated features or  
PT Alzheimer's disease-associated protein isoforms in brain tissue  
PT from the subject -  
XX  
XX Claim 7; Page 83; 427pp; English.  
XX  
XX The present invention relates to methods and compositions for the  
CC screening, diagnosis or prognosis of Alzheimer's disease (AD) in  
CC a subject. The method comprises analysing a sample of brain tissue  
CC from a subject by 2D electrophoresis to generate a 2D array of  
CC Alzheimer's disease-associated features (ADFs), whose relative  
CC abundance correlates with the presence, absence, stage or severity of  
CC AD and comparing the abundance of each feature with the abundance of  
CC that chosen feature in brain tissue from persons free from AD. The  
CC invention also describes Alzheimer's disease-associated protein  
CC isoforms (ADPIs) detectable in brain tissue. The methods and  
CC compositions of the invention are useful for the screening, diagnosis  
CC or prognosis of AD in a subject, for determining the stage or severity  
CC of AD in a subject, for identifying a subject at risk of developing AD,  
CC or for monitoring the effect of therapy administered to a subject  
CC having AD. Antibodies capable of binding to ADPIs are useful for  
CC treating or preventing AD, and for determining the efficacy of a given  
CC treatment regime. An agent that modulates the activity of ADPI is  
CC useful in the manufacture of a medicament for the treatment or  
CC prevention of AD in a subject. ABG67292-ABG68038 represent human ADPI  
CC tryptic digest peptides.  
XX  
XX Sequence 12 AA;  
SQ

Query Match 22.2%; Score 4; DB 23; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 9 YPVE 12  
Db 5 YPVE 8



Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TESQ 18  
 ||||  
 Db 4 TESQ 7

## RESULT 74

AAR63797 standard; Peptide; 13 AA.

XX AAR63797;  
 AC AC  
 XX 25-MAR-2003 (updated)  
 DT 13-JUL-1995 (first entry)  
 XX  
 DE Bacillus thuringiensis anion exchange factor N-terminal peptide.  
 XX  
 KW Vegetative insecticidal protein; VIP; Bacillus thuringiensis;  
 KW pesticide; Diabrotica virgifera virgifera; insecticide.  
 XX  
 OS Bacillus thuringiensis.

XX Key Location/Qualifiers  
 FH Misc-difference 1  
 FT /note= "any amino acid"  
 FT Misc-difference 13  
 FT /note= "any amino acid"

XX WO9421795-A1.

XX 29-SEP-1994.

XX 23-MAR-1994; 94WO-US03131.

XX 25-MAR-1993; 93US-0037057.

XX (CIBA ) CIBA GEIGY AG.

XX Carr B, Desai N, Kostichka N, Koziel MG, Mullins MA;  
 PI Nye GJ, Warren GW;

XX WPI; 1994-317015/39.

XX Novel pesticidal proteins and Bacillus strains - e.g. useful for  
 PT control of Diabrotica virgifera virgifera

XX Claim 35; Page 77; 108pp; English.

XX AAR63795-R63802 are auxiliary proteins that enhance the pesticidal  
 CC activity of the vegetative insecticidal proteins (VIPs) described  
 CC in AAR63792-R63794 and AAR75690. The protein peptide combination can  
 CC be used in a variety of systems for controlling plant and non-plant  
 CC pests, including insects, fungi, bacteria, nematodes, protozoan  
 CC pathogens and animal-parasitic liver flukes. However it is esp.  
 CC useful in the control of Diabrotica virgifera virgifera.  
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 13 AA;

Query Match 22.2%; Score 4; DB 15; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEPF 14  
 ||||  
 Db 6 VEPF 9

## RESULT 75

AAR91253  
 ID AAR91253 standard; Peptide; 13 AA.

XX

AAR91253;

XX 25-MAR-2003 (updated)  
 DT 14-AUG-1996 (first entry)

XX European corn borer-active protein N-terminal peptide.

XX Pesticide; insecticide; biological control agent; Lepidoptera;  
 KW Coleoptera; transgenic plant; maize; insect resistance;  
 KW European corn borer; Ostrinia nubilalis.

XX Bacillus thuringiensis strain AB88 (NRRL B-21225).

XX Key Location/Qualifiers  
 FH Misc-difference 1  
 FT /note= "unidentified amino acid"  
 FT Misc-difference 13  
 FT /note= "unidentified amino acid"

XX WO9610083-A1.

XX 04-APR-1996.

XX 27-SEP-1995; 95WO-EP03826.

XX 05-JUN-1995; 95US-0463483.

XX 28-SEP-1994; 94US-0314594.

XX (CIBA ) CIBA GEIGY AG.

XX Warren GW, Koziel MG, Mullins MA, Nye GJ, Carr B, Desai NM;  
 PI Kostichka K, Duck NB, Estruch JJ;

XX WPI; 1996-200921/20.

XX Bacillus strain producing insecticidal protein during vegetative  
 PT growth - used in the control of Lepidoptera and Coleoptera pests  
 XX Example 17; Page 75; 242pp; English.

XX N-terminal sequences (AAR91252 and AAR91253) were obtd. from anion  
 CC exchange fractions 23 and 28, respectively, of a European corn  
 CC borer-active 60 kDa protein of Bacillus thuringiensis AB88. This  
 CC strain also produces a protein active against black cutworm (see  
 CC also AAR91243).  
 CC (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 13 AA;

Query Match 22.2%; Score 4; DB 17; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEPF 14  
 ||||  
 Db 6 VEPF 9

Search completed: November 25, 2003, 19:27:09  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:25:48 ; Search time 28.8837 Seconds  
(without alignments)  
114.943 Million cell updates/sec

Title: US-09-641-801-22

Perfect score: 18

Sequence: 1 HKMPFPKYPVBPFTSQ 18

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 184443283 residues

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Minimum DB seq length: 3

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Database : Published Applications AA:\*

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- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
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- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
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- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
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- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	15 US-10-281-652-22	Sequence 22, Appl
2	5	27.8	15	15 US-10-281-652-5	Sequence 5, Appli
3	4	22.2	6	12 US-10-441-626-27	Sequence 27, Appl
4	4	22.2	7	9 US-09-997-900-11	Sequence 11, Appl
5	4	22.2	9	10 US-09-780-053-17	Sequence 17, Appl
6	4	22.2	9	10 US-09-780-053-319	Sequence 238, App
7	4	22.2	9	10 US-09-780-053-418	Sequence 319, App
8	4	22.2	9	10 US-09-780-053-418	Sequence 418, App
9	4	22.2	9	12 US-09-932-165-265	Sequence 285, App
10	4	22.2	9	12 US-09-932-165-851	Sequence 851, App
11	4	22.2	9	12 US-09-932-165-1238	Sequence 1238, Ap
12	4	22.2	9	12 US-10-062-109A-4	Sequence 4, Appli
13	4	22.2	9	12 US-10-062-109A-44	Sequence 44, Appl
14	4	22.2	9	12 US-10-005-480A-4	Sequence 4, Appl
15	4	22.2	9	12 US-10-005-480A-44	Sequence 44, Appl

16	4	22.2	9	12 US-10-371-069-190	Sequence 190, App
17	4	22.2	9	12 US-10-371-645-190	Sequence 190, App
18	4	22.2	10	10 US-09-780-053-68	Sequence 68, Appl
19	4	22.2	10	10 US-09-780-053-276	Sequence 276, App
20	4	22.2	10	10 US-09-780-053-398	Sequence 398, App
21	4	22.2	10	10 US-09-780-053-404	Sequence 404, App
22	4	22.2	10	10 US-09-780-053-407	Sequence 407, App
23	4	22.2	10	10 US-09-780-053-496	Sequence 496, App
24	4	22.2	10	10 US-09-780-053-715	Sequence 715, App
25	4	22.2	10	12 US-09-932-165-373	Sequence 373, App
26	4	22.2	10	12 US-09-932-165-395	Sequence 395, App
27	4	22.2	10	12 US-09-932-165-1339	Sequence 1339, Ap
28	4	22.2	10	12 US-09-932-165-1351	Sequence 1351, Ap
29	4	22.2	10	12 US-10-062-109A-55	Sequence 55, Appl
30	4	22.2	10	12 US-10-062-109A-71	Sequence 71, Appl
31	4	22.2	10	12 US-10-005-480A-55	Sequence 55, Appl
32	4	22.2	10	12 US-10-005-480A-71	Sequence 71, Appl
33	4	22.2	11	15 US-10-062-710-173	Sequence 173, App
34	4	22.2	12	15 US-10-094-401-148	Sequence 148, App
35	4	22.2	12	15 US-10-057-789-142	Sequence 142, App
36	4	22.2	12	15 US-10-212-628-142	Sequence 142, App
37	4	22.2	12	15 US-10-216-122-89	Sequence 89, Appl
38	4	22.2	13	10 US-09-966-955A-31	Sequence 31, Appl
39	4	22.2	13	10 US-09-966-955A-32	Sequence 32, Appl
40	4	22.2	13	12 US-10-371-078-26	Sequence 26, Appl
41	4	22.2	14	11 US-09-791-393-100	Sequence 100, App
42	4	22.2	14	11 US-09-791-389-100	Sequence 100, App
43	4	22.2	15	12 US-10-271-078-33	Sequence 33, Appl
44	4	22.2	15	11 US-09-892-877-381	Sequence 381, App
45	4	22.2	15	11 US-09-991-799-2	Sequence 2, Appli
46	4	22.2	15	11 US-09-948-783-381	Sequence 381, App
47	4	22.2	15	14 US-10-001-879-120	Sequence 120, App
48	4	22.2	15	15 US-10-281-652-8	Sequence 8, Appli
49	4	22.2	15	15 US-10-264-303-11	Sequence 11, Appl
50	4	22.2	16	12 US-10-175-270-13	Sequence 13, Appl
51	4	22.2	16	12 US-10-161-791-181	Sequence 181, App
52	4	22.2	16	15 US-10-225-567A-1110	Sequence 1110, Ap
53	4	22.2	16	15 US-10-225-567A-1727	Sequence 1727, Ap
54	4	22.2	17	9 US-09-864-761-46168	Sequence 46168, A
55	4	22.2	17	12 US-10-161-791-362	Sequence 362, App
56	4	22.2	18	9 US-09-864-761-48184	Sequence 48184, A
57	4	22.2	18	15 US-10-094-401-196	Sequence 196, App
58	4	22.2	20	9 US-09-841-132-236	Sequence 236, App
59	4	22.2	20	9 US-09-841-132-237	Sequence 237, App
60	4	22.2	20	9 US-09-841-132-238	Sequence 238, App
61	4	22.2	20	9 US-09-841-132-239	Sequence 239, App
62	4	22.2	20	11 US-09-983-802-664	Sequence 664, App
63	3	16.7	3	12 US-10-253-532-126	Sequence 126, App
64	3	16.7	4	10 US-09-982-172-156	Sequence 156, App
65	3	16.7	4	10 US-09-947-387-27	Sequence 27, Appl
66	3	16.7	4	11 US-09-994-078-2	Sequence 2, Appli
67	3	16.7	4	12 US-10-237-160-1	Sequence 1, Appli
68	3	16.7	4	12 US-10-253-532-122	Sequence 122, App
69	3	16.7	4	12 US-10-253-532-125	Sequence 125, App
70	3	16.7	4	12 US-10-087-942-20	Sequence 20, Appl
71	3	16.7	4	12 US-10-087-942-31	Sequence 31, Appl
72	3	16.7	4	12 US-10-313-338A-1	Sequence 1, Appli
73	3	16.7	4	12 US-10-313-790A-1	Sequence 1, Appli
74	3	16.7	4	14 US-10-138-375-27	Sequence 27, Appl
75	3	16.7	4	14 US-10-041-030-28	Sequence 28, Appl
76	3	16.7	4	15 US-10-087-905-20	Sequence 20, Appl
77	3	16.7	4	15 US-10-087-905-31	Sequence 31, Appl
78	3	16.7	4	15 US-10-059-261-25	Sequence 25, Appl
79	3	16.7	4	15 US-10-059-261-133	Sequence 133, App
80	3	16.7	4	15 US-10-006-869-199	Sequence 199, App
81	3	16.7	5	12 US-10-253-532-117	Sequence 117, App
82	3	16.7	5	12 US-10-253-532-121	Sequence 121, App
83	3	16.7	5	12 US-10-253-532-124	Sequence 124, App
84	3	16.7	5	12 US-10-226-629A-9	Sequence 9, Appli
85	3	16.7	5	12 US-10-294-891-49	Sequence 49, Appl
86	3	16.7	5	12 US-10-276-601-4	Sequence 4, Appli
87	3	16.7	5	12 US-10-020-354-112	Sequence 112, App
88	3	16.7	5	12 US-10-145-206-110	Sequence 110, App

89                   3   16.7   5   15   US-10-155-407A-12   Sequence 12, Appl  
90                   3   16.7   5   15   US-10-006-869-200   Sequence 200, App  
91                   3   16.7   5   15   US-10-006-869-202   Sequence 202, App  
92                   3   16.7   5   15   US-10-006-869-1566   Sequence 1566, Ap  
93                   3   16.7   5   15   US-10-006-869-1568   Sequence 1568, Ap  
94                   3   16.7   5   15   US-10-096-986-13   Sequence 13, Appl  
95                   3   16.7   5   15   US-10-058-613-16   Sequence 16, Appl  
96                   3   16.7   5   15   US-10-281-652-15   Sequence 15, Appl  
97                   3   16.7   5   15   US-10-206-699-199   Sequence 199, App  
98                   3   16.7   6   9   US-09-062-113-1   Sequence 1, Appl  
99                   3   16.7   6   10   US-09-529-759-26   Sequence 26, Appl  
100                  3   16.7   6   10   US-09-529-759-27   Sequence 27, Appl

## ALIGNMENTS

RESULT 1  
US-10-281-652-22  
; Sequence 22, Application US/10281652  
; Publication No. US20030091606A1  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/10/281,652  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US/09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: Peptide  
US-10-281-652-22

Query Match           100.0%;   Score 18;   DB 15;   Length 18;  
Best Local Similarity   100.0%;   Pred. No. 3.8e-13;  
Matches   18;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

QY   1   HKEMPPPKYPVPPFTESQ 18  
      |||||  
Db   1   HKEMPPPKYPVPPFTESQ 18

RESULT 2  
US-10-281-652-5  
; Sequence 5, Application US/10281652  
; Publication No. US20030091606A1  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/10/281,652  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US/09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 5  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-10-281-652-5

Query Match           27.8%;   Score 5;   DB 15;   Length 15;  
Best Local Similarity   100.0%;   Pred. No. .43;  
Matches   5;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

QY   10   PVEFP 14  
      |||||  
Db   8   PVEFP 12

RESULT 3  
US-10-441-626-27  
; Sequence 27, Application US/10441626  
; Publication No. US20030186418A1  
; GENERAL INFORMATION:  
; APPLICANT: Gualfetti, Peter  
; APPLICANT: Mitchinson, Colin  
; APPLICANT: Phillips, Jay Ian  
; TITLE OF INVENTION: No. US20030186418A1el Variant EGIII-Like Cellulase  
; TITLE OF INVENTION: Compositions  
; FILE REFERENCE: GC631  
; CURRENT APPLICATION NUMBER: US/10/441,626  
; CURRENT FILING DATE: 2003-05-19  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 27  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: EGIII-like cellulase amino acid string  
US-10-441-626-27

Query Match           22.2%;   Score 4;   DB 12;   Length 6;  
Best Local Similarity   100.0%;   Pred. No. 6e+05;  
Matches   4;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

QY   12   EPFT 15  
      |||||  
Db   3   EPFT 6

RESULT 4  
US-09-997-900-11  
; Sequence 11, Application US/09997900  
; Patent No. US20020053098A1  
; GENERAL INFORMATION:  
; APPLICANT: Kakefuda, Genichi  
; APPLICANT: Costello, Colleen  
; APPLICANT: Sun, Ming  
; APPLICANT: Hu, Weiming  
; TITLE OF INVENTION: Genes and Vectors for Conferring Herbicide Resistance  
; TITLE OF INVENTION: in Plants  
; FILE REFERENCE: 043753/241148 (5849-20A)  
; CURRENT APPLICATION NUMBER: US/09/997,900  
; CURRENT FILING DATE: 2001-11-30  
; PRIOR APPLICATION NUMBER: 60/106,239  
; PRIOR FILING DATE: 1998-10-29  
; PRIOR APPLICATION NUMBER: 09/426,568  
; PRIOR FILING DATE: 1999-10-22  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 7  
; TYPE: PRT

```

; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(7)
; OTHER INFORMATION: N-terminal of AHAS small subunit peptide from
; OTHER INFORMATION: plasmid F3
; NAME/KEY: SITE
; LOCATION: (1)..(2)
; OTHER INFORMATION: Thrombin cleavage site
US-09-997-900-11

```

```

Query Match      22.2%; Score 4; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 11 VEPF 14
    ||||
Db 3 VEPF 6

```

```

RESULT 5
US-09-780-053-17
; Sequence 17, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-17

```

```

Query Match      22.2%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 15 TESQ 18
    ||||
Db 2 TESQ 5

```

```

RESULT 6
US-09-780-053-238
; Sequence 238, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09

```

```

; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 238
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-238

```

```

Query Match      22.2%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 15 TESQ 18
    ||||
Db 2 TESQ 5

```

```

RESULT 7
US-09-780-053-319
; Sequence 319, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 319
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-319

```

```

Query Match      22.2%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 15 TESQ 18
    ||||
Db 2 TESQ 5

```

```

RESULT 8
US-09-780-053-418
; Sequence 418, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261

```

```

; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 418
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-418

Query Match      22.2%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 TESQ 18
      |||||
Db      4 TESQ 7

RESULT 9
US-09-932-165-265
; Sequence 265, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: PARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND Cat-F2E11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20014.00
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US/09/932,165
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 265
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif

US-09-932-165-265

Query Match      22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 KYPV 11
      |||||
Db      6 KYPV 9

RESULT 10
US-09-932-165-851
; Sequence 851, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: PARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND Cat-F2E11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20014.00
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US/09/932,165
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 851
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif

US-09-932-165-851

Query Match      22.2%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 TESQ 18
      |||||
Db      4 TESQ 7

RESULT 9
US-09-932-165-265
; Sequence 265, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: PARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND Cat-F2E11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20014.00
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US/09/932,165
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 265
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif

US-09-932-165-265

Query Match      22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 KYPV 11
      |||||
Db      6 KYPV 9

RESULT 10
US-09-932-165-851
; Sequence 851, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: PARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND Cat-F2E11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20014.00
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US/09/932,165
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 851
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif

US-09-932-165-851

Query Match      22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 KYPV 11
      |||||
Db      4 KYPV 7

RESULT 12
US-10-062-109A-4
; Sequence 4, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:

```

```

; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND Cat-F2E11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 851
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-851

```

```

Query Match      22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 KYPV 11
      |||||
Db      1 KYPV 4

```

```

RESULT 11
US-09-932-165-1238
; Sequence 1238, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: PARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND Cat-F2E11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1238
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-1238

```

```

Query Match      22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 KYPV 11
      |||||
Db      4 KYPV 7

```

```

RESULT 12
US-10-062-109A-4
; Sequence 4, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-4

```

```

Query Match      22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      11 VEPF 14
        ||||
Db      4 VEPF 7

```

```

RESULT 13
US-10-062-109A-44
; Sequence 44, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-44

```

```

Query Match      22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      11 VEPF 14
        ||||
Db      2 VEPF 5

```

```

RESULT 14
US-10-005-480A-4
; Sequence 4, Application US/10005480A
; Publication No. US20030191073A1

```

```

; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-4

```

```

Query Match      22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      11 VEPF 14
        ||||
Db      4 VEPF 7

```

```

RESULT 15
US-10-005-480A-44
; Sequence 44, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-44

```

```

Query Match      22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      11 VEPF 14
        ||||
Db      2 VEPF 5

```

```

RESULT 16
US-10-371-069-190
; Sequence 190, Application US/10371069
; Publication No. US20030216342A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE Inc.
; APPLICANT: Fikes, John D.

```

```
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; TITLE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.10
; CURRENT APPLICATION NUMBER: US/10/371,069
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 190
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HBV POL 655 (peptide 20.0130)
US-10-371-069-190

Query Match          22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      14 FTES 17
        ||||
Db       2 FTES 5
```

```
RESULT 17
US-10-371-645-190
; Sequence 190, Application US/10371645
; Publication No. US20030216343A1
; GENERAL INFORMATION:
; APPLICANT: EPIMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; TITLE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.11
; CURRENT APPLICATION NUMBER: US/10/371,645
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 190
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HBV POL 655 (peptide 20.0130)
US-10-371-645-190
```

```
Query Match          22.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      14 FTES 17
        ||||
Db       2 FTES 5
```

```
RESULT 18
US-09-780-053-68
; Sequence 68, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Bid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-68
```

```
Query Match          22.2%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      15 TESQ 18
        ||||
Db       2 TESQ 5
```

```
RESULT 19
US-09-780-053-276
; Sequence 276, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Bid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 276
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-276
```

```
Query Match          22.2%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      15 TESQ 18
        ||||
Db       5 TESQ 8
```

## RESULT 20

US-09-780-053-398  
; Sequence 398, Application US/09780053  
; Patent No. US20020102640A1  
; GENERAL INFORMATION:  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Mary Faris  
; APPLICANT: Elana Levin  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Ava Jakobovits  
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN  
; FILE REFERENCE: 129.5USU1  
; CURRENT APPLICATION NUMBER: US/09/780.053  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/181,261  
; PRIOR FILING DATE: 2000-02-09  
; NUMBER OF SEQ ID NOS: 716  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 398  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-09-780-053-398

Query Match 22.2%; Score 4; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TESQ 18  
|||  
Db 3 TESQ 6

## RESULT 21

US-09-780-053-404  
; Sequence 404, Application US/09780053  
; Patent No. US20020102640A1  
; GENERAL INFORMATION:  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Mary Faris  
; APPLICANT: Elana Levin  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Ava Jakobovits  
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN  
; FILE REFERENCE: 129.5USU1  
; CURRENT APPLICATION NUMBER: US/09/780.053  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/181,261  
; PRIOR FILING DATE: 2000-02-09  
; NUMBER OF SEQ ID NOS: 716  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 404  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-09-780-053-404

Query Match 22.2%; Score 4; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TESQ 18  
|||  
Db 2 TESQ 5

## RESULT 22

US-09-780-053-407  
; Sequence 407, Application US/09780053  
; Patent No. US20020102640A1  
; GENERAL INFORMATION:  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Mary Faris  
; APPLICANT: Elana Levin  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Ava Jakobovits  
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN  
; FILE REFERENCE: 129.5USU1  
; CURRENT APPLICATION NUMBER: US/09/780.053  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/181,261  
; PRIOR FILING DATE: 2000-02-09  
; NUMBER OF SEQ ID NOS: 716  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 407  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-09-780-053-407

Query Match 22.2%; Score 4; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TESQ 18  
|||  
Db 4 TESQ 7

## RESULT 23

US-09-780-053-496  
; Sequence 496, Application US/09780053  
; Patent No. US20020102640A1  
; GENERAL INFORMATION:  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Mary Faris  
; APPLICANT: Elana Levin  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Ava Jakobovits  
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN  
; FILE REFERENCE: 129.5USU1  
; CURRENT APPLICATION NUMBER: US/09/780.053  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/181,261  
; PRIOR FILING DATE: 2000-02-09  
; NUMBER OF SEQ ID NOS: 716  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 496  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-09-780-053-496

Query Match 22.2%; Score 4; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TESQ 18  
|||  
Db 5 TESQ 8

## RESULT 24



US-09-780-053-715  
; Sequence 715, Application US/09780053  
; Patent No. US20020102640A1  
; GENERAL INFORMATION:  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Mary Faris  
; APPLICANT: Elana Levin  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN  
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER  
; FILE REFERENCE: 129.5USU1  
; CURRENT APPLICATION NUMBER: US/09/780,053  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/181,261  
; PRIOR FILING DATE: 2000-02-09  
; NUMBER OF SEQ ID NOS: 716  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 715  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-09-780-053-715

Query Match 22.2%; Score 4; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0;

QY 15 TESQ 18  
|||  
DB 5 TESQ 8

RESULT 25  
US-09-932-165-373  
; Sequence 373, Application US/09932165  
; Publication No. US20030134784A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA M.  
; APPLICANT: FARIS, MARY  
; APPLICANT: SAFFRAN, DOUGLAS  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITS, AYA  
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED  
; TITLE OF INVENTION: 83P2H3 AND CatP2E11 USEFUL IN TREATMENT AND  
; TITLE OF INVENTION: DETECTION OF CANCER  
; FILE REFERENCE: 51158-20014.00  
; CURRENT APPLICATION NUMBER: US/09/932,165  
; CURRENT FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: 60/226,329  
; PRIOR FILING DATE: 2000-08-17  
; NUMBER OF SEQ ID NOS: 1508  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 373  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-932-165-373

Query Match 22.2%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0;

QY 8 KYPV 11  
|||

Db 6 KYPV 9  
RESULT 26  
US-09-932-165-395  
; Sequence 395, Application US/09932165  
; Publication No. US20030134784A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA M.  
; APPLICANT: FARIS, MARY  
; APPLICANT: SAFFRAN, DOUGLAS  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITS, AYA  
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED  
; TITLE OF INVENTION: 83P2H3 AND CatP2E11 USEFUL IN TREATMENT AND  
; TITLE OF INVENTION: DETECTION OF CANCER  
; FILE REFERENCE: 51158-20014.00  
; CURRENT APPLICATION NUMBER: US/09/932,165  
; CURRENT FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: 60/226,329  
; PRIOR FILING DATE: 2000-08-17  
; NUMBER OF SEQ ID NOS: 1508  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 395  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-932-165-395

Query Match 22.2%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0;

QY 8 KYPV 11  
|||  
DB 7 KYPV 10

RESULT 27  
US-09-932-165-1339  
; Sequence 1339, Application US/09932165  
; Publication No. US20030134784A1  
; GENERAL INFORMATION:  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: CHALLITA-EID, PIA M.  
; APPLICANT: FARIS, MARY  
; APPLICANT: SAFFRAN, DOUGLAS  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: HUBERT, RENE  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITS, AYA  
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED  
; TITLE OF INVENTION: 83P2H3 AND CatP2E11 USEFUL IN TREATMENT AND  
; TITLE OF INVENTION: DETECTION OF CANCER  
; FILE REFERENCE: 51158-20014.00  
; CURRENT APPLICATION NUMBER: US/09/932,165  
; CURRENT FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: 60/226,329  
; PRIOR FILING DATE: 2000-08-17  
; NUMBER OF SEQ ID NOS: 1508  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1339  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-932-165-1339

```
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-1339

Query Match      22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred.No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KYPV 11
Db 5 KYPV 8

RESULT 28
US-09-932-165-1351
; Sequence 1351, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1351
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-1351

Query Match      22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred.No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KYPV 11
Db 1 KYPV 4

RESULT 29
US-10-062-109A-55
; Sequence 55, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
```

```
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-55

Query Match      22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred.No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VEPF 14
Db 2 VEPF 5

RESULT 30
US-10-062-109A-71
; Sequence 71, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-71

Query Match      22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred.No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VEPF 14
Db 4 VEPF 7

RESULT 31
US-10-005-480A-55
; Sequence 55, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
```

Query Match	Best Local Similarity	Score	DB	Length	Indels	Gaps
Query Match	Best Local Similarity	Score	DB	Length	Indels	Gaps
Matches	4; Conservative	22.2%; 100.0%;	4; DB 12;	Length 10;	0; Mismatches	0; Indels
QY	11 VEPF 14					
Db	2 VEPF 5					
RESULT 32						
US-10-005-480A-71						
Sequence 71, Application US/10005480A						
Publication No. US20030191073A1						
GENERAL INFORMATION:						
APPLICANT: Agensys						
APPLICANT: Challita-Eid, Pia M.						
APPLICANT: Raitano, Arthur B.						
APPLICANT: Faris, Mary						
APPLICANT: Hubert, Rene S.						
APPLICANT: Morrison, Karen Jane Meyrick						
APPLICANT: Jakobovits, Aya						
TITLE OF INVENTION: Nucleic Acid and Corresponding Protein						
TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of						
TITLE OF INVENTION: Cancer						
FILE REFERENCE: 51158-20062.00						
CURRENT FILING DATE: 2001-11-07						
CURRENT APPLICATION NUMBER: US/10/005,480A						
NUMBER OF SEQ ID NOS: 765						
SOFTWARE: FastSeq for Windows Version 4.0						
SEQ ID NO 71						
LENGTH: 10						
TYPE: PRT						
ORGANISM: Homo Sapien						
US-10-005-480A-71						
Query Match	Best Local Similarity	Score	DB	Length	Indels	Gaps
Matches	4; Conservative	22.2%; 100.0%;	4; DB 12;	Length 10;	0; Mismatches	0; Indels
QY	11 VEPF 14					
Db	4 VEPF 7					
RESULT 33						
US-10-062-710-173						
Sequence 173, Application US/10062710						
Publication No. US20030049253A1						
GENERAL INFORMATION:						
APPLICANT: Li, Frank Q.						
APPLICANT: Chu, Yong-Liang						
APPLICANT: Qiu, Jian-Tai						
TITLE OF INVENTION: Polymeric Conjugates for Delivery of						
TITLE OF INVENTION: MHC-Recognized Epitopes						
TITLE OF INVENTION: Via Peptide Vaccines						
FILE REFERENCE: 3781-001-27						
CURRENT APPLICATION NUMBER: US/10/062,710						
CURRENT FILING DATE: 2002-02-05						
PRIOR APPLICATION NUMBER: US 60/310,498						
PRIOR FILING DATE: 2001-08-08						
NUMBER OF SEQ ID NOS: 232						
SOFTWARE: FastSeq for Windows Version 4.0						
SEQ ID NO 173						
LENGTH: 11						
TYPE: PRT						
ORGANISM: Artificial Sequence						

```
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 10
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-057-789-142

Query Match          22.2%; Score 4; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEPF 14
Db 2 VEPF 5

RESULT 36
US-10-212-628-142
; Sequence 142, Application US/10212628
; Publication No. US20030087329A1
; GENERAL INFORMATION:
; APPLICANT: Paul Haynes
; APPLICANT: Jing Wei
; APPLICANT: John Yates
; APPLICANT: Nancy Andon
; TITLE OF INVENTION: DIFFERENTIAL LABELING FOR QUANTITATIVE
; FILE REFERENCE: NADII.022CPI
; CURRENT APPLICATION NUMBER: US/10/212,628
; CURRENT FILING DATE: 2002-08-01
; PRIOR FILING DATE: 2001-01-26
; PRIOR FILING DATE: 2001-01-26 US 60/264,576
; PRIOR APPLICATION NUMBER: US 60/305,232
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 10/057,789
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 311
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 142
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 10
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-212-628-142

Query Match          22.2%; Score 4; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEPF 14
Db 2 VEPF 5

RESULT 37
US-10-216-122-89
; Sequence 89, Application US/10216122
; Publication No. US20030121063A1
; GENERAL INFORMATION:
; APPLICANT: Kazazian, Haig H.
; APPLICANT: Ostertag, Eric
; APPLICANT: DeBerardinis, Ralph
; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE OF MAMMALIAN RETROTRANSPOSONS
; FILE REFERENCE: 053893-5006-03
; CURRENT APPLICATION NUMBER: US/10/216,122
; CURRENT FILING DATE: 2002-08-09
; PRIOR FILING DATE: 2002-08-09
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: US 08/847,844
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: US 08/749,805
```

```
; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: US 60/006,831
; PRIOR FILING DATE: 1995-11-16
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 89
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-216-122-89

Query Match          22.2%; Score 4; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPVE 12
Db 5 YPVE 8

RESULT 38
US-09-966-955A-31
; Sequence 31, Application US/09966955A
; Patent No. US20020155563A1
; GENERAL INFORMATION:
; APPLICANT: Perez-Villar, Juan J.
; APPLICANT: Chang, Han
; APPLICANT: Yang, Wen-Pin
; APPLICANT: Wu, Yuli
; APPLICANT: Whitney, Gena S.
; APPLICANT: Kanner, Steven B.
; TITLE OF INVENTION: Identification and Cloning of a Full-length Human
; TITLE OF INVENTION: Clink-related Gene, MIST (Mast Cell Immunoreceptor
; FILE REFERENCE: 3053-4113US1
; CURRENT APPLICATION NUMBER: US/09/966,955A
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 60/237030
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 13
; TYPE: PRT
; ORGANISM: HUMAN
US-09-966-955A-31

Query Match          22.2%; Score 4; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PFPK 8
Db 10 PFPK 13

RESULT 39
US-09-966-955A-32
; Sequence 32, Application US/09966955A
; Patent No. US20020155563A1
; GENERAL INFORMATION:
; APPLICANT: Perez-Villar, Juan J.
; APPLICANT: Chang, Han
; APPLICANT: Yang, Wen-Pin
; APPLICANT: Wu, Yuli
; APPLICANT: Whitney, Gena S.
; APPLICANT: Kanner, Steven B.
; TITLE OF INVENTION: Identification and Cloning of a Full-length Human
; TITLE OF INVENTION: Clink-related Gene, MIST (Mast Cell Immunoreceptor
; FILE REFERENCE: 3053-4113US1
; CURRENT APPLICATION NUMBER: US/09/966,955A
; CURRENT FILING DATE: 2001-09-28
```

; PRIOR APPLICATION NUMBER: 60/237030  
; PRIOR FILING DATE: 2000-09-29  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 32  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: HUMAN  
US-09-966-955A-32

Query Match 22.2%; Score 4; DB 10; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PFPK 8  
|||  
Db 1 PFPK 4

## RESULT 40

US-10-271-078-26  
; Sequence 26, Application US/10271078  
; Publication No. US20030186267A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: NOVEL HUMAN LEUCINE-RICH REPEAT DOMAIN CONTAINING PROTEIN, HLLRCH  
; FILE REFERENCE: D0157 NP  
; CURRENT APPLICATION NUMBER: US/10/271,078  
; CURRENT FILING DATE: 2002-10-11  
; PRIOR APPLICATION NUMBER: U.S. 60/328,478  
; PRIOR FILING DATE: 2001-10-11  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 26  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-271-078-26

Query Match 22.2%; Score 4; DB 12; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KEMP 5  
|||  
Db 8 KEMP 11

## RESULT 41

US-09-791-393-100  
; Sequence 100, Application US/09791393  
; Publication No. US20030032200A1  
; GENERAL INFORMATION:  
; APPLICANT: Herath, Herath Mudiyansele Athula Chandrasiri  
; APPLICANT: Parekh, Rajesh Bhikhu  
; APPLICANT: Rohlf, Christian  
; TITLE OF INVENTION: Proteins, Genes and Their Use for  
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)  
; TITLE OF INVENTION: and Unipolar Depression  
; FILE REFERENCE: 2543-1-001 N1  
; CURRENT APPLICATION NUMBER: US/09/791,393  
; CURRENT FILING DATE: 2002-01-02  
; EARLIER APPLICATION NUMBER: GB 0004412.3  
; EARLIER FILING DATE: 2000-02-24  
; EARLIER APPLICATION NUMBER: GB 0030050.9  
; EARLIER FILING DATE: 2000-12-08  
; EARLIER APPLICATION NUMBER: US 60/254,830  
; EARLIER FILING DATE: 2000-12-12  
; NUMBER OF SEQ ID NOS: 308  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 100  
; LENGTH: 14  
; TYPE: PRT

; ORGANISM: homo sapien  
US-09-791-393-100

Query Match 22.2%; Score 4; DB 11; Length 14;  
Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 EMPF 6  
|||  
Db 2 EMPF 5

## RESULT 42

US-09-791-389-100  
; Sequence 100, Application US/09791389  
; Publication No. US20030032773A1  
; GENERAL INFORMATION:  
; APPLICANT: Herath, Herath Mudiyansele Athula Chandrasiri  
; APPLICANT: Parekh, Rajesh Bhikhu  
; APPLICANT: Rohlf, Christian  
; APPLICANT: Terrett, Jonathan Alexander  
; APPLICANT: Tyson, Kerry Louise  
; TITLE OF INVENTION: Proteins, Genes and Their Use for  
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)  
; TITLE OF INVENTION: and Unipolar Depression  
; FILE REFERENCE: 2543-1-001 N2  
; CURRENT APPLICATION NUMBER: US/09/791,389  
; CURRENT FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: GB 0004412.3  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: GB 0030050.9  
; PRIOR FILING DATE: 2000-12-08  
; PRIOR APPLICATION NUMBER: US 60/254,830  
; PRIOR FILING DATE: 2000-12-12  
; NUMBER OF SEQ ID NOS: 308  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 100  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: homo sapien  
US-09-791-389-100

Query Match 22.2%; Score 4; DB 11; Length 14;  
Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 EMPF 6  
|||  
Db 2 EMPF 5

## RESULT 43

US-10-271-078-33  
; Sequence 33, Application US/10271078  
; Publication No. US20030186267A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: NOVEL HUMAN LEUCINE-RICH REPEAT DOMAIN CONTAINING PROTEIN, HLL  
; FILE REFERENCE: D0157 NP  
; CURRENT APPLICATION NUMBER: US/10/271,078  
; CURRENT FILING DATE: 2002-10-11  
; PRIOR APPLICATION NUMBER: U.S. 60/328,478  
; PRIOR FILING DATE: 2001-10-11  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 33  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-271-078-33

Query Match 22.2%; Score 4; DB 12; Length 14;  
Best Local Similarity 100.0%; Pred. No. 4.9e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KEMP 5  
|||||  
Db 8 KEMP 11

## RESULT 44

US-09-892-877-381  
; Sequence 381, Application US/09892877  
; Publication No. US20030077809A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et. al.  
; TITLE OF INVENTION: 97 Human secreted proteins  
; FILE REFERENCE: P2028P1  
; CURRENT APPLICATION NUMBER: US/09/892,877  
; CURRENT FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/437,658  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-11-10  
; NUMBER OF SEQ ID NOS: 461  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 381  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-892-877-381

Query Match 22.2%; Score 4; DB 11; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TESQ 18  
|||||  
Db 12 TESQ 15

## RESULT 45

US-09-991-799-2  
; Sequence 2, Application US/09991799  
; Publication No. US20030100012A1  
; GENERAL INFORMATION:  
; APPLICANT: Jackowski, George  
; TITLE OF INVENTION: Plasma Protease C1 Biopolymer Markers Predictive of Alzheimers Disease  
; FILE REFERENCE: 2132.086  
; CURRENT APPLICATION NUMBER: US/09/991,799  
; CURRENT FILING DATE: 2001-11-23  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-991-799-2

Query Match 22.2%; Score 4; DB 11; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KYPV 11  
|||||  
Db 2 KYPV 5

## RESULT 46

US-09-948-783-381  
; Sequence 381, Application US/09948783  
; Publication No. US20030100051A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et. al.  
; TITLE OF INVENTION: 97 Human secreted proteins  
; FILE REFERENCE: P2028P2  
; CURRENT APPLICATION NUMBER: US/09/948,783  
; CURRENT FILING DATE: 2001-09-10

; PRIOR APPLICATION NUMBER: 60/231,846  
; PRIOR FILING DATE: 2000-09-11  
; PRIOR APPLICATION NUMBER: 09/892,877  
; PRIOR FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: 09/437,658  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: PCT/US99/09847  
; PRIOR FILING DATE: 1999-05-06  
; PRIOR APPLICATION NUMBER: 60/085,093  
; PRIOR FILING DATE: 1998-05-12  
; PRIOR APPLICATION NUMBER: 60/085,094  
; PRIOR FILING DATE: 1998-05-12  
; PRIOR APPLICATION NUMBER: 60/085,105  
; PRIOR FILING DATE: 1998-05-12  
; PRIOR APPLICATION NUMBER: 60/085,180  
; PRIOR FILING DATE: 1998-05-12  
; PRIOR APPLICATION NUMBER: 60/085,927  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,906  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,924  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,922  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,921  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,923  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,925  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,928  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,920  
; PRIOR FILING DATE: 1998-05-18  
; NUMBER OF SEQ ID NOS: 465  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 381  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-948-783-381

Query Match 22.2%; Score 4; DB 11; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TESQ 18  
|||||  
Db 12 TESQ 15

## RESULT 47

US-10-001-879-120  
; Sequence 120, Application US/10001879  
; Publication No. US20020127237A1  
; GENERAL INFORMATION:  
; APPLICANT: Salceda, Susana  
; APPLICANT: Macina, Roberto  
; APPLICANT: Recipon, Herve  
; APPLICANT: Caferkey, Robert  
; APPLICANT: Ali, Shujath  
; APPLICANT: Sun, Yongming  
; APPLICANT: Liu, Chonghua  
; TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes a  
; FILE REFERENCE: DEX-0281  
; CURRENT APPLICATION NUMBER: US/10/001,879  
; CURRENT FILING DATE: 2001-11-20  
; PRIOR APPLICATION NUMBER: 60/252,188  
; PRIOR FILING DATE: 2000-11-21  
; NUMBER OF SEQ ID NOS: 201  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 120  
; LENGTH: 15

; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-001-879-120

Query Match 22.2%; Score 4; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PPKY 9  
|||  
Db 8 PPKY 11  
|||

## RESULT 48

US-10-281-652-8  
; Sequence 8, Application US/10281652  
; Publication No. US20030091060A1  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/10/281,652  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US/09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-10-281-652-8

Query Match 22.2%; Score 4; DB 15; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PPKK 8  
|||  
Db 3 PPKK 6  
|||

## RESULT 49

US-10-264-303-11  
; Sequence 11, Application US/10264303  
; Publication No. US20030124060A1  
; GENERAL INFORMATION:  
; APPLICANT: Roux, Kenneth  
; APPLICANT: Sathe, Shridhar  
; APPLICANT: Teuber, Suzanne  
; TITLE OF INVENTION: Purified Linear Epitopes from Cashew Nuts, Nucleic Acids Encoding  
; TITLE OF INVENTION: Therefor and Associated Methods  
; FILE REFERENCE: 28396 and 30728  
; CURRENT APPLICATION NUMBER: US/10/264,303  
; CURRENT FILING DATE: 2002-10-03  
; PRIOR APPLICATION NUMBER: 60/326,793  
; PRIOR FILING DATE: 2001-10-03  
; PRIOR APPLICATION NUMBER: 60/371,774  
; PRIOR FILING DATE: 2002-04-11  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 11  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Anacardium occidentale

## US-10-264-303-11

Query Match 22.2%; Score 4; DB 15; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PFTTE 16  
|||  
Db 10 PFTTE 13  
|||

## RESULT 50

US-10-175-270-13  
; Sequence 13, Application US/10175270  
; Publication No. US20030166548A1  
; GENERAL INFORMATION:  
; APPLICANT: PETERSON, JOHNNY W.  
; APPLICANT: SAINI, SHAMSHER S.  
; APPLICANT: WOOD, THOMAS G.  
; APPLICANT: CHOPRA, ASHOK K.  
; TITLE OF INVENTION: ANTI-INFLAMMATORY AND OTHER THERAPEUTIC PROPHYLACTIC OR DIAGN  
; TITLE OF INVENTION: SYNTHETIC MELITTIN AND NE  
; TITLE OF INVENTION: W RELATED PEPTIDES  
; FILE REFERENCE: UTSG:213  
; CURRENT APPLICATION NUMBER: US/10/175,270  
; CURRENT FILING DATE: 2002-06-19  
; PRIOR APPLICATION NUMBER: US/09/458,397  
; PRIOR FILING DATE: 1999-12-10  
; PRIOR APPLICATION NUMBER: PCT/US98/12340  
; PRIOR FILING DATE: 1998-06-11  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-10-175-270-13

Query Match 22.2%; Score 4; DB 12; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 FTES 17  
|||  
Db 3 FTES 6  
|||

## RESULT 51

US-10-161-791-181  
; Sequence 181, Application US/10161791  
; Publication No. US20030186863A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/161.791  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602.999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; INFORMATION FOR SEQ ID NO: 181:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-10-161-791-181

Query Match 22.2%; Score 4; DB 12; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PPKK 8  
|  
|  
|  
|  
Db 5 PPKK 8

## RESULT 52

US-10-225-567A-1110  
; Sequence 1110, Application US/10225567A  
; Publication No. US20030113798A1  
; GENERAL INFORMATION:  
; APPLICANT: LifeSpan Biosciences  
; APPLICANT: Brown, Joseph P.  
; APPLICANT: Burner, Glenna C.  
; APPLICANT: Roush, Christine L.  
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 1920-4-4  
; CURRENT APPLICATION NUMBER: US/10/225,567A  
; CURRENT FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/257,144  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 2292  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1110  
; LENGTH: 16  
; TYPE: PPT  
; ORGANISM: Homo sapiens  
US-10-225-567A-1110

Query Match 22.2%; Score 4; DB 15; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PPKK 8  
|  
|  
|  
|  
Db 10 PPKK 13

## RESULT 53

US-10-225-567A-1727  
; Sequence 1727, Application US/10225567A  
; Publication No. US20030113798A1  
; GENERAL INFORMATION:

; APPLICANT: LifeSpan Biosciences  
; APPLICANT: Brown, Joseph P.  
; APPLICANT: Burner, Glenna C.  
; APPLICANT: Roush, Christine L.  
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPT  
; FILE REFERENCE: 1920-4-4  
; CURRENT APPLICATION NUMBER: US/10/225,567A  
; CURRENT FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/257,144  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 2292  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1727  
; LENGTH: 16  
; TYPE: PPT  
; ORGANISM: Homo sapiens  
US-10-225-567A-1727

Query Match 22.2%; Score 4; DB 15; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPVS 12  
|  
|  
|  
|  
Db 9 YPVS 12

## RESULT 54

US-09-864-761-46168  
; Sequence 46168, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO  
; FILE REFERENCE: Aeomica-x-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21





; OTHER INFORMATION: EST\_HUMAN HIT: AL121033.1, EVALUE 3.70e-02  
US-09-864-761-48184

Query Match 22.2%; Score 4; DB 9; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PFTE 16  
Db 1 PFTE 4

## RESULT 57

US-10-094-401-196  
; Sequence 196, Application US/10094401  
; Publication No. US20030069395A1  
; GENERAL INFORMATION:  
; APPLICANT: DYAX CORP.  
; APPLICANT: Sato, Aaron K.  
; APPLICANT: Ley, Arthur C.  
; APPLICANT: Cohen, Edward H.  
; TITLE OF INVENTION: SERUM ALBUMIN BINDING MOIETIES  
; FILE REFERENCE: DYX-026.2 PCT; DYX-026.2 US  
; CURRENT APPLICATION NUMBER: US/10/094.401  
; CURRENT FILING DATE: 2002-03-08  
; PRIOR APPLICATION NUMBER: 60/331,352  
; PRIOR FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/292,975  
; PRIOR FILING DATE: 2001-05-23  
; NUMBER OF SEQ ID NOS: 271  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 196  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: albumin binding peptide  
US-10-094-401-196

Query Match 22.2%; Score 4; DB 15; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 EMPF 6  
Db 10 EMPF 13

## RESULT 58

US-09-841-132-236  
; Sequence 236, Application US/09841132  
; Patent No. US20020061848A1  
; GENERAL INFORMATION:  
; APPLICANT: Bhatia, Ajay  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Probst, Peter  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND  
; FILE REFERENCE: 210121.469C8  
; CURRENT APPLICATION NUMBER: US/09/841.132  
; CURRENT FILING DATE: 2001-04-23  
; NUMBER OF SEQ ID NOS: 599  
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0  
; SEQ ID NO 236  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Made in a lab  
US-09-841-132-236

Query Match 22.2%; Score 4; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 9 YPVE 12  
Db 17 YPVE 20

## RESULT 59

US-09-841-132-237  
; Sequence 237, Application US/09841132  
; Patent No. US20020061848A1  
; GENERAL INFORMATION:  
; APPLICANT: Bhatia, Ajay  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Probst, Peter  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND  
; FILE REFERENCE: 210121.469C8  
; CURRENT APPLICATION NUMBER: US/09/841.132  
; CURRENT FILING DATE: 2001-04-23  
; NUMBER OF SEQ ID NOS: 599  
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0  
; SEQ ID NO 237  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Made in a lab  
US-09-841-132-237

Query Match 22.2%; Score 4; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 YPVE 12  
Db 12 YPVE 15

## RESULT 60

US-09-841-132-238  
; Sequence 238, Application US/09841132  
; Patent No. US20020061848A1  
; GENERAL INFORMATION:  
; APPLICANT: Bhatia, Ajay  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Probst, Peter  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND  
; FILE REFERENCE: 210121.469C8  
; CURRENT APPLICATION NUMBER: US/09/841.132  
; CURRENT FILING DATE: 2001-04-23  
; NUMBER OF SEQ ID NOS: 599  
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0  
; SEQ ID NO 238  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Made in a lab  
US-09-841-132-238

Query Match 22.2%; Score 4; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 YPVE 12  
Db 7 YPVE 10

## RESULT 61

US-09-841-132-239

; Sequence 239, Application US/09841132  
; Patent No. US20020061848A1  
; GENERAL INFORMATION:  
; APPLICANT: Bhatia, Ajay  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Probst, Peter  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND  
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION  
; FILE REFERENCE: 210121.469C8  
; CURRENT APPLICATION NUMBER: US/09/841,132  
; CURRENT FILING DATE: 2001-04-23  
; NUMBER OF SEQ ID NOS: 599  
; SOFTWARE: FastSeq for Windows Version 3.0/4.0  
; SEQ ID NO 239  
; LENGTH: 20  
; TYPE: PPT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Made in a lab  
US-09-841-132-239

Query Match 22.2%; Score 4; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPVE 12  
DB 2 YPVE 5

RESULT 62  
US-09-883-802-664  
; Sequence 664, Application US/09983802  
; Publication No. US20030022185A1  
; GENERAL INFORMATION:  
; APPLICANT: Fischer et al.  
; TITLE OF INVENTION: 123 Human Secreted Proteins  
; FILE REFERENCE: PZ010P1  
; CURRENT APPLICATION NUMBER: US/09/983,802  
; CURRENT FILING DATE: 2001-10-25  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/227,357  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US98/13684  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,926  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,793  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,925  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,929  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,803  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,732  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,931  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,932  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,916  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,930  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,918  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,920  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,733  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,795  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,919

; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,928  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,722  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,723  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,948  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,949  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,953  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,950  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,947  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,964  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/056,360  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,684  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,984  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,954  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,785  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,664  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,660  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,661  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12  
; NUMBER OF SEQ ID NOS: 672  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 664  
; LENGTH: 20  
; TYPE: PPT  
; ORGANISM: Homo sapiens  
US-09-983-802-664

Query Match 22.2%; Score 4; DB 11; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PPKK 8  
DB 16 PPKK 19

RESULT 63  
US-10-253-532-126  
; Sequence 126, Application US/10253532  
; Publication No. US20030138422A1  
; GENERAL INFORMATION:  
; APPLICANT: Aghajanian, Jane  
; APPLICANT: Wolfman, Neil  
; APPLICANT: Veldman, Geetruida  
; APPLICANT: Davies, Monique  
; APPLICANT: Whittemore, Lisa Anne  
; APPLICANT: O'Hara, Denise  
; APPLICANT: Bridges, Kristie  
; APPLICANT: Khurana, Tejiv  
; TITLE OF INVENTION: Antibody Inhibitors of GDF-8 and Uses Therefor  
; FILE REFERENCE: 08702.00012-00000  
; CURRENT APPLICATION NUMBER: US/10/253,532  
; CURRENT FILING DATE: 2002-09-25  
; PRIOR APPLICATION NUMBER: 60/324,528  
; PRIOR FILING DATE: 2001-09-26  
; NUMBER OF SEQ ID NOS: 131  
; SOFTWARE: PatentIn version 3.1

```
; SEQ ID NO 126
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-253-532-126

Query Match
Best Local Similarity 16.7%; Score 3; DB 12; Length 3;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TES 17
Db 1 TES 3

RESULT 64
US-09-982-172-156
; Sequence 156, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Email Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 156
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-156

Query Match
Best Local Similarity 16.7%; Score 3; DB 10; Length 4;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PVE 12
Db 1 PVE 3

RESULT 65
US-09-947-387-27
; Sequence 27, Application US/09947387
; Patent No. US20020150885A1
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. US20020150885A1el Fluorogenic or Fluorescent Reporter Molecule
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290005
; CURRENT APPLICATION NUMBER: US/09/947,387
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/061,582
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: US 60/145,746
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: US 09/169,888
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 4
```

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-947-387-27

Query Match
Best Local Similarity 16.7%; Score 3; DB 10; Length 4;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEP 13
Db 1 VEP 3

RESULT 66
US-09-994-078-2
; Sequence 2, Application US/09994078
; Publication No. US20030032774A1
; GENERAL INFORMATION:
; APPLICANT: BROWN, WILLIAM
; APPLICANT: DIMAIO, JOHN
; APPLICANT: SCHILLER, PETER
; APPLICANT: MARTEL, RENE
; APPLICANT: MARTEL, FRANCIS
; APPLICANT: MARTEL, DIANE
; APPLICANT: MARTEL, PIERRE
; TITLE OF INVENTION: NOVEL OPIOID PEPTIDES FOR THE TREATMENT OF PAIN
; FILE REFERENCE: MAS/81823/282437
; CURRENT APPLICATION NUMBER: US/09/994,078
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 09/159,518
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/392,918
; PRIOR FILING DATE: 1995-03-03
; PRIOR APPLICATION NUMBER: 08/718,585
; PRIOR FILING DATE: 1996-10-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-994-078-2

Query Match
Best Local Similarity 16.7%; Score 3; DB 11; Length 4;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PPT 15
Db 2 PPT 4

RESULT 67
US-10-237-160-1
; Sequence 1, Application US/10237160
; Publication No. US20030133926A1
; GENERAL INFORMATION:
; APPLICANT: Houston, Devin
; TITLE OF INVENTION: Compositions And Methods Relating To Reduction Of
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Graybeal Jackson Haley
; STREET: 777-108th Ave. NE, Suite 2460
; CITY: Bellevue
; STATE: Washington
; COUNTRY: USA
```

ZIP: 98004-5117  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows 98  
SOFTWARE: <Unknown>  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/237,160  
FILING DATE: 09-Dec-2002  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: King, Joshua  
REGISTRATION NUMBER: 35,570  
REFERENCE/DOCKET NUMBER: 1776-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (425) 455-5575  
TELEFAX: (425) 455-1046  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
FRAGMENT TYPE: N-terminal  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-237-160-1

Query Match 16.7%; Score 3; DB 12; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PPP 7  
|||  
Db 2 PPP 4

RESULT 68  
US-10-253-532-122  
; Sequence 122, Application US/10253532  
; Publication No. US20030138422A1  
; GENERAL INFORMATION:  
; APPLICANT: Aghajanian, Jane  
; APPLICANT: Wolfman, Neil  
; APPLICANT: Veldman, Geetruida  
; APPLICANT: Davies, Monique  
; APPLICANT: Whittemore, Lisa Anne  
; APPLICANT: O'Hara, Denise  
; APPLICANT: Bridges, Kristie  
; APPLICANT: Khurana, Tejiv  
; TITLE OF INVENTION: Antibody Inhibitors of GDF-8 and Uses Therefor  
; CURRENT APPLICATION NUMBER: US/10/253,532  
; CURRENT FILING DATE: 2002-09-25  
; PRIOR APPLICATION NUMBER: 60/324,528  
; PRIOR FILING DATE: 2001-09-26  
; NUMBER OF SEQ ID NOS: 131  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 122  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-253-532-122

Query Match 16.7%; Score 3; DB 12; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TES 17  
|||  
Db 2 TES 4

RESULT 69  
US-10-253-532-125  
; Sequence 125, Application US/10253532  
; Publication No. US20030138422A1  
; GENERAL INFORMATION:  
; APPLICANT: Aghajanian, Jane  
; APPLICANT: Wolfman, Neil  
; APPLICANT: Veldman, Geetruida  
; APPLICANT: Davies, Monique  
; APPLICANT: Whittemore, Lisa Anne  
; APPLICANT: O'Hara, Denise  
; APPLICANT: Bridges, Kristie  
; APPLICANT: Khurana, Tejiv  
; TITLE OF INVENTION: Antibody Inhibitors of GDF-8 and Uses Therefor  
; FILE REFERENCE: 08702.00012-00000  
; CURRENT APPLICATION NUMBER: US/10/253,532  
; CURRENT FILING DATE: 2002-09-25  
; PRIOR APPLICATION NUMBER: 60/324,528  
; PRIOR FILING DATE: 2001-09-26  
; NUMBER OF SEQ ID NOS: 131  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 125  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-253-532-125

Query Match 16.7%; Score 3; DB 12; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TES 17  
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Db 1 TES 3

RESULT 70  
US-10-087-942-20  
; Sequence 20, Application US/10087942  
; Publication No. US20030165808A1  
; GENERAL INFORMATION:  
; APPLICANT: Haaland, Perry D.  
; APPLICANT: Sherman, Douglas B.  
; APPLICANT: Stewart II, Walter W.  
; APPLICANT: Lloyd, Sheila A.  
; APPLICANT: Campbell, Robert L.  
; TITLE OF INVENTION: METHODS, APPARATUS AND COMPUTER PROGRAM PRODUCTS FOR FORMULATING CULTURE MEDIA  
; FILE REFERENCE: P3250  
; CURRENT APPLICATION NUMBER: US/10/087,942  
; CURRENT FILING DATE: 2002-03-05  
; PRIOR APPLICATION NUMBER: US/09/359,260  
; PRIOR FILING DATE: 1999-07-22  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: hypothetical  
; OTHER INFORMATION: peptide  
US-10-087-942-20

Query Match 16.7%; Score 3; DB 12; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 ESQ 18  
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Db 2 ESQ 4

RESULT 71  
US-10-087-942-31  
; Sequence 31, Application US/10087942  
; Publication No. US20030165808A1  
; GENERAL INFORMATION:  
; APPLICANT: Haaland, Perry D.  
; APPLICANT: Sherman, Douglas B.  
; APPLICANT: Stewart II, Walter W.  
; APPLICANT: Lloyd, Sheila A.  
; APPLICANT: Campbell, Robert L.  
; TITLE OF INVENTION: METHODS, APPARATUS AND COMPUTER PROGRAM PRODUCTS FOR FORMULATING CULTURE MEDIA  
; FILE REFERENCE: P3250  
; CURRENT APPLICATION NUMBER: US/10/087,942  
; CURRENT FILING DATE: 2002-03-05  
; PRIOR APPLICATION NUMBER: US/09/359,260  
; PRIOR FILING DATE: 1999-07-22  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 31  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: hypothetical  
; OTHER INFORMATION: peptide  
US-10-087-942-31

Query Match 16.7%; Score 3; DB 12; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPV 11  
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Db 2 YPV 4

RESULT 72  
US-10-313-338A-1  
; Sequence 1, Application US/10313338A  
; Publication No. US20030170226A1  
; GENERAL INFORMATION:  
; APPLICANT: Klaire Laboratories, Inc.  
; APPLICANT: Houston, Devin B.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING TO REDUCTION OF SYMPTOMS OF AU  
; FILE REFERENCE: 1776-1-7  
; CURRENT APPLICATION NUMBER: US/10/313,338A  
; CURRENT FILING DATE: 2002-12-06  
; PRIOR APPLICATION NUMBER: US 09/411,605  
; PRIOR FILING DATE: 1999-10-01  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-313-338A-1

Query Match 16.7%; Score 3; DB 12; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PFP 7  
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Db 2 PFP 4

RESULT 73  
US-10-313-790A-1  
; Sequence 1, Application US/10313790A  
; Publication No. US20030170227A1  
; GENERAL INFORMATION:

; APPLICANT: Klaire Laboratories, Inc.  
; APPLICANT: Houston, Devin B.  
; TITLE OF INVENTION: COMPOSITIONS AND MENTHODS RELATING TO REDUCTION OF SYMPTOMS OF  
; FILE REFERENCE: 1776-1-6  
; CURRENT APPLICATION NUMBER: US/10/313,790A  
; CURRENT FILING DATE: 2002-12-06  
; PRIOR APPLICATION NUMBER: US 09/411,605  
; PRIOR FILING DATE: 1999-10-01  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-313-790A-1

Query Match 16.7%; Score 3; DB 12; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PFP 7  
|||  
Db 2 PFP 4

RESULT 74  
US-10-138-375-27  
; Sequence 27, Application US/10138375  
; Publication No. US20030208037A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Han-Zhong  
; APPLICANT: Cai, Sui Xiong  
; APPLICANT: Drewe, John A.  
; APPLICANT: Yang, Wu  
; TITLE OF INVENTION: No. US20030208037A1e1 Fluorescence Dyes and Their Applications  
; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Prote  
; TITLE OF INVENTION: Other Enzymes and the Use Thereof  
; FILE REFERENCE: 1735.0030001  
; CURRENT APPLICATION NUMBER: US/10/138,375  
; CURRENT FILING DATE: 2002-05-06  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/357,952  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-21  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/093,642  
; PRIOR FILING DATE: EARLIER FILING DATE: 21-JUL-1998  
; NUMBER OF SEQ ID NOS: 139  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 27  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-10-138-375-27

Query Match 16.7%; Score 3; DB 12; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEP 13  
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Db 1 VEP 3

RESULT 75  
US-10-041-030-28  
; Sequence 28, Application US/10041030  
; Publication No. US20020150934A1  
; GENERAL INFORMATION:  
; APPLICANT: Powers, Scott  
; APPLICANT: Mu, David  
; APPLICANT: Xiang, Phil  
; APPLICANT: Peng, Yue

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; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: Diagnosis and Treatment of Cancer Using Mammalian
; FILE REFERENCE: 018781-006810US
; CURRENT APPLICATION NUMBER: US/10/041,030
; CURRENT FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 60/259,502
; PRIOR FILING DATE: 2001-01-02
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:amino acid
; OTHER INFORMATION: sequence identity in comparison of pellino 1 and
; OTHER INFORMATION: pellino 2
US-10-041-030-28

Query Match      16.7%; Score 3; DB 14; Length 4;
Best Local Similarity 100.0%; Pred.No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      14 FTE 16
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Db      2 FTE 4

Search completed: November 25, 2003, 20:37:00
Job time : 29.8837 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:16:22 ; Search time 14.5465 Seconds  
(without alignments)  
52.356 Million cell updates/sec

Title: US-09-641-801-22

Perfect score: 18

Sequence: 1 HKEMPPKYPVRFETESQ 18

Scoring table: OLIGO  
Gapex 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3  
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

Issued Patents AA:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	5	27.8	15	4	US-09-641-803-5
3	4	22.2	6	3	US-09-216-295-27
4	4	22.2	7	1	US-08-261-206A-22
5	4	22.2	7	4	US-09-426-568A-11
6	4	22.2	8	1	US-08-259-550A-30
7	4	22.2	8	2	US-08-929-922B-7
8	4	22.2	8	3	US-09-342-394-7
9	4	22.2	8	3	US-09-580-064-7
10	4	22.2	8	4	US-09-718-709-7
11	4	22.2	9	4	US-09-311-784A-190
12	4	22.2	11	1	US-08-158-351-3
13	4	22.2	11	1	US-08-482-576-3
14	4	22.2	12	3	US-08-847-844A-89
15	4	22.2	13	1	US-08-471-033-11
16	4	22.2	13	2	US-08-471-044-11
17	4	22.2	13	2	US-08-463-483A-11
18	4	22.2	13	2	US-08-471-046A-11
19	4	22.2	13	2	US-08-470-566B-11
20	4	22.2	13	2	US-08-838-219B-11
21	4	22.2	13	2	US-08-469-334-11
22	4	22.2	13	3	US-09-300-529-11
23	4	22.2	13	3	US-09-233-336A-11
24	4	22.2	13	3	US-09-233-752A-11
25	4	22.2	13	3	US-09-402-036-11
26	4	22.2	13	4	US-09-904-226-11
27	4	22.2	14	6	5171684-21
					Patent No. 5171684

28	4	22.2	15	1	US-08-080-073-25	Sequence 25, Appl
29	4	22.2	15	2	US-08-967-101-168	Sequence 168, Appl
30	4	22.2	15	2	US-08-687-956A-7	Sequence 7, Appl
31	4	22.2	15	2	US-08-687-956A-8	Sequence 8, Appl
32	4	22.2	15	2	US-08-592-541-168	Sequence 168, Appl
33	4	22.2	15	2	US-08-591-629-5	Sequence 5, Appl
34	4	22.2	15	3	US-09-124-698-168	Sequence 168, Appl
35	4	22.2	15	3	US-09-127-480-168	Sequence 168, Appl
36	4	22.2	15	3	US-08-496-841C-165	Sequence 165, Appl
37	4	22.2	15	4	US-09-124-523-168	Sequence 168, Appl
38	4	22.2	15	4	US-09-636-796A-168	Sequence 168, Appl
39	4	22.2	15	4	US-09-641-803-8	Sequence 8, Appl
40	4	22.2	16	3	US-08-602-999A-181	Sequence 181, Appl
41	4	22.2	16	3	US-09-500-124-181	Sequence 181, Appl
42	4	22.2	17	3	US-08-602-999A-362	Sequence 362, Appl
43	4	22.2	17	4	US-09-500-124-362	Sequence 362, Appl
44	4	22.2	18	3	US-08-105-454-4	Sequence 4, Appl
45	4	22.2	18	4	US-09-407-687-8	Sequence 8, Appl
46	4	22.2	20	4	US-09-227-357-664	Sequence 664, Appl
47	4	22.2	20	4	US-09-556-877-236	Sequence 236, Appl
48	4	22.2	20	4	US-09-556-877-237	Sequence 237, Appl
49	4	22.2	20	4	US-09-556-877-238	Sequence 238, Appl
50	4	22.2	20	4	US-09-556-877-239	Sequence 239, Appl
51	4	22.2	20	4	US-09-620-412C-236	Sequence 236, Appl
52	4	22.2	20	4	US-09-620-412C-237	Sequence 237, Appl
53	4	22.2	20	4	US-09-620-412C-238	Sequence 238, Appl
54	4	22.2	20	4	US-09-620-412C-239	Sequence 239, Appl
55	4	22.2	20	4	US-09-598-419-236	Sequence 236, Appl
56	4	22.2	20	4	US-09-598-419-237	Sequence 237, Appl
57	4	22.2	20	4	US-09-598-419-238	Sequence 238, Appl
58	4	22.2	20	4	US-09-598-419-239	Sequence 239, Appl
59	3	16.7	4	1	US-08-224-868-5	Sequence 5, Appl
60	3	16.7	4	2	US-08-747-137-163	Sequence 163, Appl
61	3	16.7	4	3	US-08-415-655-3	Sequence 3, Appl
62	3	16.7	4	3	US-09-330-970-19	Sequence 19, Appl
63	3	16.7	4	3	US-09-357-952-27	Sequence 27, Appl
64	3	16.7	4	3	US-09-411-531A-1	Sequence 1, Appl
65	3	16.7	4	4	US-09-521-650-27	Sequence 27, Appl
66	3	16.7	4	4	US-09-168-888-27	Sequence 27, Appl
67	3	16.7	4	4	US-09-187-859-199	Sequence 199, Appl
68	3	16.7	4	4	US-09-411-605A-1	Sequence 1, Appl
69	3	16.7	4	4	US-09-839-542B-199	Sequence 199, Appl
70	3	16.7	4	6	5215966-12	Patent No. 5215966
71	3	16.7	4	6	5215966-14	Patent No. 5215966
72	3	16.7	5	1	US-07-708-035-14	Sequence 14, Appl
73	3	16.7	5	1	US-07-657-769B-28	Sequence 28, Appl
74	3	16.7	5	1	US-07-657-769B-67	Sequence 67, Appl
75	3	16.7	5	1	US-07-895-300A-12	Sequence 12, Appl
76	3	16.7	5	1	US-08-170-360-14	Sequence 14, Appl
77	3	16.7	5	1	US-07-789-184-73	Sequence 73, Appl
78	3	16.7	5	1	US-07-789-184-81	Sequence 81, Appl
79	3	16.7	5	1	US-07-789-184-83	Sequence 83, Appl
80	3	16.7	5	1	US-07-789-184-86	Sequence 86, Appl
81	3	16.7	5	1	US-07-789-184-88	Sequence 88, Appl
82	3	16.7	5	1	US-08-475-263-73	Sequence 73, Appl
83	3	16.7	5	1	US-08-475-263-81	Sequence 81, Appl
84	3	16.7	5	1	US-08-475-263-83	Sequence 83, Appl
85	3	16.7	5	1	US-08-475-263-86	Sequence 86, Appl
86	3	16.7	5	1	US-08-475-263-88	Sequence 88, Appl
87	3	16.7	5	1	US-08-477-509B-13	Sequence 13, Appl
88	3	16.7	5	1	US-08-458-367-12	Sequence 12, Appl
89	3	16.7	5	1	US-08-485-886-73	Sequence 73, Appl
90	3	16.7	5	1	US-08-485-886-81	Sequence 81, Appl
91	3	16.7	5	1	US-08-485-886-83	Sequence 83, Appl
92	3	16.7	5	1	US-08-485-886-86	Sequence 86, Appl
93	3	16.7	5	1	US-08-485-886-88	Sequence 88, Appl
94	3	16.7	5	2	US-08-477-362-73	Sequence 73, Appl
95	3	16.7	5	2	US-08-477-362-81	Sequence 81, Appl
96	3	16.7	5	2	US-08-477-362-83	Sequence 83, Appl
97	3	16.7	5	2	US-08-477-362-86	Sequence 86, Appl
98	3	16.7	5	2	US-08-477-362-88	Sequence 88, Appl
99	3	16.7	5	2	US-08-347-335A-4	Sequence 4, Appl
100	3	16.7	5	2	US-08-477-133A-73	Sequence 73, Appl



## ALIGNMENTS

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RESULT 1
US-09-641-803-22
; Sequence 22, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-22

Query Match      100.0%; Score 18; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.7e-13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HKMPFPKYPVPEPTESQ 18
Db 1 HKMPFPKYPVPEPTESQ 18

RESULT 2
US-09-641-803-5
; Sequence 5, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-5

Query Match      27.8%; Score 5; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PVEPF 14
Db 8 PVEPF 12
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RESULT 3
US-09-216-295-27
; Sequence 27, Application US/09216295
; Patent No. 6268328
; GENERAL INFORMATION:
; APPLICANT: Mitchinson, Colin
; APPLICANT: Wendt, Dan J.
; TITLE OF INVENTION: No. 6268328el Variant EGIII-Like Cellulase Compositions
; FILE REFERENCE: GC555
; CURRENT APPLICATION NUMBER: US/09/216,295
; CURRENT FILING DATE: 1998-12-18
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide
US-09-216-295-27

Query Match      22.2%; Score 4; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 EPFT 15
Db 3 EPFT 6

RESULT 4
US-08-261-206A-22
; Sequence 22, Application US/08261206A
; Patent No. 5574007
; GENERAL INFORMATION:
; APPLICANT: Zushi, Mitichitaka
; APPLICANT: Gomi, Komakazu
; APPLICANT: Yamamoto, Shuji
; APPLICANT: Suzuki, Koji
; APPLICANT: Matsuda, Akio
; TITLE OF INVENTION: A Polypeptide Capable of Interacting
; TITLE OF INVENTION: with Thrombin
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: 301 N. Washington St.
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22046-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/261,206A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/740,492
; FILING DATE: 03-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30330
; REFERENCE/DOCKET NUMBER: 216-275P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 22:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-261-206A-22
Query Match 22.2% Score 4; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PVEP 13
Db 2 PVEP 5

RESULT 5
US-09-426-568A-11
; Sequence 11, Application US/09426568A
; Patent No. 6348643
; GENERAL INFORMATION:
; APPLICANT: Kakufuda, Genichi
; APPLICANT: Costello, Colleen
; APPLICANT: Sun, Ming
; APPLICANT: Hu, Weiming
; TITLE OF INVENTION: Genes and Vectors for Conferring Herbicide Resistance
; TITLE OF INVENTION: in Plants
; FILE REFERENCE: 008103/195497
; CURRENT APPLICATION NUMBER: US/09/426,568A
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/106,239
; PRIOR FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 11
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(7)
; OTHER INFORMATION: N-terminal of AHAS small subunit peptide from
; OTHER INFORMATION: plasmid F3
; NAME/KEY: SITE
; LOCATION: (1)..(2)
; OTHER INFORMATION: Thrombin cleavage site
; US-09-426-568A-11
Query Match 22.2% Score 4; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VEPF 14
Db 3 VEPF 6

RESULT 6
US-08-259-550A-30
; Sequence 30, Application US/08259550A
; Patent No. 5776892
; GENERAL INFORMATION:
; APPLICANT: Counts, David F.
; APPLICANT: Duff, Ronald G.
; TITLE OF INVENTION: Anti-Inflammatory Peptides
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711

; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-261-206A-22
Query Match 22.2% Score 4; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PVEP 13
Db 2 PVEP 5

RESULT 5
US-09-426-568A-11
; Sequence 11, Application US/09426568A
; Patent No. 6348643
; GENERAL INFORMATION:
; APPLICANT: Kakufuda, Genichi
; APPLICANT: Costello, Colleen
; APPLICANT: Sun, Ming
; APPLICANT: Hu, Weiming
; TITLE OF INVENTION: Genes and Vectors for Conferring Herbicide Resistance
; TITLE OF INVENTION: in Plants
; FILE REFERENCE: 008103/195497
; CURRENT APPLICATION NUMBER: US/09/426,568A
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/106,239
; PRIOR FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 11
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(7)
; OTHER INFORMATION: N-terminal of AHAS small subunit peptide from
; OTHER INFORMATION: plasmid F3
; NAME/KEY: SITE
; LOCATION: (1)..(2)
; OTHER INFORMATION: Thrombin cleavage site
; US-09-426-568A-11
Query Match 22.2% Score 4; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VEPF 14
Db 3 VEPF 6

RESULT 6
US-08-259-550A-30
; Sequence 30, Application US/08259550A
; Patent No. 5776892
; GENERAL INFORMATION:
; APPLICANT: Counts, David F.
; APPLICANT: Duff, Ronald G.
; TITLE OF INVENTION: Anti-Inflammatory Peptides
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/259,550A
; FILING DATE: 16-JUN-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7142-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-259-550A-30
Query Match 22.2% Score 4; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TESQ 18
Db 1 TESQ 4

RESULT 7
US-08-929-922B-7
; Sequence 7, Application US/08929922B
; Patent No. 5994113
; GENERAL INFORMATION:
; APPLICANT: Kauppinen, Sakari
; APPLICANT: Si, Jean Qi
; APPLICANT: Spendler, Tina
; APPLICANT: Dammann, Claus
; APPLICANT: Halkier, Torben
; APPLICANT: stergaard, Peter Rahbek
; APPLICANT: Patkar, Shamkant Anant
; APPLICANT: Hansen, Kim
; TITLE OF INVENTION: An Enzyme With Aminopeptidase Activity
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5994113o No. 5994113disk of No. 5994113th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/929,922B
; FILING DATE: 15-SEP-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4355.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
```

TELEFAX: 212-878-9655  
INFORMATION FOR SEQ ID NO: 7;  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
FRAGMENT TYPE: internal  
US-08-929-922B-7

Query Match 22.2%; Score 4; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VEPF 14  
Db 4 VEPF 7

## RESULT 8

US-09-342-394-7

; Sequence 7, Application US/09342394

; Patent No. 6143546

; GENERAL INFORMATION:

; APPLICANT: Kauppinen, Sakari

; APPLICANT: Si, Joan Qi

; APPLICANT: Spandler, Tina

; APPLICANT: Dammann, Claus

; APPLICANT: Halkier, Torben

; APPLICANT: Ostergaard, Peter Rahbek

; APPLICANT: Patkar, Shamkant Anant

; APPLICANT: Hansen, Kim

; TITLE OF INVENTION: An Enzyme With Aminopeptidase Activity

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: No. 61435460 No. 6143546disk of No. 6143546th America, Inc.

; STREET: 405 Lexington Avenue

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10174

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/342,394

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/929,922

; FILING DATE: 15-SEP-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Lambiris, Elias J

; REGISTRATION NUMBER: 33,728

; REFERENCE/DOCKET NUMBER: 4355.204-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-867-0123

; TELEFAX: 212-878-9655

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; FRAGMENT TYPE: internal

; US-09-342-394-7

Query Match 22.2%; Score 4; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VEPF 14  
Db 4 VEPF 7

## RESULT 9

US-09-580-064-7

; Sequence 7, Application US/09580064

; Patent No. 6200792

; GENERAL INFORMATION:

; APPLICANT: Kauppinen, Sakari

; APPLICANT: Si, Joan Qi

; APPLICANT: Spandler, Tina

; APPLICANT: Dammann, Claus

; APPLICANT: Halkier, Torben

; APPLICANT: stergaard, Peter Rahbek

; APPLICANT: Patkar, Shamkant Anant

; APPLICANT: Hansen, Kim

; TITLE OF INVENTION: An Enzyme With Aminopeptidase Activity

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: No. 62007920 No. 6200792disk of No. 6200792th America, Inc.

; STREET: 405 Lexington Avenue

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10174

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/580,064

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/929,922

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Lambiris, Elias J

; REGISTRATION NUMBER: 33,728

; REFERENCE/DOCKET NUMBER: 4355.204-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-867-0123

; TELEFAX: 212-878-9655

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; FRAGMENT TYPE: internal

; US-09-580-064-7

Query Match 22.2%; Score 4; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VEPF 14  
Db 4 VEPF 7

## RESULT 10

US-09-718-709-7

; Sequence 7, Application US/09718709

```
; Patent No. 6413559
; GENERAL INFORMATION:
;   APPLICANT: Kauppinen, Sakari
;   Si, Joan Qi
;   Spendler, Tina
;   Dambmann, Claus
;   Halkier, Torben
;   stergaard, Peter Rahbek
;   Patkar, Shankant Anant
;   Hansen, Kim
;
; TITLE OF INVENTION: An Enzyme With Aminopeptidase Activity
;
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: No. 6413559o No. 6413559disk of No. 6413559th America, Inc.
;   STREET: 405 Lexington Avenue
;   CITY: New York
;   STATE: NY
;   COUNTRY: USA
;   ZIP: 10174
;
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSEQ for Windows Version 2.0
;
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/718,709
;   FILING DATE: 22-No. 6413559-2000
;   CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/929,922
;   FILING DATE: 15-SEP-1997
;
; ATTORNEY/AGENT INFORMATION:
;   NAME: Lambiris, Elias J
;   REGISTRATION NUMBER: 33,728
;   REFERENCE/DOCKET NUMBER: 4355.204-US
;
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 212-867-0123
;   TELEFAX: 212-878-9655
;
; INFORMATION FOR SEQ ID NO: 7:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 8 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   HYPOTHETICAL: NO
;   FRAGMENT TYPE: internal
;   SEQUENCE DESCRIPTION: SEQ ID NO: 7:
;
; US-09-718-709-7
;
; Query Match      22.2%; Score 4; DB 4; Length 8;
; Best Local Similarity 100.0%; Pred. No. 2.5e+05;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY      11 VEPF 14
;         ||||
;         4 VEPF 7
;
; Db
;
; RESULT 11
; US-09-311-784A-190
;   Sequence 190, Application US/09311784A
;   Patent No. 6534482
;   GENERAL INFORMATION:
;     APPLICANT: Fikes, John D.
;     APPLICANT: Hermanson, Gary G.
;     APPLICANT: Sette, Alessandro
;     APPLICANT: Ishioka, Glenn Y.
;     APPLICANT: Livingston, Brian
;     APPLICANT: Chesnut, Robert W.
;     APPLICANT: EpiImmune Inc.
;   TITLE OF INVENTION: Expression Vectors for Stimulating an
;   TITLE OF INVENTION: Immune Response and Methods of Using the Same
```

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; FILE REFERENCE: 39963-20022.01
; CURRENT APPLICATION NUMBER: US/09/311,784A
; CURRENT FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 190
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: HBV POL 655 (peptide 20.0130)
;
; US-09-311-784A-190
;
; Query Match      22.2%; Score 4; DB 4; Length 9;
; Best Local Similarity 100.0%; Pred. No. 2.5e+05;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY      14 FTES 17
;         ||||
;         2 FTES 5
;
; Db
;
; RESULT 12
; US-08-158-351-3
;   Sequence 3, Application US/08158351
;   Patent No. 5445820
;   GENERAL INFORMATION:
;     APPLICANT: SEIDEL, Christoph
;     APPLICANT: BURNS, Geoffrey
;     APPLICANT: ENGEL, Wolf-Dieter
;   TITLE OF INVENTION: STREPTOLYSIN O PEPTIDE ANTIGENS AND
;   TITLE OF INVENTION: METHODS FOR THE DETERMINATION OF STREPTOLYSIN ANTIBODIES
;   NUMBER OF SEQUENCES: 5
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Nikaido, Marmelstein, Murray & Oram
;     STREET: 655 Fifteenth Street N.W., Suite 330
;     CITY: Washington
;     STATE: D.C.
;     COUNTRY: USA
;     ZIP: 2005-5701
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA: US/08/158,351
;   FILING DATE:
;   CLASSIFICATION: 424
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: DE P 42 40 056.2
;     FILING DATE: 28-NOV-1992
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Kitts, Monica C.
;     REGISTRATION NUMBER: 36,105
;     REFERENCE/DOCKET NUMBER: 1614-3052
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (202) 638-5000
;     TELEFAX: (202) 638-4810
;   INFORMATION FOR SEQ ID NO: 3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 11 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: peptide
;
; US-08-158-351-3
;
; Query Match      22.2%; Score 4; DB 1; Length 11;
; Best Local Similarity 100.0%; Pred. No. 1.8e+02;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      2 KEMP 5
      ||||
Db      6 KEMP 9

RESULT 13
US-08-482-576-3
; Sequence 3, Application US/08482576
; Patent No. 5688659
; GENERAL INFORMATION:
; APPLICANT: SEIDEL, Christoph
; APPLICANT: BURNS, Geoffrey
; APPLICANT: ENGEL, Wolf-Dieter
; TITLE OF INVENTION: STREPTOLYSIN O PEPTIDE ANTIGENS AND
; TITLE OF INVENTION: METHODS FOR THE DETERMINATION OF STREPTOLYSIN
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram
; STREET: 655 Fifteenth Street N.W., Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,576
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 42 40 056.2
; FILING DATE: 28-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitts, Monica C.
; REGISTRATION NUMBER: 36,105
; REFERENCE/DOCKET NUMBER: 1614-3052
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-5000
; TELEFAX: (202) 638-4810
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-482-576-3

Query Match      22.2%; Score 4; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 KEMP 5
      ||||
Db      6 KEMP 9

RESULT 14
US-08-847-844A-89
; Sequence 89, Application US/08847844A
; Patent No. 6150160
; GENERAL INFORMATION:
; APPLICANT: KAZAZIAN JR., HAIG H.
; APPLICANT: BOEKE, JEF D.
; APPLICANT: MORAN, JOHN V.
; APPLICANT: DOMEROSKI, BETH A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE OF
; TITLE OF INVENTION: MAMMALIAN RETROTRANSPOSONS
```

```
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND FL.
; CITY: PHILADELPHIA
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103-7086
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/847,844A
; FILING DATE: 28-APR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/749,805
; FILING DATE: 16-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/006,831
; FILING DATE: 16-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DOYLE LEARY Ph.D., KATHRYN
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: 9596-2302
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020
; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 89:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-847-844A-89

Query Match      22.2%; Score 4; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 YPVE 12
      ||||
Db      5 YPVE 8

RESULT 15
US-08-471-033-11
; Sequence 11, Application US/08471033
; Patent No. 5770696
; GENERAL INFORMATION:
; APPLICANT: Warren, Gregory W
; APPLICANT: Koziel, Michael G
; APPLICANT: Mullins, Martha A
; APPLICANT: Nye, Gordon J
; APPLICANT: Carr, Brian
; APPLICANT: Desai, Nalini M
; APPLICANT: Kostichka, N. Kristy
; APPLICANT: Duck, Nicholas B
; APPLICANT: Estruch, Juan J
; TITLE OF INVENTION: No. 5770696el Pesticidal Proteins and Strains
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,033
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,594
; FILING DATE: 09-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/218,018
; FILING DATE: 23-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/037,057
; FILING DATE: 25-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: P-40,403
; REFERENCE/DOCKET NUMBER: CGC 1695/CIP3/DIV7 - SOLv3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8582
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORGANISM: Bacillus thuringiensis
; ORIGINAL SOURCE:
; US-08-471-033-11

Query Match 22.2%; Score 4; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VEPF 14
Db 6 VEPF 9

RESULT 16
US-08-471-044-11
; Sequence 11, Application US/08471044
; Patent No. 5840868
; GENERAL INFORMATION:
; APPLICANT: Warren, Gregory W
; APPLICANT: Koziel, Michael G
; APPLICANT: Mullins, Martha A
; APPLICANT: Nye, Gordon J
; APPLICANT: Carr, Brian
; APPLICANT: Desai, Nalini M
; APPLICANT: Kostichka, N. Kristy
; APPLICANT: Duck, Nicholas B
; APPLICANT: Estruch, Juan J
; TITLE OF INVENTION: No. 5840868el Pesticidal Proteins and Strains
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,044
; FILING DATE: 06-JUN-1995

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; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/463,483
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,594
; FILING DATE: 09-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/218,018
; FILING DATE: 23-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/037,057
; FILING DATE: 25-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40,403
; REFERENCE/DOCKET NUMBER: CGC 1695/CIP3/DIV6 - SOLv3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8582
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; ORIGINAL SOURCE:
; US-08-471-044-11

Query Match 22.2%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VEPF 14
Db 6 VEPF 9

RESULT 17
US-08-463-483A-11
; Sequence 11, Application US/08463483A
; Patent No. 5849870
; GENERAL INFORMATION:
; APPLICANT: Warren, Gregory W
; APPLICANT: Koziel, Michael G
; APPLICANT: Mullins, Martha A
; APPLICANT: Nye, Gordon J
; APPLICANT: Carr, Brian
; APPLICANT: Desai, Nalini M
; APPLICANT: Kostichka, N. Kristy
; APPLICANT: Duck, Nicholas B
; APPLICANT: Estruch, Juan J
; TITLE OF INVENTION: No. 5849870el Pesticidal Proteins and Strains
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,483A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,594

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; FILING DATE: 09-SEP-1994
; APPLICATION NUMBER: US 08/218,018
; PRIOR APPLICATION DATA:
; FILING DATE: 23-MAR-1994
; APPLICATION NUMBER: US 08/037,057
; FILING DATE: 25-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murry
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: CGC 1695/CIP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8615
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORGANISM: Bacillus thuringiensis
; ORIGINAL SOURCE:
; US-08-463-483A-11

Query Match 22.2%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred.No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEPF 14
DB 6 VEPF 9

RESULT 18
US-08-471-046A-11
; Sequence 11, Application US/08471046A
; Patent No. 5866326
; GENERAL INFORMATION:
; APPLICANT: Warren, Gregory W
; APPLICANT: Kozziel, Michael G
; APPLICANT: Mullins, Martha A
; APPLICANT: Nye, Gordon J
; APPLICANT: Carr, Brian
; APPLICANT: Desai, Nalini M
; APPLICANT: Kostichka, N. Kristy
; APPLICANT: Estruch, Juan J
; APPLICANT: Duck, Nicholas B
; TITLE OF INVENTION: Method For Isolating Vegetative Insecticidal
; PROTEIN GENES
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5866326artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,046A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/463,483
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,594
; FILING DATE: 09-SEP-1994
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US 08/218,018
; FILING DATE: 23-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/037,057
; FILING DATE: 25-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC1695/CIP3/DIV8 - SQLv4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; US-08-471-046A-11

Query Match 22.2%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred.No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEPF 14
DB 6 VEPF 9

RESULT 19
US-08-470-566B-11
; Sequence 11, Application US/08470566B
; Patent No. 5872212
; GENERAL INFORMATION:
; APPLICANT: Warren, Gregory W
; APPLICANT: Kozziel, Michael G
; APPLICANT: Mullins, Martha A
; APPLICANT: Nye, Gordon J
; APPLICANT: Carr, Brian
; APPLICANT: Desai, Nalini M
; APPLICANT: Kostichka, N. Kristy
; APPLICANT: Duck, Nicholas B
; APPLICANT: Estruch, Juan J
; APPLICANT: Estruch, Juan J
; TITLE OF INVENTION: No. 5872212el Pesticidal Proteins and Strains
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5872212artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,566B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/463,483
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,594
; FILING DATE: 09-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/218,018
; FILING DATE: 23-MAR-1994
; PRIOR APPLICATION DATA:
```

```
; APPLICATION NUMBER: US 08/037,057
; FILING DATE: 25-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC1695/CIP3/DIV4 - SQLV4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORGANISM: Bacillus thuringiensis
; US-08-470-566B-11
Query Match 22.2%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEPF 14
Db 6 VEPF 9

RESULT 20
US-08-838-219B-11
; Sequence 11, Application US/08838219B
; Patent No. 5877012
; GENERAL INFORMATION:
; APPLICANT: Warren, Gregory W
; APPLICANT: Koziel, Michael G
; APPLICANT: Mullins, Martha A
; APPLICANT: Nye, Gordon J
; APPLICANT: Carr, Brian
; APPLICANT: Desai, Nalini M
; APPLICANT: Kostichka, N. Kristy
; APPLICANT: Duck, Nicholas B
; APPLICANT: Estruch, Juan J
; TITLE OF INVENTION: A No. 5877012el Class of Proteins for the
; TITLE OF INVENTION: Control of Plant Pests
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/838,219B
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/463,483
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,594
; FILING DATE: 09-SEP-1994
; APPLICATION NUMBER: US 08/218,018
; FILING DATE: 23-MAR-1994
; APPLICATION NUMBER: US 08/037,057
; FILING DATE: 25-MAR-1993

; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: CGC 1695/CIP3
```

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; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40,403
; REFERENCE/DOCKET NUMBER: CGC 1925
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8582
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORGANISM: Bacillus thuringiensis
; US-08-838-219B-11
Query Match 22.2%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEPF 14
Db 6 VEPF 9

RESULT 21
US-08-469-334-11
; Sequence 11, Application US/08469334
; Patent No. 5990383
; GENERAL INFORMATION:
; APPLICANT: Warren, Gregory W
; APPLICANT: Koziel, Michael G
; APPLICANT: Mullins, Martha A
; APPLICANT: Nye, Gordon J
; APPLICANT: Carr, Brian
; APPLICANT: Desai, Nalini M
; APPLICANT: Kostichka, N. Kristy
; APPLICANT: Duck, Nicholas B
; APPLICANT: Estruch, Juan J
; TITLE OF INVENTION: No. 5990383el Pesticidal Proteins and Strains
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/469,334
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/463,483
; FILING DATE:
; APPLICATION NUMBER: US 08/314,594
; FILING DATE: 09-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/218,018
; FILING DATE: 23-MAR-1994
; APPLICATION NUMBER: US 08/037,057
; FILING DATE: 25-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: CGC 1695/CIP3
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; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-541-8615  
; TELEFAX: 919-541-8689  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; ORIGINAL SOURCE:  
; ORGANISM: Bacillus thuringiensis  
US-08-469-334-11

Query Match 22.2%; Score 4; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEPF 14  
Db 6 VEPF 9

## RESULT 22

US-09-300-529-11  
; Sequence 11, Application US/09300529

; Patent No. 6066783  
; GENERAL INFORMATION:  
; APPLICANT: Warren, Gregory W  
; APPLICANT: Koziel, Michael G  
; APPLICANT: Mullins, Martha A  
; APPLICANT: Nye, Gordon J  
; APPLICANT: Carr, Brian  
; APPLICANT: Desai, Nalini M  
; APPLICANT: Kostichka, N. Kristy  
; APPLICANT: Duck, Nicholas B  
; APPLICANT: Estruch, Juan J  
; TITLE OF INVENTION: Genes Encoding Insecticidal Proteins  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 6066783artis Corporation  
; STREET: 3054 Cornwallis Road  
; CITY: Research Triangle Park  
; STATE: NC  
; COUNTRY: USA  
; ZIP: 27709

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30B  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/300,529  
; FILING DATE: TBA

; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/469,334  
; FILING DATE: 06-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/463,483  
; FILING DATE: 05-JUN-1995

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/314,594  
; FILING DATE: 09-SEP-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/218,018  
; FILING DATE: 23-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/037,057  
; FILING DATE: 25-MAR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meigs, J. Timothy  
; REGISTRATION NUMBER: 38,241  
; REFERENCE/DOCKET NUMBER: S-19506L

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-541-8587  
; TELEFAX: 919-541-8689  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; ORIGINAL SOURCE:  
; ORGANISM: Bacillus thuringiensis  
US-09-300-529-11

Query Match 22.2%; Score 4; DB 3; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEPF 14  
Db 6 VEPF 9

## RESULT 23

US-09-233-336A-11  
; Sequence 11, Application US/09233336A

; Patent No. 6107279  
; GENERAL INFORMATION:  
; APPLICANT: Warren, Gregory W  
; APPLICANT: Koziel, Michael G  
; APPLICANT: Mullins, Martha A  
; APPLICANT: Nye, Gordon J  
; APPLICANT: Carr, Brian  
; APPLICANT: Desai, Nalini M  
; APPLICANT: Kostichka, N. Kristy  
; APPLICANT: Duck, Nicholas B  
; APPLICANT: Estruch, Juan J  
; TITLE OF INVENTION: A No. 6107279el Class of Proteins for the  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CIBA-GEIGY Corporation  
; STREET: 7 Skyline Drive  
; CITY: Hawthorne  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10532

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30B  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/233,336A  
; FILING DATE:

; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/838,219  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/314,594  
; FILING DATE: 09-SEP-1994

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/218,018  
; FILING DATE: 23-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/037,057  
; FILING DATE: 25-MAR-1993

; ATTORNEY/AGENT INFORMATION:  
; NAME: Pace, Gary M.  
; REGISTRATION NUMBER: 40,403  
; REFERENCE/DOCKET NUMBER: CGC 1925  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-541-8582

; TELEFAX: 919-541-8689  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; ORIGINAL SOURCE:  
; ORGANISM: Bacillus thuringiensis  
; US-09-233-336A-11

Query Match 22.2%; Score 4; DB 3; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 11 VEPF 14  
Db 6 VEPF 9

RESULT 24  
US-09-233-752A-11  
; Sequence 11, Application US/09233752A  
; Patent No. 6137033  
; GENERAL INFORMATION:  
; APPLICANT: Warren, Gregory W  
; APPLICANT: Koziel, Michael G  
; APPLICANT: Mullins, Martha A  
; APPLICANT: Nye, Gordon J  
; APPLICANT: Carr, Brian  
; APPLICANT: Desai, Nalini M  
; APPLICANT: Kostichka, N. Kristy  
; APPLICANT: Duck, Nicholas B  
; APPLICANT: Estruch, Juan J  
; TITLE OF INVENTION: A No. 6137033el Class of Proteins for the  
; TITLE OF INVENTION: Control of Plant Pests  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CIBA-GEIGY Corporation  
; STREET: 7 Skyline Drive  
; CITY: Hawthorne  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10532  
; COMPUTER READABLE FORM: disk  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30B  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/233,752A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/838,219  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/314,594  
; FILING DATE: 09-SEP-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/218,018  
; FILING DATE: 23-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/037,057  
; FILING DATE: 25-MAR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pace, Gary M.  
; REGISTRATION NUMBER: 40,403  
; REFERENCE/DOCKET NUMBER: CGC 1925  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-541-8582  
; TELEFAX: 919-541-8689

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; ORIGINAL SOURCE:  
; ORGANISM: Bacillus thuringiensis  
; US-09-233-752A-11

Query Match 22.2%; Score 4; DB 3; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 11 VEPF 14  
Db 6 VEPF 9

RESULT 25  
US-09-402-036-11  
; Sequence 11, Application US/09402036  
; Patent No. 6291156  
; GENERAL INFORMATION:  
; APPLICANT: Estruch, Juan J.  
; APPLICANT: Yu, Cao-Guo  
; APPLICANT: Warren, Gregory W.  
; APPLICANT: Desai, Nalini  
; APPLICANT: Koziel, Michael  
; APPLICANT: Nye, Gordon  
; TITLE OF INVENTION: Plant Pest Control  
; FILE REFERENCE: S-21284C  
; CURRENT APPLICATION NUMBER: US/09/402,036  
; PRIOR FILING DATE: 2000-02-08  
; PRIOR APPLICATION NUMBER: PCT/EP98/01952  
; PRIOR FILING DATE: 1998-04-02  
; PRIOR APPLICATION NUMBER: 08/838,219  
; PRIOR FILING DATE: 1997-04-03  
; PRIOR APPLICATION NUMBER: 08/832,263  
; PRIOR FILING DATE: 1997-04-03  
; PRIOR APPLICATION NUMBER: 08/832,265  
; PRIOR FILING DATE: 1997-04-03  
; PRIOR APPLICATION NUMBER: 08/463,483  
; PRIOR FILING DATE: 1995-06-05  
; PRIOR APPLICATION NUMBER: 08/314,594  
; PRIOR FILING DATE: 1994-09-09  
; PRIOR APPLICATION NUMBER: 08/218,018  
; PRIOR FILING DATE: 1994-03-24  
; PRIOR APPLICATION NUMBER: 08/037,057  
; PRIOR FILING DATE: 1993-03-25  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (1)..(13)  
; OTHER INFORMATION: Xaa represents any amino acid  
; US-09-402-036-11

Query Match 22.2%; Score 4; DB 3; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 11 VEPF 14  
Db 6 VEPF 9

RESULT 26  
US-09-904-226-11  
; Sequence 11, Application US/09904226

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; Patent No. 6429360
; GENERAL INFORMATION:
; APPLICANT: Estruch, Juan J.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Desai, Nalini
; APPLICANT: Koziel, Michael
; APPLICANT: Nye, Gordon
; TITLE OF INVENTION: Plant Pest Control
; FILE REFERENCE: S-21284D
; CURRENT APPLICATION NUMBER: US/09/904,226
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/EP98/01952
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: 08/838,219
; PRIOR FILING DATE: 1997-04-03
; PRIOR APPLICATION NUMBER: 08/832,263
; PRIOR FILING DATE: 1997-04-03
; PRIOR APPLICATION NUMBER: 08/832,265
; PRIOR FILING DATE: 1997-04-03
; PRIOR APPLICATION NUMBER: 08/463,483
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: 08/314,594
; PRIOR FILING DATE: 1994-09-09
; PRIOR APPLICATION NUMBER: 08/218,018
; PRIOR FILING DATE: 1994-03-24
; PRIOR APPLICATION NUMBER: 08/037,057
; PRIOR FILING DATE: 1993-03-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
; FEATURE: <221> SITE<222> (1)..(13)<223> Xaa represents any amino acid
US-09-904-226-11

Query Match      22.2%; Score 4; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 VEPF 14
DB      6 VEPF 9

RESULT 27
5171684-21
; Patent No. 5171684
; APPLICANT: YEN, KWANG-MU;BLATT, LAWRENCE M.;KARL, MICHAEL R.
; TITLE OF INVENTION: BIOCONVERSIONS CATALYZED BY THE TOULUENE
; MONOOXYGENASE OF PSEUDOMONAS MENDOCINA KR-1
; NUMBER OF SEQUENCES: 41
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/590,374
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 177,631
; FILING DATE: 05-APR-1988
; SEQ ID NO:21:
; LENGTH: 14
5171684-21

Query Match      22.2%; Score 4; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 YPEF 12
DB      9 YPEF 12

RESULT 28
US-08-080-073-25
; Sequence 25, Application US/08080073
; Patent No. 5384255
; GENERAL INFORMATION:
; APPLICANT: Ciechanover, Aaron J.
; APPLICANT: Blumenfeld, Nava
; APPLICANT: Gonen, Hedva
; TITLE OF INVENTION: Ubiquitin Carrier Enzyme E2-F1.
; TITLE OF INVENTION: Purification, Production, and Use
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/080,073
; FILING DATE: 21-JUN-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 1448.0050000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-080-073-25

Query Match      22.2%; Score 4; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PKYP 10
DB      7 PKYP 10

RESULT 29
US-08-967-101-168
; Sequence 168, Application US/08967101
; Patent No. 5840540
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; APPLICANT: ROMMENS, JOHANNA M
; APPLICANT: FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 183
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: High Street Tower - 125 High Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/967,101

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; FILING DATE: 10-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/592,541
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 168:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-967-101-168

Query Match      22.2%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 PFTE 16
Db      9 PFTE 12

RESULT 30
US-08-687-956A-7
; Sequence 7, Application US/08687956A
; Patent No. 5861157
; GENERAL INFORMATION:
; APPLICANT: BURNIE, JAMES P
; APPLICANT: MATTHEWS, RUTH C
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: INFECTIONS DUE TO STREPTOCOCCI AND ENTEROCOCCI
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO, LLP
; STREET: 1100 NEW YORK AVENUE, N.W., EAST TOWER, 9TH
; STREET: FLOOR
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,956A
; FILING DATE: 29-JUL-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9401689.6
; FILING DATE: 28-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 50885/222892
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/861-3000
; TELEFAX: 202/822-0944
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus sobrinus
; STRAIN: Streptococcus sobrinus MUCOB 263
US-08-687-956A-8

Query Match      22.2%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 PVEP 13
Db      11 PVEP 14

RESULT 31
US-08-687-956A-8
; Sequence 8, Application US/08687956A
; Patent No. 5861157
; GENERAL INFORMATION:
; APPLICANT: BURNIE, JAMES P
; APPLICANT: MATTHEWS, RUTH C
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: INFECTIONS DUE TO STREPTOCOCCI AND ENTEROCOCCI
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO, LLP
; STREET: 1100 NEW YORK AVENUE, N.W., EAST TOWER, 9TH
; STREET: FLOOR
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,956A
; FILING DATE: 29-JUL-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9401689.6
; FILING DATE: 28-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 50885/222892
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/861-3000
; TELEFAX: 202/822-0944
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus sobrinus
; STRAIN: Streptococcus sobrinus MUCOB 263
US-08-687-956A-8

Query Match      22.2%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 PVEP 13
Db      11 PVEP 14
```

```

RESULT 32
US-08-592-541-168
; Sequence 168, Application US/08592541
; Patent No. 5986054
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; APPLICANT: ROMMENS, JOHANNA M
; APPLICANT: FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 183
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: High Street Tower - 125 High Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 168:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-592-541-168

Query Match 22.2%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred.No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PFTE 16
DB 9 PFTE 12

RESULT 33
US-08-591-629-5
; Sequence 5, Application US/08591629
; Patent No. 5993808
; GENERAL INFORMATION:
; APPLICANT: MELCHERS, Leo Sjoerd
; APPLICANT: APOTHEKER-DE GROOT, Marion
; APPLICANT: BOL, John Ferdinand
; APPLICANT: CORNELISSEN, Bernardus Johannes Clemens
; APPLICANT: LINTHORST, Hubertus Josephus Maria
; APPLICANT: PONSTEIN, Anne Silene
; APPLICANT: SELA-BUURLAGE, Marianne Beatrix
; TITLE OF INVENTION: plant chitinases, DNA coding therefor and
; TITLE OF INVENTION: plants containing same
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ladas & Parry
; STREET: 26 West 61st Street
; CITY: New York
; STATE: NY
; COUNTRY: USA

```

```

; ZIP: 10023-7604
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
; COMPUTER: IEM PC 4.86 SX 50 Mhz
; OPERATING SYSTEM: DOS 6.20
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,629
; FILING DATE: 15-FEB-96
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP94/02761
; FILING DATE: 17-AUG-94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93202425.0
; FILING DATE: 17-AUG-93
; ATTORNEY/AGENT INFORMATION:
; NAME: MASS. CLIFFORD J.
; REGISTRATION NUMBER: 30,086
; REFERENCE/DOCKET NUMBER: U-010627-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 708-1800
; TELEFAX: (212) 246-8959
; TELEX: 233288
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Nicotiana tabacum
; DEVELOPMENTAL STAGE: TMV-induced
; TISSUE TYPE: leaf
US-08-591-629-5

Query Match 22.2%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred.No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPVE 12
DB 4 YPVE 7

RESULT 34
US-09-124-698-168
; Sequence 168, Application US/09124698
; Patent No. 6117978
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; APPLICANT: ROMMENS, JOHANNA M
; APPLICANT: FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 183
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: High Street Tower - 125 High Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/124,698
; FILING DATE:

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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/592,541
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 168:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-124-698-168

Query Match 22.2%; Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PFTE 16
Db 9 PFTE 12

RESULT 35
US-09-127-480-168
; Sequence 168, Application US/09127480
; Patent No. 6194153
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; APPLICANT: ROMMENS, JOHANNA M
; APPLICANT: FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TO ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 183
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/127,480
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,541
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 168:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-127-480-168

Query Match 22.2%; Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PFTE 16
Db 9 PFTE 12

RESULT 36
US-08-496-841C-165
; Sequence 165, Application US/08496841C
; Patent No. 6210919
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; APPLICANT: ROMMENS, JOHANNA M
; APPLICANT: FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TO ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 175
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby, PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/496,841C
; FILING DATE: 28-Jun-1995
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul F. Fehlner, Ph.D.
; REGISTRATION NUMBER: 35,135
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 527-7700
; TELEFAX: (212) 753-6237
; INFORMATION FOR SEQ ID NO: 165:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 165:
US-08-496-841C-165

Query Match 22.2%; Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PFTE 16
Db 9 PFTE 12

RESULT 37
US-09-124-523-168
; Sequence 168, Application US/09124523
; Patent No. 6395960
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; APPLICANT: ROMMENS, JOHANNA M
; APPLICANT: FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TO ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 183
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: High Street Tower - 125 High Street
; US-09-124-523-168
```

```
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/124,523
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,541
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 168:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; MOLECULE TYPE: peptide
US-09-124-523-168

Query Match 22.2%; Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PFTE 16
Db 9 PFTE 12

RESULT 38
US-09-636-796A-168
; Sequence 168, Application US/09636796A
; Patent No. 6485911
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; ROMMENS, JOHANNA M
; FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TO ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 183
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: High Street Tower - 125 High Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/636,796A
; FILING DATE: 11-Aug-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,541
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000

; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/124,523
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,541
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000

; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 168:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; MOLECULE TYPE: peptide
US-09-636-796A-168

Query Match 22.2%; Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PFTE 16
Db 9 PFTE 12

RESULT 39
US-09-641-803-8
; Sequence 8, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDODGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-8

Query Match 22.2%; Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PFPK 8
Db 3 PFPK 6

RESULT 40
US-08-602-999A-181
; Sequence 181, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
```

;; CITY: New York  
;; STATE: New York  
;; COUNTRY: U.S.A.  
;; ZIP: 10036-2711  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/602,999A  
;; FILING DATE: 16-FEB-1996  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Mistrock, S. Leslie  
;; REGISTRATION NUMBER: 18,872  
;; REFERENCE/DOCKET NUMBER: 1101-202  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212) 790-9090  
;; TELEFAX: (212) 869-9741/8864  
;; TELEX: 66141 PENNIE  
;; INFORMATION FOR SEQ ID NO: 181:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 16 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: peptide  
;; US-08-602-999A-181

Query Match 22.2%; Score 4; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 5 PFPK 8  
Db 5 PFPK 8

RESULT 41  
US-09-500-124-181  
; Sequence 181, Application US/09500124  
; Patent No. 6432920  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/500,124  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:

;; NAME: Mistrock, S. Leslie  
;; REGISTRATION NUMBER: 18,872  
;; REFERENCE/DOCKET NUMBER: 1101-202  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212) 790-9090  
;; TELEFAX: (212) 869-9741/8864  
;; TELEX: 66141 PENNIE  
;; INFORMATION FOR SEQ ID NO: 181:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 16 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: peptide  
;; US-09-500-124-181

Query Match 22.2%; Score 4; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 5 PFPK 8  
Db 5 PFPK 8

RESULT 42  
US-08-602-999A-362  
; Sequence 362, Application US/08602999A  
; Patent No. 6184205  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999A  
; FILING DATE: 16-FEB-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 362:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; US-08-602-999A-362

Query Match 22.2%; Score 4; DB 3; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;



Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PVEP 13  
||||  
Db 10 PVEP 13

## RESULT 43

US-09-500-124-362  
; Sequence 362, Application US/09500124  
; Patent No. 6432920  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/500,124  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mierock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 869-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 362:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-09-500-124-362

Query Match 22.2%; Score 4; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PVEP 13  
||||  
Db 10 PVEP 13

## RESULT 44

US-08-105-454-4  
; Sequence 4, Application US/08105454  
; Patent No. 6071715  
; GENERAL INFORMATION:  
; APPLICANT: Qian, Yue-Wei  
; APPLICANT: Lee, Eva Y.-H. P.

; TITLE OF INVENTION: No. 6071715el Proteins Which Bind to  
; TITLE OF INVENTION: Retinoblastoma Proteins and Their  
; TITLE OF INVENTION: Encoding DNA Sequences  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: 2300 One American Center  
; CITY: Austin  
; STATE: TX  
; COUNTRY: USA  
; ZIP: 78701  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/105,454  
; FILING DATE: Concurrently herewith  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kitchell, Barbara  
; REGISTRATION NUMBER: 33,928  
; REFERENCE/DOCKET NUMBER: UTSK:196/KIT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 512-320-7200  
; TELEFAX: 512-474-7577  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-105-454-4

Query Match 22.2%; Score 4; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KEMP 5  
||||  
Db 7 KEMP 10

## RESULT 45

US-09-407-687-8  
; Sequence 8, Application US/09407687  
; Patent No. 6548634  
; GENERAL INFORMATION:  
; APPLICANT: Ballinger, Marcus  
; APPLICANT: Kavanaugh, Michael  
; TITLE OF INVENTION: Synthetic Peptides Having FGF Receptor  
; TITLE OF INVENTION: Affinity  
; FILE REFERENCE: 1517.001  
; CURRENT APPLICATION NUMBER: US/09/407,687  
; CURRENT FILING DATE: 1999-09-28  
; EARLIER APPLICATION NUMBER: 60/102,667  
; EARLIER FILING DATE: 1998-09-30  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 8  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide  
US-09-407-687-8

Query Match 22.2%; Score 4; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	4	MPP	7
Db	2	MPP	5

```

RESULT 46
US-09-227-357-664
; Sequence 664, Application US/09227357
; Patent No. 6342581
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: P2010P1
; CURRENT APPLICATION NUMBER: US/09/227,357
; CURRENT FILING DATE: 1999-01-08
; EARLIER APPLICATION NUMBER: PCT/US98/13684
; EARLIER FILING DATE: 1998-07-07
; EARLIER APPLICATION NUMBER: 60/051,926
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,793
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,925
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,929
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,803
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,732
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,931
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,932
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,916
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,930
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,918
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,920
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,733
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,795
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,919
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,928
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/055,722
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,723
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,948
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,949
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,953
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,950
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,947
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,964
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,360
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,684
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,984
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,954
; EARLIER FILING DATE: 1997-08-18

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; EARLIER APPLICATION NUMBER: 60/058,785
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,664
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,660
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,661
; EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 664
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-227-357-664

Query Match
Best Local Similarity 22.2%; Score 4; DB 4; Length 20;
Matches 4; Conservative 0; Mismatches 0; Indels 0

Qy 5 PPKK 8
Db 16 PPKK 19

RESULT 47
US-09-556-877-236
; Sequence 236, Application US/09556877
; Patent No. 6432916
; GENERAL INFORMATION:
; APPLICANT: Probst, Peter
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir
; APPLICANT: Fling, Steve
; APPLICANT: Maisonneuve, Jeff
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C5
; CURRENT APPLICATION NUMBER: US/09/556,877
; CURRENT FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 236
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-556-877-236

Query Match
Best Local Similarity 22.2%; Score 4; DB 4; Length 20;
Matches 4; Conservative 0; Mismatches 0; Indels 0

Qy 9 YPVE 12
Db 17 YPVE 20

RESULT 48
US-09-556-877-237
; Sequence 237, Application US/09556877
; Patent No. 6432916
; GENERAL INFORMATION:
; APPLICANT: Probst, Peter
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir
; APPLICANT: Fling, Steve
; APPLICANT: Maisonneuve, Jeff
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C5
; CURRENT APPLICATION NUMBER: US/09/556,877

```

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; CURRENT FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 237
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-556-877-237

Query Match      22.2%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 YPVE 12
      ||||
Db      12 YPVE 15

RESULT 49
US-09-556-877-238
; Sequence 238, Application US/09556877
; Patent No. 6432916
; GENERAL INFORMATION:
; APPLICANT: Probet, Peter
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir
; APPLICANT: Fling, Steve
; APPLICANT: Maisonneuve, Jeff
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C5
; CURRENT FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 238
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-556-877-238

Query Match      22.2%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 YPVE 12
      ||||
Db      7 YPVE 10

RESULT 50
US-09-556-877-239
; Sequence 239, Application US/09556877
; Patent No. 6432916
; GENERAL INFORMATION:
; APPLICANT: Probet, Peter
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir
; APPLICANT: Fling, Steve
; APPLICANT: Maisonneuve, Jeff
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C5
; CURRENT APPLICATION NUMBER: US/09/556,877
; CURRENT FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 239
; LENGTH: 20

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-556-877-239

Query Match      22.2%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 YPVE 12
      ||||
Db      12 YPVE 15

RESULT 51
US-09-620-412C-236
; Sequence 236, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 236
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-620-412C-236

Query Match      22.2%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 YPVE 12
      ||||
Db      17 YPVE 20

RESULT 52
US-09-620-412C-237
; Sequence 237, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 237
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-620-412C-237

Query Match      22.2%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 YPVE 12
      ||||
Db      12 YPVE 15
```

```
RESULT 53
US-09-620-412C-238
; Sequence 238, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 238
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-620-412C-238

Query Match      22.2%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      9 YPVE 12
        |||||
Db      7 YPVE 10

RESULT 54
US-09-620-412C-239
; Sequence 239, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 239
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-620-412C-239

Query Match      22.2%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      9 YPVE 12
        |||||
Db      2 YPVE 5

RESULT 55
US-09-598-419-236
; Sequence 236, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598,419
```

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; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 236
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-598-419-236

Query Match      22.2%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      9 YPVE 12
        |||||
Db      17 YPVE 20

RESULT 56
US-09-598-419-237
; Sequence 237, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 237
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-598-419-237

Query Match      22.2%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      9 YPVE 12
        |||||
Db      12 YPVE 15

RESULT 57
US-09-598-419-238
; Sequence 238, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 238
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-598-419-238
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Query Match 22.2%; Score 4; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPVE 12  
|||  
Db 7 YPVE 10

RESULT 58  
US-09-598-419-239  
; Sequence 239, Application US/09598419  
; Patent No. 6565856  
; GENERAL INFORMATION:  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Scholler, John  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND  
; FILE REFERENCE: 210121.46906  
; CURRENT APPLICATION NUMBER: US/09/598,419  
; CURRENT FILING DATE: 2000-06-20  
; NUMBER OF SEQ ID NOS: 357  
; SOFTWARE: FastSeq for Windows Version 3.0/4.0  
; SEQ ID NO 239  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Made in a lab  
US-09-598-419-239

Query Match 22.2%; Score 4; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 YPVE 12  
|||  
Db 2 YPVE 5

RESULT 59  
US-08-224-868-5  
; Sequence 5, Application US/08224868  
; Patent No. 569844B  
; GENERAL INFORMATION:  
; APPLICANT: Soldin, Steven J.  
; TITLE OF INVENTION: IMMUNOSUPPRESSIVE DRUG BINDING PROTEINS  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/224,868  
; FILING DATE: 08-APR-1995  
; CLASSIFICATION: 436  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/200,404  
; FILING DATE: 23-FEB-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/782,761  
; FILING DATE: 22-OCT-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/487,115

; FILING DATE: 02-MAR-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/279,176  
; FILING DATE: 02-DEC-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/841,792  
; FILING DATE: 26-FEB-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/521,074  
; FILING DATE: 09-MAY-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bett, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 64688/125/CHRE  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-224-868-5  
Query Match 16.7%; Score 3; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EPF 14  
|||  
Db 2 EPF 4

RESULT 60  
US-08-747-137-163  
; Sequence 163, Application US/08747137  
; Patent No. 5945033  
; GENERAL INFORMATION:  
; APPLICANT: Yen, Richard C.K.  
; TITLE OF INVENTION: NON-CROSSLINKED PROTEIN PARTICLES FOR  
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC USE  
; NUMBER OF SEQUENCES: 184  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/747,137  
; FILING DATE: 12-NOV-1996  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/212,546  
; FILING DATE: 14-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/069,831  
; FILING DATE: 01-JUN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/959,560  
; FILING DATE: 13-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/641,720  
; FILING DATE: 15-JAN-1991

ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 016197-000840US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-576-0200  
; INFORMATION FOR SEQ ID NO: 163:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: not relevant  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 4  
; OTHER INFORMATION: /product= "Pro-Amide"  
US-08-747-137-163

Query Match 16.7%; Score 3; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 YPV 11  
Db 1 YPV 3

## RESULT 61

US-08-415-655-3  
; Sequence 3, Application US/08415655  
; Patent No. 6025480  
; GENERAL INFORMATION:  
; APPLICANT: Massague, Joan  
; APPLICANT: Lee, Mong-hong  
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING  
; TITLE OF INVENTION: p75KIP2, A CYCLIN-DEPENDENT KINASE INHIBITOR AND USES OF  
; TITLE OF INVENTION: SAME  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/415,655  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 1747/47418  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0525  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-415-655-3

Query Match 16.7%; Score 3; DB 3; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 10 PVE 12  
Db 2 PVE 4  
RESULT 62  
US-09-330-970-19  
; Sequence 19, Application US/09330970  
; Patent No. 6146876  
; GENERAL INFORMATION:  
; APPLICANT: Robison, Keith E.  
; APPLICANT: Kapeller-libermann, Rosana  
; APPLICANT: White, David  
; TITLE OF INVENTION: A No. 6146876el Human Cyclic Nucleotide  
; TITLE OF INVENTION: Phosphodiesterase  
; FILE REFERENCE: 5800-28  
; CURRENT APPLICATION NUMBER: US/09/330,970  
; EARLIER FILING DATE: 1999-06-11  
; EARLIER APPLICATION NUMBER: 09/277,423  
; EARLIER FILING DATE: 1999-03-26  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 19  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-330-970-19

Query Match 16.7%; Score 3; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TES 17  
Db 1 TES 3

## RESULT 63

US-09-357-952-27  
; Sequence 27, Application US/09357952  
; Patent No. 6248904  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Han-Zhong  
; APPLICANT: Cai, Sui Xiong  
; APPLICANT: Drewe, John A.  
; APPLICANT: Yang, Wu  
; TITLE OF INVENTION: No. 6248904el Fluorescence Dyes and Their Applications for Who  
; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Protea  
; TITLE OF INVENTION: Other Enzymes and the Use Thereof  
; FILE REFERENCE: 1735.0030001  
; CURRENT APPLICATION NUMBER: US/09/357,952  
; CURRENT FILING DATE: 1999-07-21  
; EARLIER APPLICATION NUMBER: US 60/093,642  
; EARLIER FILING DATE: 21-JUL-1998  
; NUMBER OF SEQ ID NOS: 139  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 27  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic  
; OTHER INFORMATION: Peptide  
US-09-357-952-27

Query Match 16.7%; Score 3; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VEP 13

Db 1 VEP 3

RESULT 64

US-09-411-531A-1

; Sequence 1, Application US/09411531A

; Patent No. 6251391

; GENERAL INFORMATION:

; APPLICANT: Wilkinson, Randall

; Houston, Devin

; TITLE OF INVENTION: Compositions and methods relating to the

; inhibition of casomorphin and glutuomorphin

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Graybeal Jackson Haley

; STREET: 777-108th Ave. NE, Suite 2460

; CITY: Bellevue

; STATE: Washington

; COUNTRY: USA

; ZIP: 98004-5117

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Windows 98

; SOFTWARE: Microsoft Word 97

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/411,531A

; FILING DATE: 01-Oct-1999

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: King, Joshua

; REGISTRATION NUMBER: 35,570

; REFERENCE/DOCKET NUMBER: 1776-2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (425) 455-5575

; TELEFAX: (425) 455-1046

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 4 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; FRAGMENT TYPE: N-terminal

; SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-411-531A-1

Query Match 16.7%; Score 3; DB 3; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PFP 7

Db 2 PFP 4

RESULT 65

US-09-521-650-27

; Sequence 27, Application US/09521650

; Patent No. 6335429

; GENERAL INFORMATION:

; APPLICANT: Weber, Eckard

; APPLICANT: Cai, Sui Xiong

; APPLICANT: Keana, John F.W.

; APPLICANT: Drewe, John A.

; APPLICANT: Zhang, Han-Zhong

; TITLE OF INVENTION: No. 6335429el Fluorogenic or Fluorescent Reporter Molecules and

; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence

; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the

; TITLE OF INVENTION: Use Thereof

; FILE REFERENCE: 1735.0290002

Query Match 16.7%; Score 3; DB 3; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PFP 7

Db 2 PFP 4

us-09-641-801-22.oligo.ra1

Query Match 16.7%; Score 3; DB 4; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEP 13

Db 1 VEP 3

RESULT 66

US-09-168-888-27

; Sequence 27, Application US/09168888

; Patent No. 6342611

; GENERAL INFORMATION:

; APPLICANT: Weber, Eckard

; APPLICANT: Cai, Sui Xiong

; APPLICANT: Keana, John F.W.

; APPLICANT: Drewe, John A.

; APPLICANT: Zhang, Han-Zhong

; TITLE OF INVENTION: No. 6342611el Fluorogenic or Fluorescent Reporter Molecules a:

; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence

; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the

; TITLE OF INVENTION: Use Thereof

; FILE REFERENCE: 1735.0290002

Query Match 16.7%; Score 3; DB 4; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEP 13

Db 1 VEP 3

RESULT 67

US-09-187-859-199

; Sequence 199, Application US/09187859A

; Patent No. 6358920

```
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 199
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative linear modulating agent based on
; OTHER INFORMATION: cadherin-7 cell adhesion recognition sequence
US-09-187-859-199

Query Match          16.7%; Score 3; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      11 VEP 13
      |||
Db      1 VEP 3

RESULT 68
US-09-411-605A-1
; Sequence 1, Application US/09411605A
; Patent No. 644772
; GENERAL INFORMATION:
; APPLICANT: Houston, Devin
; TITLE OF INVENTION: Compositions And Methods Relating To Reduction Of Symptoms Of Au
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/411,605A
; CURRENT FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-411-605A-1

Query Match          16.7%; Score 3; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 PFP 7
      |||
Db      2 PFP 4

RESULT 69
US-09-839-542B-199
; Sequence 199, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 199
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: Representative linear modulating agent based on
; OTHER INFORMATION: cadherin-7 cell adhesion recognition sequence
US-09-839-542B-199

Query Match          16.7%; Score 3; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      11 VEP 13
      |||
Db      1 VEP 3

RESULT 70
5215966-12
; Patent No. 5215966
; APPLICANT: HOLZMANN, GUNTER; RADDATZ, PETER; SCHMITGES,
; CLAUD J.; MINCK, KLAUS OTTO; JONCZYK, ALFRED; SOMBROEK,
; JOHANNES; GANTE, JOACHIM
; TITLE OF INVENTION: PEPTIDE AND RENIN INHIBITORS
; NUMBER OF SEQUENCES: 22
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/126,060
; FILING DATE: 27-NOV-1987
; SEQ ID NO:12
; LENGTH: 4
5215966-12

Query Match          16.7%; Score 3; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 PFP 7
      |||
Db      2 PFP 4

RESULT 71
5215966-14
; Patent No. 5215966
; APPLICANT: HOLZMANN, GUNTER; RADDATZ, PETER; SCHMITGES,
; CLAUD J.; MINCK, KLAUS OTTO; JONCZYK, ALFRED; SOMBROEK,
; JOHANNES; GANTE, JOACHIM
; TITLE OF INVENTION: PEPTIDE AND RENIN INHIBITORS
; NUMBER OF SEQUENCES: 22
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/126,060
; FILING DATE: 27-NOV-1987
; SEQ ID NO:14
; LENGTH: 4
5215966-14

Query Match          16.7%; Score 3; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      13 PFT 15
      |||
Db      2 PFT 4

RESULT 72
US-07-708-035-14
; Sequence 14, Application US/07708035
; Patent No. 5215964
; GENERAL INFORMATION:
; APPLICANT: Goldstein, Gideon
; APPLICANT: Audhya, Tapan
; APPLICANT: Heavner, George
; APPLICANT: Anwer, Mohamad K.
; TITLE OF INVENTION: Peptides Useful in Regulating The Immune
; and Nervous Systems
```



```

; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Howson and Howson
; STREET: 321 No. 5215964ristown Road, Box 457
; CITY: Spring House
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19477
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/708,035
; FILING DATE: 19910603
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: IRIP-US40
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 540-9206
; TELEFAX: (215) 540-5818
; TELEX: 910-250-6892
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= Acetyl
; OTHER INFORMATION: /note= "Acetyl is attached to the amino terminus
; OTHER INFORMATION: of the peptide."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 5
; OTHER INFORMATION: /label= NH2
; OTHER INFORMATION: /note= "NH2 is attached to the carboxy terminus of
; OTHER INFORMATION: the peptide."
;
US-07-708-035-14

Query Match 16.7%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EPF 14
Db 3 EPF 5

RESULT 73
US-07-657-769B-28
; Sequence 28, Application US/07657769B
; Patent No. 5256766
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; TITLE OF INVENTION: RECOMBINANT RECEPTOR AND RELATED
; TITLE OF INVENTION: PHARMACEUTICALS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSES: IRELL & MANELLA
; STREET: 545 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/657,769B
; FILING DATE: 19910219
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2000-0502.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-07-657-769B-67

Query Match 16.7%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EPF 14
Db 3 EPF 5

RESULT 74
US-07-657-769B-67
; Sequence 67, Application US/07657769B
; Patent No. 5256766
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; TITLE OF INVENTION: RECOMBINANT RECEPTOR AND RELATED
; TITLE OF INVENTION: PHARMACEUTICALS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSES: IRELL & MANELLA
; STREET: 545 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/657,769B
; FILING DATE: 19910219
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2000-0502.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-07-657-769B-67

Query Match 16.7%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEP 13
Db 1 VEP 3
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/657,769B
; FILING DATE: 19910219
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2000-0502.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-07-657-769B-28

Query Match 16.7%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEP 13
Db 1 VEP 3

RESULT 74
US-07-657-769B-67
; Sequence 67, Application US/07657769B
; Patent No. 5256766
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; TITLE OF INVENTION: RECOMBINANT RECEPTOR AND RELATED
; TITLE OF INVENTION: PHARMACEUTICALS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSES: IRELL & MANELLA
; STREET: 545 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/657,769B
; FILING DATE: 19910219
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2000-0502.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-07-657-769B-67

Query Match 16.7%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEP 13
Db 1 VEP 3
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:28:30 ; Search time 12.3488 Seconds  
(without alignments)  
140.178 Million cell updates/sec

Title: US-09-641-801-23

Perfect score: 18

Sequence: 1 SLTLTDVEKLHLPPLVQ 18

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

PIR\_76:\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	5	27.8	18	2	S04229	N4-(beta-N-acetylglucosaminyl) tetrameric protein
2	4	22.2	15	2	S66419	protein kinase (EC 2.7.1.37)
3	4	22.2	16	2	S20410	protein p12E - Pri
4	4	22.2	19	2	S66613	H4-transporting tw
5	4	22.2	20	1	S60633	tet leader peptide
6	4	22.2	20	2	LFBSIU	urinary tract ston
7	4	22.2	20	2	S23742	lysosomal protein
8	4	22.2	20	2	S56005	ig mu chain D regi
9	4	22.2	6	2	B33932	hypothetical prote
10	3	16.7	7	2	P00663	enamelin f - bovin
11	3	16.7	8	2	T14906	unspecific monooxy
12	3	16.7	8	2	S10783	apolipoprotein A-I
13	3	16.7	9	2	P00080	probable glucose-6
14	3	16.7	10	2	C39745	urease (EC 3.5.1.5
15	3	16.7	10	2	C26997	sphingomyelinase -
16	3	16.7	10	2	I36893	hematin (EC 3.4.-
17	3	16.7	10	2	S18396	neomycin suppressin
18	3	16.7	10	2	C35389	ig heavy chain C r
19	3	16.7	10	2	C39745	platelet activatin
20	3	16.7	10	2	A61007	Fc mu (IgM) recept
21	3	16.7	10	2	A56633	placental lactogen
22	3	16.7	10	2	C39111	carnitine medium/1
23	3	16.7	10	2	B45482	lysosome-associate
24	3	16.7	10	2	C39388	cytochrome-c oxida
25	3	16.7	10	2	A47364	
26	3	16.7	10	2	A61354	
27	3	16.7	10	2	PX0060	
28	3	16.7	10	2	T13838	
29	3	16.7	10	2	T14219	

30	3	16.7	10	2	C54226	light-harvesting p
31	3	16.7	10	2	PA0116	ferredoxin-NADP re
32	3	16.7	10	2	P50220	ferredoxin-NADP re
33	3	16.7	11	2	S42449	ant1 protein - pha
34	3	16.7	11	2	D58502	27K bile and gallb
35	3	16.7	11	2	I33098	173K exoantigen -
36	3	16.7	11	2	I52304	gene RSSR4 protei
37	3	16.7	11	2	T17081	cytochrome-c oxida
38	3	16.7	11	2	P00034	dextranucrase (EC
39	3	16.7	12	2	S29764	alpha-macroglobuli
40	3	16.7	12	2	S65136	kallikrein K2 - hu
41	3	16.7	12	2	P80663	dystrophin-associ
42	3	16.7	12	2	B60228	Fc mu (IgM) recept
43	3	16.7	12	4	JX0315	aminotransferase c
44	3	16.7	12	4	S49073	frame shifted cyta
45	3	16.7	13	2	P00491	self-incompatibili
46	3	16.7	13	2	A60856	inhibin alpha chai
47	3	16.7	13	2	S15755	actin 7 - soybean
48	3	16.7	13	2	JZVHP1	crabrolin - Europe
49	3	16.7	13	2	PN0125	serine proteinase
50	3	16.7	13	2	PC4055	hypothetical 13 pr
51	3	16.7	13	2	D56661	S-locus specific g
52	3	16.7	13	2	S09019	hemolytic protein
53	3	16.7	13	2	I84603	deoxynucleotidyltr
54	3	16.7	13	2	A61458	Ig kappa chain V-I
55	3	16.7	13	2	S57571	T-cell receptor al
56	3	16.7	13	2	PH0138	histamine-releasein
57	3	16.7	14	2	JN0390	ubiquitin - potato
58	3	16.7	14	2	S19803	translatoin initia
59	3	16.7	14	2	B29743	223K exoantigen -
60	3	16.7	14	2	C33098	hemocyanin chain 5
61	3	16.7	14	2	D61308	Ig heavy chain CRD
62	3	16.7	14	2	PT0259	T-cell receptor V-
63	3	16.7	14	2	S57572	dehydrin 4.5K poly
64	3	16.7	14	2	PC4382	unspecific monooxy
65	3	16.7	15	2	A26997	S-locus specific g
66	3	16.7	15	2	B56661	photosystem I 19.0
67	3	16.7	15	2	PQ0681	capsid protein VP1
68	3	16.7	15	2	PQ0545	hypothetical 1.5K
69	3	16.7	15	2	B39109	gentisate 1,2-diox
70	3	16.7	15	2	A35232	phosphoprotein, 80
71	3	16.7	15	2	S61284	protein disulfide-
72	3	16.7	15	2	S62620	protein QF200016 -
73	3	16.7	15	2	PA0051	protein QF200037 -
74	3	16.7	15	2	PA0060	protein QF200076 -
75	3	16.7	15	2	PA0106	ubiquitin - fungus
76	3	16.7	15	2	PA0063	gastrin-releasing
77	3	16.7	15	2	PS0221	T cell receptor al
78	3	16.7	15	2	PH1788	urinary tract ston
79	3	16.7	15	2	A56049	hypothetical TEL/M
80	3	16.7	15	4	I38336	gene c-fms protein
81	3	16.7	16	2	I57530	cytochrome P450-th
82	3	16.7	16	2	A61268	beta-glucosidase (
83	3	16.7	16	2	S29631	superoxide dismuta
84	3	16.7	16	2	E58503	photosystem I chai
85	3	16.7	16	2	T09741	photosystem I chai
86	3	16.7	16	2	G24687	T-cell receptor be
87	3	16.7	16	2	H49039	insulin-like growt
88	3	16.7	16	2	JH0517	hemoglobin beta-x
89	3	16.7	16	2	I46275	Ig H chain V-D-J r
90	3	16.7	16	2	PH1637	cytochrome P450mtf
91	3	16.7	16	2	B40291	light-harvesting p
92	3	16.7	16	2	F54226	alcohol dehydrogen
93	3	16.7	17	2	S66198	ribosomal protein
94	3	16.7	17	2	JP0046	actin 6 - soybean
95	3	16.7	17	2	S15754	caldesmon - rabbit
96	3	16.7	17	2	B44873	vitamin D binding
97	3	16.7	17	2	I54269	excretory gland al
98	3	16.7	17	2	A59069	sex-lethal protein
99	3	16.7	17	2	S60171	fatty acid ethyl e
100	3	16.7	17	2	A42920	

## ALIGNMENTS

## RESULT 1

S04229  
 N4-(beta-N-acetylglucosaminyl)-L-asparaginase (EC 3.5.1.26) 24K chain - rat (fragment)  
 N:Alternate names: glycosylasparaginase  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 30-Sep-1993  
 C:Accession: S04229  
 R:Tollersrud, O.K.; Aronson Jr., N.N.  
 Biochem. J. 260, 101-108, 1989  
 A:Title: Purification and characterization of rat liver glycosylasparaginase.  
 A:Reference number: S04228; MUID:89374025; PMID:2775174  
 A:Accession: S04229  
 A:Molecule type: protein  
 A:Residues: 1-18 <TOL>  
 C:Superfamily: N4-(beta-N-acetylglucosaminyl)-L-asparaginase  
 C:Keywords: hydrolase

Query Match 27.8%; Score 5; DB 2; Length 18;  
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 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## QY 13 PLPLV 17

Db 3 PLPLV 7

## RESULT 2

S66419  
 tetrameric proteinase precursor, 60K, dithiothreitol-sensitive - spinach (fragment)  
 C:Species: Spinacia oleracea (spinach)  
 C:Date: 19-Mar-1997 #sequence\_revision 29-Aug-1997 #text\_change 29-Aug-1997  
 C:Accession: S66419  
 R:Kuwabata, T.  
 FEBS Lett. 371, 195-198, 1995  
 A:Title: The 60-kDa precursor to the dithiothreitol-sensitive tetrameric proteinase of spi  
 A:Reference number: S66419; MUID:95402209; PMID:7672127  
 A:Accession: S66419  
 A:Molecule type: protein  
 A:Residues: 1-9 <KUM>

Query Match 22.2%; Score 4; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## QY 6 DVEK 9

Db 6 DVEK 9

## RESULT 3

S20410  
 protein kinase (EC 2.7.1.37) - spinach chloroplast (fragment)  
 N:Alternate names: LHCI protein kinase  
 C:Species: chloroplast Spinacia oleracea (spinach)  
 C:Date: 19-Mar-1997 #sequence\_revision 11-Jun-1999 #text\_change 11-Jun-1999  
 C:Accession: S20410  
 R:Gal, A.; Herrmann, R.G.; Lottspeich, F.; Ohad, I.  
 FEBS Lett. 298, 33-35, 1992  
 A:Title: Phosphorylation of cytochrome b6 by the LHC II kinase associated with the cyto  
 A:Reference number: S20410; MUID:92183823; PMID:1544419  
 A:Accession: S20410  
 A:Molecule type: protein  
 A:Residues: 1-15 <GAL>  
 C:Genetics:  
 A:Genome: chloroplast  
 C:Function:

A:Description: is responsible for the regulation of energy distribution between photosys  
 A>Note: does not exhibit redox-controlled activation  
 C:Keywords: chloroplast; light-harvesting complex; membrane-associated complex; phospho

Query Match 22.2%; Score 4; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## QY 6 DVEK 9

Db 6 DVEK 9

## RESULT 4

S66613  
 protein p12E - Friend murine leukemia virus (fragments)  
 C:Species: Friend murine leukemia virus  
 C:Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997  
 C:Accession: S66613  
 R:Hensel, J.; Hintz, M.; Karas, M.; Linder, D.; Stahl, B.; Geyer, R.  
 Eur. J. Biochem. 232, 373-380, 1995  
 A:Title: Localization of the palmitoylation site in the transmembrane protein p12E of  
 A:Reference number: S66613; MUID:96035869; PMID:7556184  
 A:Accession: S66613  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-9;10-16 <HEN>

Query Match 22.2%; Score 4; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 6.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## QY 1 SLTL 4

Db 4 SLTL 7

## RESULT 5

S60633  
 H+-transporting two-sector ATPase (EC 3.6.3.14) protein 8 - brine shrimp mitochondrion  
 C:Species: mitochondrion Artemia sp. (brine shrimp)  
 A:Variety: Strain La Mata  
 C:Date: 27-Apr-1996 #sequence\_revision 13-Mar-1997 #text\_change 03-Jun-2002  
 C:Accession: S60633  
 R:Perez, M.L.; Valverde, J.R.; Batuecas, B.; Amat, F.; Marco, R.; Garesse, R.  
 J. Mol. Evol. 38, 156-168, 1994  
 A:Title: Speciation in the Artemia genus: mitochondrial DNA analysis of bisexual and  
 A:Reference number: S60624; MUID:94223692; PMID:8169960  
 A:Accession: S60633  
 A>Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-19 <PER>

A:Cross-references: EMBL:X67263; NID:g11210; PIDN:CAA47685.1; PID:g11211  
 A:Experimental source: strain La Mata  
 A>Note: the source is designated as Artemia parthenogenetica  
 C:Genetics:  
 A:Gene: ATP8  
 A:Genome: mitochondrion  
 A:Genetic code: SGC4  
 C:Superfamily: H+-transporting ATP synthase protein 8  
 C:Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion;

Query Match 22.2%; Score 4; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 7.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## QY 12 LPLP 15

Db 5 LPLP 8

## RESULT 6

LFESTU  
 tet leader peptide - Bacillus cereus plasmid pBC16  
 C:Species: Bacillus cereus  
 C:Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 16-Jul-1999

C;Accession: S09233  
 R;Palva, A.; Vidgren, G.; Simonen, M.; Rintala, H.; Laamanen, P.  
 Nucleic Acids Res. 18, 1635, 1990  
 A;Title: Nucleotide sequence of the tetracycline resistance gene of pBC16 from *Bacillus*  
 A;Reference number: S09233; MUID:90221899; PMID:2109312  
 A;Accession: S09233  
 A;Status: translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-20 <PAL>  
 A;Cross-references: EMBL:X51366; NID:G39459; PIDN:CAA35750.1; PID:G39460  
 C;Genetics:  
 A;Genome: plasmid  
 C;Superfamily: tet leader peptide

Query Match 22.2%; Score 4; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTL 4  
 ||||  
 Db 17 SLTL 20

RESULT 7  
 S23742  
 tet leader peptide - *Staphylococcus hyicus*  
 C;Species: *Staphylococcus hyicus*  
 C;Date: 19-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 26-Aug-1999  
 C;Accession: S23742  
 R;Schwarz, S.; Cardoso, M.; Wegener, H.C.  
 Antimicrob. Agents Chemother. 36, 580-588, 1992  
 A;Title: Nucleotide sequence and phylogeny of the tet(L) tetracycline resistance determi  
 A;Reference number: S23742; MUID:92321725; PMID:1622166  
 A;Accession: S23742  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-20 <SCH>  
 A;Cross-references: EMBL:X60828; NID:G43682; PIDN:CAA43219.1; PID:G43683  
 A;Note: the authors translated the codon GGA for residue 14 as Ala  
 C;Superfamily: tet leader peptide

Query Match 22.2%; Score 4; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTL 4  
 ||||  
 Db 17 SLTL 20

RESULT 8  
 F56046  
 urinary tract stone matrix protein 8, 14K - human (fragment)  
 C;Species: *Homo sapiens* (man)  
 C;Date: 12-Apr-1995 #sequence\_revision 12-Apr-1995 #text\_change 12-Apr-1995  
 C;Accession: F56046  
 R;Binette, J.P.; Binette, M.B.; Gawinowicz, M.A.; Kendrick, N.  
 Submitted to the Protein Sequence Database, February 1995  
 A;Description: Isolation, characterization and sequence of stone proteins.  
 A;Reference number: A56046  
 A;Accession: F56046  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-20 <BIN>

Query Match 22.2%; Score 4; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TLTD 6  
 ||||  
 Db 12 TLTD 15

RESULT 9  
 S56005  
 lysosomal protein 22K - rat (fragment)  
 C;Species: *Rattus norvegicus* (Norway rat)  
 C;Date: 10-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 07-May-1999  
 C;Accession: S56005  
 R;Kuwana, T.; Mullock, B.M.; Luzio, J.P.  
 Biochem. J. 308, 937-946, 1995  
 A;Title: Identification of a lysosomal protein causing lipid transfer, using a fluores  
 A;Reference number: S56005; MUID:97104296; PMID:8948454  
 A;Accession: S56005  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-20 <KUW>

Query Match 22.2%; Score 4; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTL 4  
 ||||  
 Db 17 SLTL 20

RESULT 10  
 B33932  
 Ig mu chain D region (D23) - mouse  
 C;Species: *Mus musculus* (house mouse)  
 C;Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 16-Aug-1996  
 C;Accession: B33932  
 R;Baccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.  
 Proc. Natl. Acad. Sci. U.S.A. 86, 4624-4628, 1989  
 A;Title: Two murine natural polyreactive autoantibodies are encoded by nonmutated germ  
 A;Reference number: A33932; MUID:89282823; PMID:2499887  
 A;Accession: B33932  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-6 <BAC>  
 A;Cross-references: GB:M27107  
 C;Keywords: immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 EKL 10  
 ||||  
 Db 1 EKL 3

RESULT 11  
 PQ0663  
 membrane protein - porcine epidemic diarrhea virus (isolate Belgian CV777) (fragment)  
 C;Species: porcine epidemic diarrhea virus  
 C;Date: 14-Jul-1994 #sequence\_revision 14-Jul-1994 #text\_change 08-Oct-1999  
 C;Accession: PQ0663  
 R;Bridgen, A.; Duarte, M.; Tobler, K.; Laude, H.; Ackermann, M.  
 J. Gen. Virol. 74, 1795-1804, 1993  
 A;Title: Sequence determination of the nucleocapsid protein gene of the porcine epidem  
 issible gastroenteritis virus.  
 A;Reference number: JQ2191; MUID:93389433; PMID:8397280  
 A;Accession: PQ0663  
 A;Molecule type: mRNA  
 A;Residues: 1-7 <BRI>  
 A;Cross-references: GB:Z14976; NID:G311650; PIDN:CAA78699.1; PID:G584083  
 C;Comment: This virus is coronavirus related to human coronavirus 229E.  
 C;Keywords: membrane protein

Query Match 16.7%; Score 3; DB 2; Length 7;  
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 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LHL 12  
|||  
Db 4 LHL 6

## RESULT 12

T14906  
hypothetical protein - parsley  
C;Species: Petroselinum crispum (parsley)  
C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
C;Accession: T14906  
R;Feldbrugge, M.; Sprenger, M.; Dinkelbach, M.; Yazaki, K.; Harter, K.; Weisshaar, B.  
Plant Cell 6, 1607-1621, 1994  
A;Title: Functional analysis of a light-responsive plant bZIP transcriptional regulator.  
A;Reference number: Z18259; MUID:95128172; PMID:7827494  
A;Accession: T14906  
A;Status: preliminary;  
A;Molecule type: DNA  
A;Residues: 1-8 <FE>  
A;Cross-references: EMBL:S75395; NID:g913201; PID:e194245

Query Match 16.7%; Score 3; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TLT 5  
|||  
Db 4 TLT 6

## RESULT 13

S10783  
enamelin f - bovine (fragment)  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 19-Mar-1997 #sequence\_revision 21-Nov-1998 #text\_change 21-Nov-1998  
C;Accession: S10783  
R;Strawich, E.; Glimcher, M.J.  
Eur. J. Biochem. 191, 47-56, 1990  
A;Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is albu  
A;Reference number: S10780; MUID:90336641; PMID:2379503  
A;Accession: S10783  
A;Molecule type: protein  
A;Residues: 1-8 <STR>  
C;Keywords: enamel; phosphoprotein

Query Match 16.7%; Score 3; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLP 15  
|||  
Db 2 PLP 4

## RESULT 14

PT0080  
60K Ca binding protein - edible frog (fragment)  
C;Species: Rana esculenta (edible frog)  
C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C;Accession: PT0080  
R;Treveso, S.; Zorzato, F.; Chiozzi, P.; Melandri, P.; Volpe, P.; Pozzan, T.  
Biochem. Biophys. Res. Commun. 175, 444-450, 1991  
A;Title: Frog brain expresses a 60 kDa Ca2+ binding protein similar to mammalian calreti  
A;Reference number: PT0080; MUID:91207333; PMID:2018493  
A;Accession: PT0080  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-9 <TRE>

Query Match 16.7%; Score 3; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PLV 17  
|||  
Db 2 PLV 4

## RESULT 15

C26997  
unspecific monooxygenase (EC 1.14.14.1) isozyme E, phenobarbital-inducible, hepatic -  
N;Alternate names: cytochrome P450  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 30-Jun-1988 #sequence\_revision 30-Jun-1988 #text\_change 05-Mar-1999  
C;Accession: C26997  
R;Graves, P.E.; Kaminsky, L.S.; Halpert, J.  
Biochemistry 26, 3887-3894, 1987  
A;Title: Evidence for functional and structural multiplicity of pregnenolone-16-alpha  
A;Reference number: A26997; MUID:8800604; PMID:3651420  
A;Accession: C26997  
A;Molecule type: protein  
A;Residues: 1-10 <GRA>  
A;Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology  
C;Keywords: electron transfer; heme; liver; monooxygenase; oxidoreductase; transmembr

Query Match 16.7%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LTL 4  
|||  
Db 7 LTL 9

## RESULT 16

I36893  
apolipoprotein A-I - green monkey (fragment)  
C;Species: Cercopithecus aethiops (green monkey, grivet)  
C;Date: 16-Feb-1996 #sequence\_revision 16-Feb-1996 #text\_change 13-Aug-1999  
C;Accession: I36893  
R;Sorci-Thomas, M.; Kearns, M.W.  
J. Biol. Chem. 266, 18045-18050, 1991  
A;Title: Transcriptional regulation of the apolipoprotein A-I gene.  
A;Reference number: A57766; MUID:92011532; PMID:1917942  
A;Accession: I36893  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-10 <RES>  
A;Cross-references: GB:M69224; NID:g176486; PIDN:AAA35357.1; PID:g553152  
C;Superfamily: apolipoprotein A-I

Query Match 16.7%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LTL 4  
|||  
Db 6 LTL 8

## RESULT 17

S18396  
probable glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) - Acetobacter hansenii (fr.  
C;Species: Acetobacter hansenii  
C;Date: 19-Mar-1997 #sequence\_revision 01-Feb-1999 #text\_change 01-Feb-1999  
C;Accession: S18396  
R;Levy, H.R.; Cook, C.  
Arch. Biochem. Biophys. 291, 161-167, 1991  
A;Title: Purification and properties of NADP-linked glucose-6-phosphate dehydrogenase  
A;Reference number: S18396; MUID:92027789; PMID:1929428  
A;Accession: S18396  
A;Molecule type: protein  
A;Residues: 1-10 <LEV>  
A;Experimental source: ATCC 23769  
C;Function:  
A;Description: catalyzes reduction of glucose-6-phosphate to gluconolactone 6-phospha

A;Pathway: pentose phosphate pathway  
 C;Keywords: oxidoreductase; homotetramer; NADP; pentose phosphate pathway

Query Match 16.7%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 HLP 13  
 ||||  
 Db 2 HLP 4

RESULT 18  
 C35389  
 urease (BC 3.5.1.5) 6K chain - Morganella morganii (fragment)  
 C;Species: Morganella morganii  
 C;Date: 31-Aug-1990 #sequence\_revision 31-Aug-1990 #text\_change 23-Jun-1993  
 C;Accession: C35389  
 R;Hu, L.F.; Nicholson, E.B.; Jones, B.D.; Lynch, M.J.; Mobley, H.L.T.  
 J. Bacteriol. 172, 3073-3080, 1990  
 A;Title: Morganella morganii urease: purification, characterization, and isolation of gene  
 A;Reference number: A35389; PMID:90264298; PMID:2345135  
 A;Accession: C35389  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-10 <HUA>  
 C;Keywords: hydrolase

Query Match 16.7%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VEK 9  
 ||||  
 Db 8 VEK 10

RESULT 19  
 C39745  
 sphingomyelinase - Rhodococcus sp. (fragment)  
 C;Species: Rhodococcus sp.  
 C;Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 30-Sep-1993  
 C;Accession: C39745  
 R;Ito, M.; Ikegami, Y.; Yamagata, T.  
 J. Biol. Chem. 266, 7919-7926, 1991  
 A;Title: Activator proteins for glycosphingolipid hydrolysis by endoglycoceramidas. E  
 ble using these activator proteins.  
 A;Reference number: A39745; PMID:91210321; PMID:1850427  
 A;Accession: C39745  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-10 <ITO>

Query Match 16.7%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLP 15  
 ||||  
 Db 3 PLP 5

RESULT 20  
 A61007  
 hementin (BC 3.4.-.-) - Amazon leech (fragment)  
 C;Species: Haementeria ghilianii (Amazon leech)  
 C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 07-May-1999  
 C;Accession: A61007  
 R;Swadesh, J.K.; Huang, I.Y.; Budzynski, A.Z.  
 J. Chromatogr. 502, 359-369, 1990  
 A;Title: Purification and characterization of hementin, a fibrinogenolytic protease from  
 A;Reference number: A61007; PMID:90256973; PMID:2187898  
 A;Accession: A61007

A;Molecule type: protein  
 A;Residues: 1-10 <SWA>  
 C;Keywords: anticoagulant; hydrolase; saliva

Query Match 16.7%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TLT 5  
 ||||  
 Db 2 TLT 4

RESULT 21  
 A56633  
 neomysuppressin - flesh fly (Sarcophaga bullata)  
 N;Alternate names: Neb-MS  
 C;Species: Sarcophaga bullata  
 C;Date: 21-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 20-Jun-2000  
 C;Accession: A56633  
 R;Fonagy, A.; Schoofs, L.; Proost, P.; Van Damme, J.; Bueds, H.; De Loof, A.  
 Comp. Biochem. Physiol. C 102, 239-245, 1992  
 A;Title: Isolation, primary structure and synthesis of neomysuppressin, a myoinhibit  
 A;Reference number: A56633; PMID:93047886; PMID:1359537  
 A;Accession: A56633  
 A;Molecule type: protein  
 A;Residues: 1-10 <FON>  
 A;Experimental source: head  
 A;Note: sequence extracted from NCBI backbone (NCBIP:119072)  
 C;Keywords: amidated carboxyl end; neuropeptide  
 F;10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 16.7%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TDV 7  
 ||||  
 Db 1 TDV 3

RESULT 22  
 C39111  
 Ig heavy chain C region - Pacific hagfish (fragment)  
 C;Species: Eptatretus stoutii (Pacific hagfish)  
 C;Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 16-Aug-1996  
 C;Accession: C39111  
 R;Varner, J.; Neame, P.; Litman, G.W.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 1746-1750, 1991  
 A;Title: A serum heterodimer from hagfish (Eptatretus stoutii) exhibits structural s  
 A;Reference number: A39111; PMID:91156684; PMID:2000382  
 A;Accession: C39111  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-10 <VAR>  
 C;Keywords: heterotetramer; immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PLV 17  
 ||||  
 Db 7 PLV 9

RESULT 23  
 B45482  
 platelet activating factor acetylhydrolase - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 05-May-1995 #sequence\_revision 05-May-1995 #text\_change 05-May-1995  
 C;Accession: B45482  
 R;Stafforini, D.M.; Rollins, E.N.; Prescott, S.M.; McIntyre, T.M.

J. Biol. Chem. 268, 3857-3865, 1993  
 A;Title: The platelet-activating factor acetylhydrolase from human erythrocytes. Purified  
 A;Reference number: A45482; MUID:93179380; PMID:8440681  
 A;Accession: B45482  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-10 <STR>

Query Match 16.7%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PLV 17  
 Db 2 PLV 4

## RESULT 24

C39398  
 FC mu (IgM) receptor surface complex gamma chain - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 28-Feb-1992 #sequence\_revision 28-Feb-1992 #text\_change 20-Mar-1998  
 C;Accession: C39398  
 R;Campbell, K.S.; Hager, E.J.; Friedrich, R.J.; Cambier, J.C.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 3982-3986, 1991  
 A;Title: IgM antigen receptor complex contains phosphoprotein products of B29 and mb-1 g  
 A;Reference number: A39398; MUID:91219496; PMID:2023945  
 A;Accession: C39398  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-10 <CAM>

Query Match 16.7%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPL 14  
 Db 4 LPL 6

## RESULT 25

A47364  
 Placental lactogen-I precursor - mouse (fragment)  
 C;Species: Mus sp. (mouse)  
 C;Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 12-Aug-1996  
 C;Accession: A47364  
 R;Shida, M.M.; Ng, Y.K.; Soares, M.J.; Linzer, D.I.  
 Mol. Endocrinol. 7, 181-188, 1993  
 A;Title: Trophoblast-specific transcription from the mouse placental lactogen-I gene pro  
 A;Reference number: A47364; MUID:93225959; PMID:8469232  
 A;Accession: A47364  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-10 <RES>  
 A;Cross-references: GB:S58124; NID:G299449

Query Match 16.7%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LTL 4  
 Db 3 LTL 5

## RESULT 26

A61354  
 carnitine medium/long chain acyltransferase (EC 2.3.1.-) - rat (fragment)  
 N;Alternate names: endoplasmic reticulum protein ERP61; glucose regulated protein GRP58;  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 07-May-1999  
 C;Accession: A61354

R;Murthy, M.S.R.; Pande, S.V.  
 Mol. Cell. Biochem. 122, 133-138, 1993  
 A;Title: Carnitine medium/long chain acyltransferase of microsomes seems to be the p  
 A;Reference number: A61354; MUID:94049728; PMID:8232244  
 A;Accession: A61354  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-10 <MUR>  
 C;Keywords: acyltransferase

Query Match 16.7%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LTD 6  
 Db 6 LTD 8

## RESULT 27

PX0060  
 lysosome-associated membrane glycoprotein 2 - rat (fragment)  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 03-Mar-1995  
 C;Accession: PX0060  
 R;Akasaki, K.; Yamaguchi, Y.; Furuno, K.; Tsuji, H.  
 J. Biochem. 110, 922-927, 1991  
 A;Title: Purification, some properties, and tissue distribution of a major lysosome-  
 A;Reference number: PX0060; MUID:92176167; PMID:1794981  
 A;Accession: PX0060  
 A;Molecule type: protein  
 A;Residues: 1-10 <AKA>  
 A;Experimental source: liver  
 C;Keywords: glycoprotein; membrane protein

Query Match 16.7%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LTD 6  
 Db 5 LTD 7

## RESULT 28

T13838  
 cytochrome-c oxidase (EC 1.9.3.1) chain I - Bipes biporus mitochondrion (fragment)  
 C;Species: mitochondrion Bipes biporus  
 C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 11-May-2000  
 C;Accession: T13838  
 R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Fang, Z.; Papenfuss, T.J.  
 Mol. Biol. Evol. 14, 91-104, 1997  
 A;Title: Two novel gene orders and the role of light-strand replication in rearrange  
 A;Reference number: Z17789; MUID:97153826; PMID:9000757  
 A;Accession: T13838  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-10 <MAC>  
 A;Cross-references: EMBL:U71335; NID:G1753232; PID:G1753235; PIDN:AAB48271.1  
 C;Genetics:  
 A;Genome: mitochondrion  
 A;Note: COI  
 C;Keywords: mitochondrion; oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLT 3  
 Db 2 SLT 4

RESULT 29  
 T14219  
 Cytochrome-c oxidase (EC 1.9.3.1) chain I - Xenosaurus grandis mitochondrion (fragment)  
 C:Species: mitochondrion Xenosaurus grandis  
 C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 21-Jul-2000  
 C/Accession: T14219  
 R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Fang, Z.; Papenfuss, T.J.  
 Mol. Biol. Evol. 14, 91-104, 1997  
 A>Title: Two novel gene orders and the role of light-strand replication in rearrangement  
 A/Reference number: Z17789; MUID:97153826; PMID:9000757  
 A/Accession: T14219  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-10 <MAC>  
 A/Cross-references: EMBL:U71333; NID:g5739536; PIDN:AAC62821.1; PID:g1753275  
 C/Genetics:  
 A/Genome: mitochondrion  
 A/Note: Col  
 C/Keywords: mitochondrion; oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TLT 5  
 |||  
 Db 2 TLT 4

RESULT 30  
 C54226  
 light-harvesting protein B-830 alpha-3 chain - Chromatium purpuratum (fragment)  
 C:Species: Chromatium purpuratum  
 C/Date: 05-Jan-1996 #sequence\_revision 05-Jan-1996 #text\_change 05-Jan-1996  
 C/Accession: C54226  
 R;Kerfeld, C.A.; Yeates, T.O.; Thornber, J.P.  
 Biochemistry 33, 2178-2184, 1994  
 A>Title: Purification and characterization of the peripheral antenna of the purple-sulfur  
 A/Reference number: A54226; MUID:94162224; PMID:8117674  
 A/Accession: C54226  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-10 <KR>  
 C/Keywords: antenna complex; light-harvesting polypeptide

Query Match 16.7%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 LVQ 18  
 |||  
 Db 7 LVQ 9

RESULT 31  
 PA0116  
 ferredoxin-NADP reductase (EC 1.18.1.2) - rice (fragment)  
 C:Species: Oryza sativa (rice)  
 C/Date: 07-Apr-1995 #sequence\_revision 26-May-1995 #text\_change 03-Jun-2002  
 C/Accession: PA0116  
 R;Kamo, M.; Tsugita, A.  
 submitted to JIPID, March 1995  
 A/Reference number: PA0114  
 A/Accession: PA0116  
 A/Molecule type: protein  
 A/Residues: 1-10 <KAM>  
 A/Experimental source: leaf  
 C/Keywords: NADP; oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VEX 9  
 |||  
 Db 1 VEX 3

RESULT 32  
 PS0220  
 ferredoxin-NADP reductase (EC 1.18.1.2) - rice (fragment)  
 C:Species: Oryza sativa (rice)  
 C/Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 03-Jun-2002  
 C/Accession: PS0220  
 R;Uchiyama, Y.; Tsugita, A.  
 submitted to JIPID, August 1991  
 A/Reference number: PS0205  
 A/Accession: PS0220  
 A/Molecule type: protein  
 A/Residues: 1-10 <UCH>  
 C/Keywords: NADP; oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VEX 9  
 |||  
 Db 1 VEX 3

RESULT 33  
 S42449  
 ant1 protein - phase P7  
 C/Species: phase P7  
 C/Date: 07-Sep-1994 #sequence\_revision 26-May-1995 #text\_change 08-Oct-1999  
 C/Accession: S42449  
 R;Citron, M.; Schuster, H.  
 Cell 62, 591-598, 1990  
 A>Title: The c4 repressors of bacteriophages P1 and P7 are antisense RNAs.  
 A/Reference number: S42448; MUID:90335969; PMID:1696181  
 A/Accession: S42449  
 A/Status: preliminary; translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-11 <CIT>  
 A/Cross-references: EMBL:M35139; NID:g215705; PIDN:AAA32437.1; PID:g215707

Query Match 16.7%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PLV 17  
 |||  
 Db 4 PLV 6

RESULT 34  
 D58502  
 27K bile and gallbladder stone protein - unidentified bacterium (fragment)  
 C:Species: unidentified bacterium  
 C/Date: 07-Feb-1997 #sequence\_revision 07-Feb-1997 #text\_change 10-Jul-1998  
 C/Accession: D58502  
 R;Binette, J.P.; Binette, M.B.  
 submitted to the Protein Sequence Database, October 1996  
 A/Description: The proteins of kidney and gallbladder stones.  
 A/Reference number: A58501  
 A/Accession: D58502  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-11 <BIN>  
 A/Experimental source: human bile and gallbladder stones

Query Match 16.7%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 4 LTD 6  
|||  
Db 4 LTD 6

RESULT 35  
I33098  
173K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)  
C:Species: Plasmodium falciparum  
C:Date: 24-Aug-1990 #sequence\_revision 24-Aug-1990 #text\_change 09-Jun-2000  
C:Accession: I33098  
R;Nichols, J.H.; Hager, L.P.  
submitted to the Protein Sequence Database, May 1990  
A:Reference number: A33098  
A:Accession: I33098  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-11 <NIC>

Query Match 16.7%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPL 14  
|||  
Db 6 LPL 8

RESULT 36  
I52304  
gene rSSTR4 protein - rat (fragment)  
C:Species: Rattus sp. (rat)  
C:Date: 23-May-1998 #sequence\_revision 29-May-1998 #text\_change 17-Mar-1999  
C:Accession: I52304  
R;Xu, Y.; Bruno, J.F.; Berelowitz, M.  
Biochem. Biophys. Res. Commun. 206, 935-941, 1995  
A:Title: Characterization of the proximal promoter region of the rat somatostatin receptor  
A:Reference number: I52304; MUID:95134278; PMID:7832807  
A:Accession: I52304  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-11 <RES>  
A:Cross-references: GB:S75475; NID:G914315  
C:Genetics:  
A:Gene: rSSTR4

Query Match 16.7%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPL 14  
|||  
Db 7 LPL 9

RESULT 37  
T17081  
cytochrome-c oxidase (EC 1.9.3.1) chain I - Phrynocephalus raddei mitochondrion (fragment)  
C:Species: mitochondrion Phrynocephalus raddei  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 22-Oct-1999  
C:Accession: T17081  
R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.  
J. Mol. Evol. 44, 660-674, 1997  
A:Title: Evolutionary shifts in three major structural features of the mitochondrial gene  
A:Reference number: Z18674; MUID:97315309; PMID:9169559  
A:Accession: T17081  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-11 <MAC>  
A:Cross-references: EMBL:U82691; NID:G3603148; PID:G3603151; PIDN:AA62302.1  
C:Genetics:  
A:Genome: mitochondrion  
A>Note: COI

C:Keywords: mitochondrion; oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TLT 5  
|||  
Db 3 TLT 5

RESULT 38  
PU0034  
dextranucrase (EC 2.4.1.5) - Streptococcus bovis (fragment)  
C:Species: Streptococcus bovis  
C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 18-Sep-1996  
C:Accession: PU0034  
R;Uezono, Y.; Tsumori, H.; Mukasa, H.  
submitted to JIPID, October 1993  
A:Description: Purification and properties of glucosyltransferase synthesizing 1,6-a  
A:Reference number: PU0034  
A:Accession: PU0034  
A:Molecule type: protein  
A:Residues: 1-11 <UEZ>  
A:Experimental source: ATCC 9809  
C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 16.7%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TLT 5  
|||  
Db 7 TLT 9

RESULT 39  
S29764  
alpha-macroglobulin proteinase inhibitor - bullfrog (fragment)  
C:Species: Rana catesbeiana (bullfrog)  
C:Date: 19-Mar-1997 #sequence\_revision 24-Mar-1999 #text\_change 07-May-1999  
C:Accession: S29764  
R;Rubenstein, D.S.; Thoenes, I.B.; Pizzo, S.V.; Englund, J.J.  
Biochem. J. 290, 85-95, 1993  
A:Title: Identification of monomeric alpha-macroglobulin proteinase inhibitors in bi  
teasinase inhibitor from the American bullfrog Rana catesbeiana.  
A:Reference number: S29764; MUID:93176138; PMID:7679897

Query Match 16.7%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 HLP 13  
|||  
Db 3 HLP 5

RESULT 40  
S65136  
kalikrein K2 - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 07-May-1999  
C:Accession: S65136  
R;Deperthes, D.; Chapdelaine, P.; Tremblay, R.R.; Brunet, C.; Berton, J.; Hebert, J.  
Biochim. Biophys. Acta 1245, 311-316, 1995

A:Title: Isolation of prostatic kallikrein hK2, also known as hGK-1, in human seminal plasma  
 A:Reference number: S65136; MUID:96125726; PMID:8541306  
 A:Accession: S65136  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-12 <DEP>

Query Match 16.7%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LHL 12  
 |||  
 Db 7 LHL 9

RESULT 41  
 PNO663  
 dystrophin-associated glycoprotein A3a-II - rabbit (fragment)  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C:Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 07-May-1999  
 C:Accession: PNO663  
 R:Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.

A:Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained in the dystrophic muscle  
 A:Reference number: PNO662; MUID:94156881; PMID:8113213  
 A:Accession: PNO663  
 A:Molecule type: protein  
 A:Residues: 1-12 <VS>

C:Comment: This protein is retained in Duchenne type muscular dystrophy muscle.  
 C:Keywords: glycoprotein; skeletal muscle

Query Match 16.7%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLP 15  
 |||  
 Db 3 PLP 5

RESULT 42  
 B60228  
 Fc mu (IgM) receptor surface complex beta chain - mouse (fragment)  
 N:Alternate names: membrane protein B29  
 C:Species: Mus musculus (house mouse)  
 C:Date: 08-Dec-1992 #sequence\_revision 08-Dec-1992 #text\_change 20-Mar-1998  
 C:Accession: B60228; B39398  
 R:Hombach, J.; Lottspeich, F.; Reth, M.

A:Title: Identification of the genes encoding the Igm-alpha and Ig-beta components of the mouse IgM receptor complex  
 A:Reference number: A60228; MUID:91099432; PMID:2269334  
 A:Accession: B60228  
 A:Molecule type: protein  
 A:Residues: 1-12 <HOM>  
 R:Cambelli, K.S.; Hager, E.J.; Friedrich, R.J.; Cambier, J.C.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 3982-3986, 1991  
 A:Title: Igm antigen receptor complex contains phosphoprotein products of B29 and mb-1 genes  
 A:Reference number: A39398; MUID:91219496; PMID:2023945  
 A:Accession: B39398

A:Molecule type: protein  
 A:Residues: 'XX', 3-10 <CAM>  
 C:Keywords: membrane protein

Query Match 16.7%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPL 14  
 |||  
 Db 4 LPL 6

# RESULT 43

JX0315  
 aminotransferase chimera DY18 - synthetic (fragment)  
 C:Species: synthetic  
 C:Date: 28-May-1999 #sequence\_revision 28-May-1999 #text\_change 28-May-1999  
 C:Accession: JX0315  
 R:Miyaizawa, K.; Kawaguchi, S.; Okamoto, A.; Kato, R.; Ogawa, T.; Kuramitsu, S.  
 J. Biochem. 115, 568-577, 1994  
 A:Title: Construction of aminotransferase chimeras and analysis of their substrate specificity  
 A:Reference number: JX0315; MUID:94334304; PMID:8056774  
 A:Accession: JX0315  
 A:Molecule type: DNA  
 A:Residues: 1-12 <MY>  
 C:Comment: This enzyme is a chimeric enzyme of Escherichia coli aspartate aminotransferase and aminotransferase  
 C:Keywords: aminotransferase

Query Match 16.7%; Score 3; DB 4; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LTL 4  
 |||  
 Db 7 LTL 9

# RESULT 44

S49073  
 frame shifted cytochrome accessory protein HMW3 - Mycoplasma pneumoniae (fragment)  
 N:Alternate names: H-transferring ATP synthase (EC 3.6.3.14) alpha chain (misidentified)  
 C:Species: Mycoplasma pneumoniae  
 C:Date: 28-Aug-1998 #sequence\_revision 28-Aug-1998 #text\_change 19-Apr-2002  
 C:Accession: S49073  
 R:Proft, T.; Herrmann, R.  
 Mol. Microbiol. 13, 337-348, 1994  
 A:Title: Identification and characterization of hitherto unknown Mycoplasma pneumoniae cytochrome accessory protein HMW3  
 A:Reference number: S49059; MUID:95075318; PMID:7984111  
 A:Accession: S49073  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-12 <PRO>  
 A:Cross-references: EMBL:Z32665; NID:G474163; PIDN:CAA83583.1; PID:G581348  
 A:Experimental source: clone D2-16  
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1994  
 A:Note: the GenBank entry MPDASAL, release 106.0, translates the ATC codon, 1 in this sequence, to a stop codon. The nucleotide sequence translated in an alternative reading frame is identical to the sequence in this entry.  
 C:Comment: The nucleotide sequence translated in an alternative reading frame is identical to the sequence in this entry.  
 C:Genetics: SGC3

Query Match 16.7%; Score 3; DB 4; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TLT 5  
 |||  
 Db 3 TLT 5

# RESULT 45

PQ0491  
 self-incompatibility locus glycoprotein delta - wild cabbage (fragment)  
 C:Species: Brassica oleracea (wild cabbage)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 31-Oct-1997  
 C:Accession: PQ0491  
 R:Gaude, T.; Friry, A.; Heizmann, P.; Mariac, C.; Rougier, M.; Fobis, I.; Dumas, C.  
 Plant Cell 5, 75-86, 1993  
 A:Title: Expression of a self-incompatibility gene in a self-compatible line of Brassica oleracea  
 A:Reference number: JQ1733; MUID:93177215; PMID:8439745  
 A:Accession: PQ0491  
 A:Molecule type: protein  
 A:Residues: 1-13 <GAU>  
 A:Experimental source: stigma, var. acephala P57S1  
 C:Superfamily: S-receptor kinase; protein kinase homology; S-locus-specific glycoprotein

C;Keywords: glycoprotein

Query Match 16.7%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 5.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLT 3  
|||  
DB 9 SLT 11

#### RESULT 46

A60856  
inhibin alpha chain - sheep (fragment)  
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C;Accession: A60856  
R;Leversha, L.J.; Robertson, D.M.; de Vos, F.L.; Morgan, F.J.; Hearn, M.T.W.; Wattenhall  
J. Endocrinol. 113, 213-221, 1987  
A;Title: Isolation of inhibin from ovine follicular fluid.  
A;Reference number: A60856; MUID:87224684; PMID:3585232  
A;Accession: A60856  
A;Molecule type: protein  
A;Residues: 1-13 <LSV>  
C;Comment: Inhibin suppresses follicle-stimulating hormone secretion.  
C;Superfamily: inhibin  
C;Keywords: disulfide bond; glycoprotein; gonad; heterodimer; hormone

Query Match 16.7%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 5.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLP 15  
|||  
DB 4 PLP 6

#### RESULT 47

S15755  
actin 7 - soybean (fragment)  
C;Species: Glycine max (soybean)  
C;Date: 20-Feb-1995 #sequence\_revision 29-May-1998 #text\_change 13-Aug-1999  
C;Accession: S15755  
R;Pearson, L.; Meagher, R.B.  
Plant Mol. Biol. 14, 513-526, 1990  
A;Title: Diverse soybean actin transcripts contain a large intron in the 5' untranslated  
A;Reference number: S15754; MUID:91346640; PMID:2102831  
A;Accession: S15755  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-13 <PEA>  
A;Cross-references: EMBL:X17120; NID:g18527; PIDN:CAA34980.1; PID:g18528  
C;Superfamily: actin  
C;Keywords: cytoskeleton; structural protein

Query Match 16.7%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 5.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PLV 17  
|||  
DB 9 PLV 11

#### RESULT 48

JZVHP1  
crabrolin - European hornet  
C;Species: Vespa crabro (European hornet)  
C;Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000  
C;Accession: A01781  
R;Argiolas, A.; Pisano, J.J.  
J. Biol. Chem. 259, 10106-10111, 1984  
A;Title: Isolation and characterization of two new peptides, mastoparan C and crabrolin,

A;Reference number: A92441; MUID:84289390; PMID:6206053

A;Accession: A01781

A;Molecule type: protein

A;Residues: 1-13 <ARG>

C;Comment: This cytoactive peptide from hornet venom induces mast cell degranulation

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; venom

F;13/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 16.7%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 5.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPL 14  
|||  
DB 2 LPL 4

#### RESULT 49

PN0125  
serine proteinase (BC 3.4.21.-) - Actinomyces sp. (fragment)  
C;Species: Actinomyces sp.  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 27-Jan-1995  
C;Accession: PN0125  
R;Mosolova, O.V.; Rudenskaya, G.N.; Stepanov, V.M.; Khodova, O.M.; Tsaplina, I.A.  
Biochimia 52, 414-422, 1987  
A;Title: Glu, Asp-specific proteinase from Actinomycetes.  
A;Reference number: PN0125  
A;Accession: PN0125  
A;Molecule type: protein  
A;Residues: 1-13 <MOS>  
A;Note: article in Russian with English abstract  
C;Keywords: hydrolase; serine proteinase

Query Match 16.7%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 5.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TDV 7  
|||  
DB 5 TDV 7

#### RESULT 50

PC4055  
hypothetical 13 protein - Frankia sp. (fragment)  
C;Species: Frankia sp.  
C;Date: 10-Sep-1995 #sequence\_revision 27-Oct-1995 #text\_change 27-Oct-1995  
C;Accession: PC4055  
R;Harriott, O.T.; Hosted, T.J.; Benson, D.R.  
Gene 161, 63-67, 1995  
A;Title: Sequences of nifX, nifW, nifZ, nifB and two ORF in the Frankia nitrogen fix  
A;Reference number: JC4203; MUID:95369734; PMID:7642138  
A;Accession: PC4055  
A;Molecule type: DNA  
A;Residues: 1-13 <HAR>  
A;Cross-references: GB:L29299

Query Match 16.7%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 5.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LTD 6  
|||  
DB 10 LTD 12

#### RESULT 51

D56661  
S-locus specific glycoprotein (allele S3) - wild cabbage (fragment)  
C;Species: Brassica oleracea (wild cabbage)  
C;Date: 05-Jan-1996 #sequence\_revision 05-Jan-1996 #text\_change 05-Jan-1996  
C;Accession: D56661

R;Gaude, T.; Denoroy, L.; Dumas, C.  
Electrophoresis 12, 646-653, 1991  
A:Title: Use of a fast protein electrophoretic purification procedure for N-terminal seq  
A:Reference number: A56661; MUID:92090397; PMID:1752245  
A:Accession: D56661  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-13 <GAU>  
A:Experimental source: stigma extracts, var. acephala  
A:Note: sequence extracted from NCBI backbone (NCBIP:72300)  
C:Comment: This glycoprotein, expressed only in stigmas, plays an important role in the  
C:Keywords: glycoprotein; polymorphism

Query Match 16.7%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 5.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SUT 3  
|||  
Db 9 SUT 11

RESULT 52  
S03019  
hemolytic protein B9 - edible frog (fragment)  
C:Species: Rana esculenta (edible frog)  
C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 18-Jun-1993  
C:Accession: S03019  
R;Simmaco, M.; De Biase, D.; Severini, C.; Aita, M.; Erpamer, G.F.; Barra, D.; Bossa, F.  
Biochim. Biophys. Acta 1033, 318-323, 1990  
A:Title: Purification and characterization of bioactive peptides from skin extracts of R  
A:Reference number: S03018; MUID:90198965; PMID:2317508  
A:Accession: S03019  
A:Molecule type: protein  
A:Residues: 1-13 <SIM>

Query Match 16.7%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 5.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPL 14  
|||  
Db 2 LPL 4

RESULT 53  
I84603  
deoxynucleotidyltransferase - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 21-Jul-2000  
C:Accession: I84603  
R;Koiwai, O.; Kaneda, T.; Morishita, R.  
Biochem. Biophys. Res. Commun. 144, 185-190, 1987  
A:Title: Analysis of human terminal deoxynucleotidyl transferase cDNA expressible in man  
A:Reference number: I45884; MUID:87213162; PMID:3579900  
A:Accession: I84603  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-13 <RES>  
A:Cross-references: GB:M26144; NID:G951194; PIDN:AAA74588.1; PID:G951195  
C:Genetics:  
A:Gene: GDB:DNTT  
A:Cross-references: GDB:119100; OMIM:187410  
A:Map position: 10q23-10q24

Query Match 16.7%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 5.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLP 15  
|||  
Db 9 PLP 11

RESULT 54  
A61458  
Ig kappa chain V-L region (BOU) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 15-Oct-1994 #sequence\_revision 15-Oct-1994 #text\_change 16-Aug-1996  
C:Accession: A61458; PLO156  
R;Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.  
J. Exp. Med. 170, 1551-1558, 1989  
A:Title: Expression of a public idiotype by human monoclonal IGM directed to myelin-  
A:Reference number: A61458; MUID:90039128; PMID:2478651  
A:Accession: A61458  
A:Molecule type: protein  
A:Residues: 1-13 <BRO>  
C:Comment: This protein is one of monoclonal IGM reactive with myeloma-associated gly  
C:Keywords: heterotetramer; immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 5.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TLT 5  
|||  
Db 10 TLT 12

RESULT 55  
S57571  
T cell receptor alpha chain V-J region (clone PP7 and others) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 19-Oct-1995 #sequence\_revision 17-Nov-1995 #text\_change 05-Nov-1999  
C:Accession: S57571; S57573; S57576  
R;Burrows, S.R.; Silins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Argae, V.P.  
submitted to the EMBL Data Library, June 1995  
A:Description: T cell receptor repertoire for a viral epitope in humans is diversifie  
A:Reference number: S57494  
A:Accession: S57571  
A:Molecule type: mRNA  
A:Residues: 1-13 <BUR>  
A:Cross-references: EMBL:Z49948; NID:G887496; PIDN:CAA90219.1; PID:G887497  
A:Experimental source: clone PP7  
A:Accession: S57573  
A:Molecule type: mRNA  
A:Residues: 1-13 <BUL>  
A:Cross-references: EMBL:Z49950; NID:G887500; PIDN:CAA90221.1; PID:G887501  
A:Experimental source: clone TFI  
A:Accession: S57576  
A:Molecule type: mRNA  
A:Residues: 1-13 <BUW>  
A:Cross-references: EMBL:Z49952; NID:G887512; PIDN:CAA90223.1; PID:G887513  
A:Experimental source: clone RL16  
C:Keywords: T-cell receptor

Query Match 16.7%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 5.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EKL 10  
|||  
Db 8 EKL 10

RESULT 56  
PH0138  
T-cell receptor beta chain V-D-J region C8 - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 30-May-1997  
C:Accession: PH0138  
R;Martin, R.; Howell, M.D.; Jaraquemada, D.; Flierlage, M.; Richert, J.; Brostoff, S.;  
J. Exp. Med. 173, 19-24, 1991  
A:Title: A myelin basic protein peptide is recognized by cytotoxic T cells in the cor  
A:Reference number: PH0135; MUID:91086843; PMID:1702137  
A:Accession: PH0138

A:Molecule type: mRNA  
A:Residues: 1-13 <MAR>  
C:Keywords: T-cell receptor

Query Match 16.7%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 5.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EKL 10  
|||  
Db 11 EKL 13

## RESULT 57

JN0390  
histamine-releasing peptide II - oriental hornet  
N:Alternate names: venom protein HR-2  
C:Species: Vespa orientalis (oriental hornet)  
C>Date: 15-Jan-1993 #sequence\_revision 15-Jan-1993 #text\_change 23-Aug-1997  
R:Miroschnikov, A.I.; Shezhkova, L.G.; Nazimov, I.V.; Reshetova, O.I.; Rozinov, B.V.; Gus  
Bioorg. Khim. 7, 1467-1477, 1981  
A:Title: Structure and properties of histamine releasing peptides from the venom of Vesp  
A:Reference number: JN0389  
A:Accession: JN0390  
A:Molecule type: protein  
A:Residues: 1-14 <MR>  
R:Tuichibaev, M.U.; Akmedova, N.U.; Kazakov, I.; Korneev, A.S.; Gagel'gans, A.I.  
Biochemistry (N.Y.) 53, 183-190, 1988  
A:Title: Low-molecular-weight peptides of venom of the giant hornet Vespa orientalis. S  
A:Reference number: S06445  
A:Accession: S10919  
A:Molecule type: protein  
A:Residues: 1-14 <TUI>  
C:Superfamily: crabrolin  
C:Keywords: amidated carboxyl end; venom  
F:14/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 16.7%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 5.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPL 14  
|||  
Db 2 LPL 4

## RESULT 58

S19803  
ubiquitin - potato (fragment)  
C:Species: Solanum tuberosum (potato)  
C>Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 30-Sep-1993  
C:Accession: S19803  
R:Belknap, W.  
submitted to the EMBL Data Library, January 1992  
A:Reference number: S19798  
A:Accession: S19803  
A:Molecule type: mRNA  
A:Residues: 1-14 <BEL>  
A:Cross-references: EMBL:Z11667  
C:Superfamily: ubiquitin; ubiquitin homology

Query Match 16.7%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 5.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TLT 5  
|||  
Db 7 TLT 9

## RESULT 59

B29743  
Ig heavy chain CRD3 region (clone 2-118C) - human (fragment)

translation initiation factor eIF-2 alpha chain-associated kinase phosphopeptide - r.  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C>Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 31-Oct-1997  
C:Accession: B29743

R:Rose, D.W.; Wettenhall, R.E.H.; Kudlicki, W.; Kramer, G.; Hardesty, B.  
Biochemistry 26, 6593-6597, 1987  
A:Title: The 90-kilodalton peptide of the heme-regulated eIF-2-alpha kinase has sequ  
A:Reference number: A90521; MUID:88107571; PMID:3427028  
A:Accession: B29743  
A:Molecule type: protein  
A:Residues: 1-14 <ROS>  
A:Experimental source: reticulocyte  
C:Superfamily: heat shock protein 90

Query Match 16.7%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 5.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLT 3  
|||  
Db 3 SLT 5

## RESULT 60

C33098  
23k exoantigen - malaria parasite (Plasmodium falciparum) (fragments)  
C:Species: Plasmodium falciparum  
C>Date: 24-Aug-1990 #sequence\_revision 24-Aug-1990 #text\_change 09-Jun-2000  
C:Accession: C33098

R:Nichols, J.H.; Hager, L.P.  
submitted to the Protein Sequence Database, May 1990  
A:Reference number: A33098  
A:Accession: C33098  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-14 <NIC>

Query Match 16.7%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 5.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EKL 10  
|||  
Db 6 EKL 8

## RESULT 61

D61308  
hemocyanin chain 5A - Sahara scorpion (fragment)  
C:Species: Androctonus australis (Sahara scorpion)  
C>Date: 17-Jul-1994 #sequence\_revision 17-Jul-1994 #text\_change 07-May-1999  
C:Accession: D61308  
R:Jolles, J.; Jolles, P.; Lamy, J.; Lamy, J.  
FEBS Lett. 106, 283-291, 1979  
A:Title: Structural characterization of seven different subunits in Androctonus aust  
A:Reference number: A61308; MUID:80047238; PMID:499512  
A:Accession: D61308  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-14 <JOL>

Query Match 16.7%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 5.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPL 14  
|||  
Db 10 LPL 12

## RESULT 62

PT0259  
Ig heavy chain CRD3 region (clone 2-118C) - human (fragment)

C:Species: Homo sapiens (man)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
 C:Accession: PT0259  
 R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shabe, S.; Caton, A.J.; Rovera, G.  
 J. Exp. Med. 173, 395-407, 1991  
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J  
 A:Reference number: PT0222; MUID:91108337; PMID:1899102  
 A:Accession: PT0259  
 A:Molecule type: DNA  
 A:Residues: 1-14 <YAM>  
 A:Experimental source: B lymphocyte  
 C:Keywords: heterotetramer; immunoglobulin

Query Match 16.7%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 5.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TLT 5  
 |||  
 Db 2 TLT 4  
 |||

RESULT 63  
 S57572  
 T cell receptor V-J junctional alpha chain region - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 19-Oct-1995 #sequence\_revision 17-Nov-1995 #text\_change 05-Nov-1999  
 C:Accession: S57572  
 R:Burrows, S.R.; Silins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Arguet, V.P.  
 submitted to the EMBL Data Library, June 1995  
 A:Description: T cell receptor repertoire for a viral epitope in humans is diversified b  
 A:Reference number: S57494  
 A:Accession: S57572  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-14 <BUR>  
 A:Cross-references: EMBL:249957; NID:g887478; PIDN:CAA90228.1; PID:g887479  
 C:Keywords: T-cell receptor

Query Match 16.7%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 5.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 PLV 17  
 |||  
 Db 10 PLV 12  
 |||

RESULT 64  
 PC4382  
 dehydrin 4.5K polypeptide - Soybean (fragment)  
 N:Alternate names: acid soluble 26K protein  
 C:Species: Glycine max  
 C:Date: 06-Nov-1997 #sequence\_revision 06-Nov-1997 #text\_change 18-Jul-2001  
 C:Accession: PC4382  
 R:Momma, M.; Haraguchi, K.; Saito, M.; Chikuni, K.; Harada, K.  
 Biosci. Biotechnol. Biochem. 61, 1286-1291, 1997  
 A:Title: Purification and characterization of the acid soluble 26-kDa polypeptide from s  
 A:Reference number: PC4380; MUID:97446521; PMID:9301109  
 A:Accession: PC4382  
 A:Molecule type: protein  
 A:Residues: 1-14 <MOM>  
 A:Experimental source: seed  
 C:Comment: This protein is rich in hydrophilic amino acid, and highly heat stable.

Query Match 16.7%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 5.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 EKL 10  
 |||  
 Db 6 EKL 8  
 |||

RESULT 65  
 A26997  
 unspecific monooxygenase (EC 1.14.14.1) cytochrome P450 2B1, hepatic - rat (fragment  
 N:Alternate names: cytochrome P450b  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 30-Jun-1988 #sequence\_revision 30-Jun-1988 #text\_change 05-Mar-1999  
 C:Accession: A26997  
 R:Graves, P.E.; Kaminsky, L.S.; Halpert, J.  
 Biochemistry 26, 3887-3894, 1987  
 A:Title: Evidence for functional and structural multiplicity of pregnenolone-16- $\alpha$ -  
 A:Reference number: A26997; MUID:88000604; PMID:3651420  
 A:Accession: A26997  
 A:Molecule type: protein  
 A:Residues: 1-15 <GRA>  
 A:Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology  
 C:Keywords: electron transfer; heme; liver; monooxygenase; oxidoreductase; transmemb:

Query Match 16.7%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LTL 4  
 |||  
 Db 7 LTL 9  
 |||

RESULT 66  
 B56661  
 S-locus specific glycoprotein P57 beta - wild cabbage (fragment)  
 C:Species: Brassica oleracea (wild cabbage)  
 C:Date: 05-Jan-1996 #sequence\_revision 05-Jan-1996 #text\_change 31-Oct-1997  
 C:Accession: B56661  
 R:Gaude, I.; Denoroy, L.; Dumas, C.  
 Electrophoresis 12, 646-653, 1991  
 A:Title: Use of a fast protein electrophoretic purification procedure for N-terminal  
 A:Reference number: A56661; MUID:92090397; PMID:1752245  
 A:Accession: B56661  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-15 <GAU>  
 A:Experimental source: stigma extracts, var. acephala, self-compatible line P57  
 A:Note: sequence extracted from NCBI backbone (NCBIP:72302)  
 C:Comment: This glycoprotein, expressed only in stigmas, plays an important role in  
 C:Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology  
 C:Keywords: glycoprotein; polymorphism

Query Match 16.7%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLT 3  
 |||  
 Db 11 SLT 13  
 |||

RESULT 67  
 PQ0681  
 photosystem I 19.0K D1 chain - common tobacco (fragment)  
 C:Species: Nicotiana tabacum (common tobacco)  
 C:Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 17-Mar-1999  
 C:Accession: PQ0681  
 R:Obokata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugitara, M.  
 Plant Physiol. 102, 1259-1267, 1993  
 A:Title: Molecular heterogeneity of photosystem I. psdA, psbE, psbF, psbH and psbL a;  
 A:Reference number: PQ0667; MUID:94105345; PMID:8278548  
 A:Accession: PQ0681  
 A:Molecule type: protein  
 A:Residues: 1-15 <OBO>  
 C:Superfamily: photosystem I chain II  
 C:Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 16.7%; Score 3; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 5.9e+03; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VEK 9  
Db 2 VEK 4

## RESULT 68

Capsid protein VP19C - human herpesvirus 1 (fragment)  
C/Species: human herpesvirus 1  
C/Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 07-May-1999  
C/Accession: PQ0545  
R/Davison, M.D.; Rixon, F.J.; Davison, A.J.  
J. Gen. Virol. 73, 2709-2713, 1992  
A/Title: Identification of genes encoding two capsid proteins (VP24 and VP26) of herpes  
A/Reference number: PQ0544; MUID:93019027; PMID:1328483  
A/Accession: PQ0545  
A/Molecule type: protein  
A/Residues: 1-15 <DAV>  
A/Experimental source: strain 17  
C/Genetics:  
A/Gene: UL38  
C/Keywords: capsid protein

Query Match 16.7%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PLP 15  
Db 5 PFP 7

## RESULT 69

B39109  
Hypothetical 1.5K protein - hepatitis C virus  
N/Alternate names: hypothetical protein 2  
C/Species: hepatitis C virus  
C/Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 07-May-1999  
C/Accession: B39109; JQ1585  
R/Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Tekamp-  
Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991  
A/Title: Characterization of the terminal regions of hepatitis C viral RNA: identification  
A/Reference number: A39109; MUID:91156678; PMID:1705704  
A/Accession: B39109  
A/Status: not compared with conceptual translation  
A/Molecule type: mRNA  
A/Residues: 1-15 <HAN>  
A/Cross-references: GB:M58406  
R/Kumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.  
J. Gen. Virol. 73, 1521-1525, 1992

A/Title: Cloning and sequencing of the structural region and expression of putative core  
A/Reference number: JQ1584; MUID:92300349; PMID:1318944  
A/Accession: JQ1585  
A/Molecule type: genomic RNA  
A/Residues: 1-15 <KUM>  
A/Experimental source: strain U.K.

Query Match 16.7%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PLP 15  
Db 10 PLP 12

## RESULT 70

A35232  
Gentisate 1,2-dioxygenase (EC 1.13.11.4) - Comamonas testosteroni (fragment)  
C/Species: Comamonas testosteroni

C/Date: 10-Aug-1990 #sequence\_revision 10-Aug-1990 #text\_change 23-Jun-1993  
C/Accession: A35232  
R/Harpe, M.R.; Lipscomb, J.D.  
J. Biol. Chem. 265, 6301-6311, 1990  
A/Title: Gentisate 1,2-dioxygenase from Pseudomonas. Purification, characterization,  
A/Reference number: A35232; MUID:90202907; PMID:2156846  
A/Accession: A35232  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-15 <HAR>  
C/Keywords: oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LVQ 18  
Db 2 LVQ 4

## RESULT 71

S61284  
Phosphoprotein, 80K - Escherichia coli (fragment)  
C/Species: Escherichia coli  
C/Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 25-Apr-1997  
C/Accession: S61284  
R/Freestone, P.; Grant, S.; Toth, I.; Norris, V.  
Mol. Microbiol. 15, 573-580, 1995  
A/Title: Identification of phosphoproteins in Escherichia coli.  
A/Reference number: S61284; MUID:95302968; PMID:7783627  
A/Accession: S61284  
A/Molecule type: protein  
A/Residues: 1-15 <FRE>

Query Match 16.7%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 EKL 10  
Db 3 EKL 5

## RESULT 72

S62620  
Protein disulfide-isomerase (EC 5.3.4.1) - castor bean (fragment)  
C/Species: Ricinus communis (castor bean)  
C/Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 17-Mar-1999  
C/Accession: S62620  
R/Coughlan, S.J.; Hastings, C.; Winfrey Jr., R.J.  
Eur. J. Biochem. 235, 215-224, 1996

A/Title: Molecular characterisation of plant endoplasmic reticulum: identification c  
A/Reference number: S62620; MUID:96202938; PMID:8631332  
A/Accession: S62620

A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-15 <COU>  
C/Keywords: intramolecular oxidoreductase; isomerase

Query Match 16.7%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LTL 4  
Db 11 LTL 13

## RESULT 73

PA0051  
Protein QF200016 - fungus (Fusarium sporotrichioides) (fragment)  
C/Species: Fusarium sporotrichioides

C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001  
 C;Accession: PA0051  
 R;Chow, L.P.; Fukaya, N.; Sugitara, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.  
 submitted to JIPID, October 1994  
 A;Description: Two dimensional polyacrylamide gel electrophoresis of *Fusarium sporotrichioides*  
 A;Reference number: PA0051  
 A;Accession: PA0051  
 A;Molecule type: protein  
 A;Residues: 1-15 <CHO>

Query Match 16.7%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VEK 9  
 |||  
 Db 2 VEK 4

## RESULT 74

PA0060  
 protein QP200037 - fungus (*Fusarium sporotrichioides*) (fragment)  
 C;Species: *Fusarium sporotrichioides*  
 C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001  
 C;Accession: PA0060  
 R;Chow, L.P.; Fukaya, N.; Sugitara, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.  
 submitted to JIPID, October 1994  
 A;Description: Two dimensional polyacrylamide gel electrophoresis of *Fusarium sporotrichioides*  
 A;Reference number: PA0051  
 A;Accession: PA0060  
 A;Molecule type: protein  
 A;Residues: 1-15 <CHO>

Query Match 16.7%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PLP 15  
 |||  
 Db 4 PLP 6

## RESULT 75

PA0106  
 protein QP200076 - fungus (*Fusarium sporotrichioides*) (fragment)  
 C;Species: *Fusarium sporotrichioides*  
 C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001  
 C;Accession: PA0106  
 R;Chow, L.P.; Fukaya, N.; Sugitara, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.  
 submitted to JIPID, October 1994  
 A;Description: Two dimensional polyacrylamide gel electrophoresis of *Fusarium sporotrichioides*  
 A;Reference number: PA0051  
 A;Accession: PA0106  
 A;Molecule type: protein  
 A;Residues: 1-15 <CHO>

Query Match 16.7%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LTL 4  
 |||  
 Db 6 LTL 8

Search completed: November 25, 2003, 19:36:09  
 Job time : 13.3488 secs



GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: November 25, 2003, 18:17:40 ; Search time 6.38372 Seconds  
(without alignments)  
132.600 Million cell updates/sec

Title: US-09-641-801-23

Perfect score: 18  
Sequence: 1 SLTLTDVKEHLPLPLVQ 18

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	22.2	13	1	TEJA_RANJA
2	4	22.2	17	1	PH3_PERAM
3	4	22.2	20	1	LPFR_BACST
4	3	16.7	8	1	ALL6_CDPPO
5	3	16.7	10	1	ESL_LACCA
6	3	16.7	10	1	NS1_MYCTU
7	3	16.7	10	1	URE3_MORMO
8	3	16.7	11	1	TIN4_HOPTI
9	3	16.7	12	1	PPK4_PERAM
10	3	16.7	12	1	TIN2_HOPTI
11	3	16.7	12	1	TIN3_HOPTI
12	3	16.7	12	1	TM2A_METWA
13	3	16.7	13	1	ACT7_SOYBN
14	3	16.7	13	1	CRBL_VESCR
15	3	16.7	13	1	CRTC_RANES
16	3	16.7	13	1	FR12_PEA
17	3	16.7	13	1	HPB9_RANES
18	3	16.7	13	1	IDHP_RAT
19	3	16.7	13	1	TEMA_RANTE
20	3	16.7	13	1	TEMF_RANTE
21	3	16.7	14	1	CRBL_VESOR
22	3	16.7	14	1	ECDC_LYMDI
23	3	16.7	15	1	CYSK_GLOPA
24	3	16.7	15	1	GTS_ASADI
25	3	16.7	15	1	ONC1_ONCMY
26	3	16.7	15	1	UC29_MAIZE
27	3	16.7	16	1	ARCD_PSEPU
28	3	16.7	16	1	FIBA_MELME
29	3	16.7	16	1	IBPA_RIG
30	3	16.7	16	1	MMPA_SOLTU
31	3	16.7	17	1	ACT6_SOYBN
32	3	16.7	17	1	EPG_THEAQ
33	3	16.7	18	1	RL23_HALCU

34	3	16.7	18	1	UC21_MAIZE
35	3	16.7	19	1	HI790_RAT
36	3	16.7	19	1	LANA_ACTIG
37	3	16.7	19	1	LPGE_ECOLI
38	3	16.7	19	1	MIFB_TRISP
39	3	16.7	20	1	FIBB_SHEEP
40	3	16.7	20	1	FRHA_METBA
41	3	16.7	20	1	HETI_RADMG
42	3	16.7	20	1	M117_BOVIN
43	3	16.7	20	1	TENA_ACTTE
44	3	16.7	20	1	TENB_ACTTE
45	3	16.7	20	1	TL22_SFIOL
46	3	16.7	20	1	YPRB_SERMA
47	2	11.1	5	1	BIOA_CITFR
48	2	11.1	5	1	PRCT_PERAM
49	2	11.1	6	1	TMOF_SARBU
50	2	11.1	6	1	TRPI_PSEPU
51	2	11.1	6	1	VP19_HSV1K
52	2	11.1	7	1	CCFI_ENTFA
53	2	11.1	7	1	MNFI_LEPDE
54	2	11.1	7	1	UN06_PINPS
55	2	11.1	8	1	ACT_CARMA
56	2	11.1	8	1	AKH_TABAT
57	2	11.1	8	1	CAD1_ENTFA
58	2	11.1	8	1	COM2_CONPU
59	2	11.1	8	1	CPD1_ENTFA
60	2	11.1	8	1	HTF2_PERAM
61	2	11.1	8	1	PLP_BRANA
62	2	11.1	8	1	PPK3_PERAM
63	2	11.1	8	1	RT34_BOVIN
64	2	11.1	8	1	UPAA_HUMAN
65	2	11.1	9	1	ALC_CHLRE
66	2	11.1	9	1	BUK_CLOPA
67	2	11.1	9	1	FAR5_PANRE
68	2	11.1	9	1	FAR5_PENMO
69	2	11.1	9	1	FAR9_ASCSU
70	2	11.1	9	1	FIBB_MAFPU
71	2	11.1	9	1	MGMT_BOVIN
72	2	11.1	9	1	MOSH_CLYJA
73	2	11.1	9	1	OXYA_SQUAC
74	2	11.1	9	1	OXYT_RABIT
75	2	11.1	9	1	PH1_LYCES
76	2	11.1	9	1	RT33_BOVIN
77	2	11.1	9	1	SAMP_MUSCA
78	2	11.1	9	1	TAL1_PICJA
79	2	11.1	9	1	TAL3_PICJA
80	2	11.1	9	1	UHA2_HUMAN
81	2	11.1	9	1	ULAD_HUMAN
82	2	11.1	9	1	ULAE_HUMAN
83	2	11.1	9	1	UPA3_HUMAN
84	2	11.1	9	1	UPA6_HUMAN
85	2	11.1	9	1	UPA7_HUMAN
86	2	11.1	10	1	AH3_PRUSE
87	2	11.1	10	1	AL19_CARMA
88	2	11.1	10	1	ANGT_BOVIN
89	2	11.1	10	1	ANGT_CHICK
90	2	11.1	10	1	APE_CARGI
91	2	11.1	10	1	BRK_ONCMY
92	2	11.1	10	1	CATB_SHEEP
93	2	11.1	10	1	COXA_ONCMY
94	2	11.1	10	1	COXK_ONCMY
95	2	11.1	10	1	FARP_LOCOMI
96	2	11.1	10	1	FARP_MANSE
97	2	11.1	10	1	GAJU_HUMAN
98	2	11.1	10	1	GON1_PETWA
99	2	11.1	10	1	GON2_CHEPR
100	2	11.1	10	1	GON3_ONCKE

ALIGNMENTS

RESULT 1

P80527	zea mays (m
P21794	rattus norv
P56650	actinoplane
P33236	escherichia
P81529	trichinella
P14470	ovis aries
P80489	methanosarc
P58689	radianthus
P35451	bos taurus
P30833	actinia ten
P30834	actinia ten
P82796	spinacia ol
P22581	serratia ma
P13071	citrobacter
P01373	periplaneta
P41495	sarcophaga
P36414	pseudomonas
P23210	herpes simp
P20104	enterococcu
P42984	leptinotars
P81675	pinus pinas
P80709	carcinus ma
P14595	tabanus atr
P13268	enterococcu
P58785	conus purpu
P13269	enterococcu
P04549	periplaneta
P81707	brassica na
P82618	periplaneta
P82929	bos taurus
P30096	homo sapien
P82678	chlamydomon
P81337	clostridium
P82661	panagrellus
P83320	penaeus mon
P43172	ascaris suu
P19345	macaca fusc
P29177	bos taurus
P19852	clypeaster
P42999	squalus aca
P32878	oryctolagus
P83380	lycopersico
P82926	bos taurus
P19095	mustelus ca
P17440	pichia jadi
P17441	pichia jadi
P40929	homo sapien
P31929	homo sapien
P31931	homo sapien
P30089	homo sapien
P30092	homo sapien
P30093	homo sapien
P29261	prunus sero
P81822	carcinus ma
P01017	bos taurus
P01018	gallus gall
P80474	capnocytoph
Q9prz1	oncorhynch
P83205	ovis aries
P83328	oncorhynch
P80332	oncorhynch
P38553	locusta mig
P18523	manduca sex
P01358	homo sapien
P04378	petromyzon
P80678	chelyosoma
P20367	oncorhynch

TEJA\_RANJA  
ID TEJA\_RANJA STANDARD; PRT; 13 AA.  
AC P83307;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Temporalin-1Ja.  
OS Rana japonica (Japanese reddish frog).  
OC Amphibia; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.  
OX NCBI\_TaxID=8402;  
RN [1]  
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
RC TISSUE=Skin secretion;  
RX MEDLINE=21826910; PubMed=11835990;  
RA Isaacson T., Soto A., Iwamuro S., Knoop F.C., Conlon J.M.;  
RT "Antimicrobial peptides with atypical structural features from the  
RL skin of the Japanese brown frog Rana japonica.";  
PEptides 23:419-425(2002).  
CC -!- FUNCTION: Antibacterial activity against the Gram-negative  
CC bacterium E.coli and the Gram-positive bacterium S.aureus.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
CC -!- MASS SPECTROMETRY: MW=1405; METHOD=Electrospray.  
CC -!- SIMILARITY: Belongs to the brevinin family.  
KW Amphibian defense peptide; Antibiotic; Amidation.  
FT MOD RES 13  
13  
SQ SEQUENCE 13 AA; 1407 MW; 3EF713EA610A2448 CRC64;  
Query Match 22.2%; Score 4; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 14 LPLV 17  
DB 2 LPLV 5

RESULT 2  
ID PH3\_PPRAM STANDARD; PRT; 17 AA.  
AC P82696;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DE Peptide hormone 3 (Pea-VEAacid 1).  
OS Periplaneta americana (American cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Blattodea;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
OC Blattidae; Periplaneta.  
OX NCBI\_TaxID=6978;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Abdominal perisymphathetic organs;  
RX MEDLINE=20140865; PubMed=10676456;  
RA Pradel R., Eckert M., Holman G.M.;  
RT "The unique neuropeptide pattern in abdominal perisymphathetic organs  
RT of insects.";  
RL Ann. N.Y. Acad. Sci. 897:282-290(1999).  
CC -!- FUNCTION: UNKNOWN.  
CC -!- MASS SPECTROMETRY: MW=1651.35; METHOD=MALDI.  
KW Neuropeptide.  
SQ SEQUENCE 17 AA; 1807 MW; 2374AC8B1F86E8EB CRC64;  
Query Match 22.2%; Score 4; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 LTLT 5  
DB 3 LTLT 6

RESULT 3  
ID LPTR\_BACST STANDARD; PRT; 20 AA.  
AC P05658;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-NOV-1988 (Rel. 09, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Tetracycline resistance leader peptide.  
GN TETL.  
OS Bacillus stearothermophilus,  
OS Bacillus cereus, and  
OS Staphylococcus hyicus.  
OG Plasmid pTHT15, Plasmid pBC16, and Plasmid pSTEL.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.  
OX NCBI\_TaxID=1422, 1396, 1284;  
RN [1]\_TaxID=1422, 1396, 1284;  
RP SEQUENCE FROM N.A.  
RC SPECIES=B.stearothermophilus; PLASMID=pTHT15;  
RX MEDLINE=86031344; PubMed=2996983;  
RA Hoshino T., Ikeda T., Tomizuka N., Furukawa K.;  
RT "Nucleotide sequence of the tetracycline resistance gene of pTHT15, a  
RT thermophilic Bacillus plasmid: comparison with staphylococcal Tcr  
RT controls.";  
RL Gene 37:131-138(1985).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC SPECIES=B.cereus; PLASMID=pBC16;  
RX MEDLINE=90221899; PubMed=2109312;  
RA Palva A., Vidgren G., Simonen M., Rintala H., Laamanen P.;  
RT "Nucleotide sequence of the tetracycline resistance gene of pBC16  
RT from Bacillus cereus.";  
RL Nucleic Acids Res. 18:1635-1635(1990).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC SPECIES=S.hyicus; PLASMID=pSTEL;  
RX MEDLINE=92321725; PubMed=1622166;  
RA Schwarz S., Cardoso M., Wegener H.C.;  
RT "Nucleotide sequence and phylogeny of the tet(L) tetracycline  
RT resistance determinant encoded by plasmid pSTEL from Staphylococcus  
RL Antimicrob. Agents Chemother. 36:580-588(1992).  
CC -----  
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CC -----  
DR EMBL; D000006; BAA00004.1; -;  
DR EMBL; M11036; AAA22850.1; -;  
DR EMBL; X51366; CAA35750.1; -;  
DR EMBL; X60828; CAA43219.1; -;  
DR PIR; S09233; LFBSTU.  
DR PIR; S23742; S23742.  
KW Leader peptide; Antibiotic resistance; plasmid.  
SQ SEQUENCE 20 AA; 2253 MW; 18D0F4A6CA231CA1 CRC64;  
Query Match 22.2%; Score 4; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SLTL 4  
DB 17 SLTL 20

RESULT 4  
ID ALL6\_CYPDPO STANDARD; PRT; 8 AA.  
AC P82157;  
DT 30-MAY-2000 (Rel. 39, Created)

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DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Cydiastatin 6.
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;
RN [1]
RP SEQUENCE
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Dave H., Johnson A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309(1997).
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 8
SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LPL 14
Db 1 LPL 3

RESULT 5
ESL LACCA
ID ESL LACCA STANDARD; PRT; 10 AA.
AC P81758;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Putative esterase/lipase (EC 3.1.1.-) (Fragment).
OS Lactobacillus casei
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1582;
RN [1]
RP SEQUENCE
RC STRAIN=IFPL731;
RA Lopez de Felipe F.;
RL Submitted (MAR-1999) to the SWISS-PROT data bank.
KW Hydrolase; Serine esterase.
FT NON TER 10
SQ SEQUENCE 10 AA; 1070 MW; 1C6132D732CAB1A0 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TDV 7
Db 4 TDV 6

RESULT 6
NS1 MYCTU
ID NS1 MYCTU STANDARD; PRT; 10 AA.
AC P81135;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 30 kDa non-secretory protein 1 (Fragment).
OS Mycobacterium tuberculosis
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]

DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Cydiastatin 6.
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;
RN [1]
RP SEQUENCE
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Dave H., Johnson A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309(1997).
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 8
SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LPL 14
Db 1 LPL 3

RESULT 5
ESL LACCA
ID ESL LACCA STANDARD; PRT; 10 AA.
AC P81758;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Putative esterase/lipase (EC 3.1.1.-) (Fragment).
OS Lactobacillus casei
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1582;
RN [1]
RP SEQUENCE
RC STRAIN=IFPL731;
RA Lopez de Felipe F.;
RL Submitted (MAR-1999) to the SWISS-PROT data bank.
KW Hydrolase; Serine esterase.
FT NON TER 10
SQ SEQUENCE 10 AA; 1070 MW; 1C6132D732CAB1A0 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TDV 7
Db 4 TDV 6

RESULT 6
NS1 MYCTU
ID NS1 MYCTU STANDARD; PRT; 10 AA.
AC P81135;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 30 kDa non-secretory protein 1 (Fragment).
OS Mycobacterium tuberculosis
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]

RP SEQUENCE
RC STRAIN=H37Rv;
RL Submitted (DEC-1997) to the SWISS-PROT data bank.
CC -1- CAUTION: We are unable to find this protein in the translation of
CC the genome of strain H37Rv.
FT NON TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1042 MW; 8767FE6AB2C73771 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 PLV 17
Db 4 PLV 6

RESULT 7
URE3 MORMO
ID URE3 MORMO STANDARD; PRT; 10 AA.
AC P17339;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Urease gamma subunit (EC 3.5.1.5) (6 kDa subunit) (Urea
DE amidohydrolase) (Fragment).
GN UREA.
OS Morganella morganii (Proteus morganii).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Morganella.
OX NCBI_TaxID=582;
RN [1]
RP SEQUENCE
RX MEDLINE=90264298; PubMed=2345135;
RA Hu L.-T., Nicholson E.B., Jones B.D., Lynch M.J., Mobley H.L.T.;
RT "Morganella morganii urease: purification, characterization, and
RT isolation of gene sequences.";
RL J. Bacteriol. 172:3073-3080(1990).
CC -1- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
CC -1- SUBUNIT: (ALPHA, BETA, GAMMA) (3) (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE UREASE GAMMA SUBUNIT FAMILY.
DR PIR; C35389; C35389.
KW Hydrolase.
FT NON TER 10
SQ SEQUENCE 10 AA; 1171 MW; 4B313BCB077771A7 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VEK 9
Db 8 VEK 10

RESULT 8
TIN4 HOPTI
ID TIN4 HOPTI STANDARD; PRT; 11 AA.
AC P82654;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tigerin-4.
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae;
OC Hoplobatrachus.
OX NCBI_TaxID=103373;
RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
RC TISSUE=Skin secretion;

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RX PubMed=11031261;
RA Purna Sai K., Jagannadham M.V., Vairamani M., Raju N.P.,
RA Devi A.S., Nagaraj R., Sitaram N.;
RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
RT tigerina.";
RL J. Biol. Chem. 276:2701-2707(2001).
CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST B.SUBTILIS, E.COLI,
CC S.AUREUS, M.LUTEUS, P.PUTIDA AND S.CEREVISIAE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=1247; METHOD=MALDI.
KW Amphibian defense peptide; Antibiotic.
FT DISULFID 3 11
SQ SEQUENCE 11 AA; 1248 MW; 117D8EFD37605DCB CRC64;

Query Match 16.7%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLP 15
DB 7 PLP 9

RESULT 9
ID PPK4 PERAM STANDARD; PRT; 12 AA.
AC P82619;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinin-4 (Pea-PK-4) (YXPRU-amide).
OS Periplaneta americana (American cockroach).
CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
CC Blattidae; Periplaneta.
CC NCBI_TaxID=6978;
RN [1]
SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
TISSUE=Retrocerebral complex;
RX MEDLINE=99212469; PubMed=10196736;
RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;
RT "Differential distribution of pyrokinin-isoforms in cerebral and
RT abdominal neurohemal organs of the American cockroach.";
RL Insect Biochem. Mol. Biol. 29:139-144(1999).
RN [2]
TISSUE SPECIFICITY.
RX MEDLINE=20189894; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Tagma-specific distribution of FXPRlamides in the nervous system of
RT the American cockroach.";
RL J. Comp. Neurol. 419:352-363(2000).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.
CC -!- MASS SPECTROMETRY: MW=1147.9; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD RES 12 12
SQ SEQUENCE 12 AA; 1449 MW; FA7A3049FF42CAA1 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 HLP 13
DB 2 HLP 4

RESULT 10
ID TIN2 HOPTI STANDARD; PRT; 12 AA.

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AC P82652;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tigerin-2.
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae;
CC Hoplobatrachus.
CC NCBI_TaxID=103373;
RN [1]
SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
RP TISSUE=Skin secretion;
RX PubMed=11031261;
RA Purna Sai K., Jagannadham M.V., Vairamani M., Raju N.P.,
RA Devi A.S., Nagaraj R., Sitaram N.;
RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
RT tigerina.";
RL J. Biol. Chem. 276:2701-2707(2001).
CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST B.SUBTILIS, E.COLI,
CC S.AUREUS, M.LUTEUS, P.PUTIDA AND S.CEREVISIAE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=1368; METHOD=MALDI.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT DISULFID 3 11
FT MOD RES 12 12
SQ SEQUENCE 12 AA; 1369 MW; C2627D8EFD37605D CRC64;

Query Match 16.7%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLP 15
DB 7 PLP 9

RESULT 11
ID TIN3 HOPTI STANDARD; PRT; 12 AA.
AC P82653;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tigerin-3.
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae;
CC Hoplobatrachus.
CC NCBI_TaxID=103373;
RN [1]
SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
RP TISSUE=Skin secretion;
RX PubMed=11031261;
RA Purna Sai K., Jagannadham M.V., Vairamani M., Raju N.P.,
RA Devi A.S., Nagaraj R., Sitaram N.;
RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
RT tigerina.";
RL J. Biol. Chem. 276:2701-2707(2001).
CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST B.SUBTILIS, E.COLI,
CC S.AUREUS, M.LUTEUS, P.PUTIDA AND S.CEREVISIAE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=1409; METHOD=MALDI.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT DISULFID 3 11
FT MOD RES 12 12
SQ SEQUENCE 12 AA; 1411 MW; C0717D8EFD37605D CRC64;

Query Match 16.7%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      13 PLP 15
      |||
Db      7 PLP 9

RESULT 12
TM2A METMA
ID      TW2A METMA      STANDARD;      PRT;      12 AA.
AC      PS0652;
DT      01-OCT-1996 (Rel. 34, Created)
DT      01-OCT-1996 (Rel. 34, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Alternative tetrahydromethanopterin S-methyltransferase 28 kDa subunit
DE      (EC 2.1.1.86) (N5-methyltetrahydromethanopterin--coenzyme M
DE      methyltransferase 28 kDa subunit) (Fragment).
OS      Methanosarcina mazei (Methanosarcina frisia).
OS      Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
OC      Methanosarcinales; Methanosarcinaceae; Methanosarcina.
OX      NCBI_TaxID=2209;
RN      [1]
RP      SEQUENCE.
RC      STRAIN=Goel / Go1 / ATCC BAA-199 / DSM 3647 / OCM 88;
RX      MEDLINE=96370840; PubMed=9774736;
RA      Lienard T., Becher B., Marschall M., Bowien S., Gottschalk G.;
RT      "Sodium ion translocation by N5-methyltetrahydromethanopterin:
RT      coenzyme M methyltransferase from Methanosarcina mazei Go1
RT      reconstituted in ether lipid liposomes.";
RL      Eur. J. Biochem. 239:857-864 (1996).
CC      -!- FUNCTION: THIS ENZYME COMPLEX CATALYZES AN INTERMEDIATE STEP IN
CC      METHANOGENESIS, THE FORMATION OF METHYL-COENZYME M AND
CC      TETRAHYDROMETHANOPTERIN FROM COENZYME M AND N5-METHYL-
CC      TETRAHYDROMETHANOPTERIN.
CC      -!- CATALYTIC ACTIVITY: 5-methyl-5,6,7,8-tetrahydromethanopterin + 2-
CC      mercaptoethanesulfonate = 5,6,7,8-tetrahydromethanopterin + 2-
CC      (methylthio)ethanesulfonate.
CC      -!- SUBUNIT: COMPOSED OF SIX DIFFERENT SUBUNITS.
CC      -!- SUBCELLULAR LOCATION: Integral membrane protein.
KW      Transferase; Methyltransferase; Transmembrane; Methanogenesis.
FT      NON TER 12
FT      SEQUENCE 12 AA; 1321 MW; 6DE4A5766232D76B CRC64;

QY      8 EXL 10
      |||
Db      2 EXL 4

RESULT 13
ACT7 SOYBN
ID      ACT7 SOYBN      STANDARD;      PRT;      13 AA.
AC      P15987;
DT      01-APR-1990 (Rel. 14, Created)
DT      01-APR-1990 (Rel. 14, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      Actin 7 (Fragment).
GN      SACT.
OS      Glycine max (Soybean).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC      eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX      NCBI_TaxID=3847;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=cv. Wayne;
RX      MEDLINE=91346640; PubMed=2102831;
RA      Pearson L., Meagher R.B.;
RT      "Diverse soybean actin transcripts contain a large intron in the 5'
RT      untranslated leader: structural similarity to vertebrate muscle actin
RT      genes.";

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RL      Plant Mol. Biol. 14:513-526(1990).
CC      -!- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED
CC      IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBIQUITOUSLY EXPRESSED
CC      IN ALL EUKARYOTIC CELLS.
CC      -!- FUNCTION: ESSENTIAL COMPONENT OF CELL CYTOSKELETON; PLAYS AN
CC      IMPORTANT ROLE IN CYTOPLASMIC STREAMING, CELL SHAPE DETERMINATION,
CC      CELL DIVISION, ORGANELLE MOVEMENT AND EXTENSION GROWTH.
CC      -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC      -!- MISCELLANEOUS: THERE ARE AT LEAST 16 ACTIN GENES IN SOYBEAN.
CC      -!- SIMILARITY: Belongs to the actin family.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; X17120; CAA34980.1; -
DR      PIR; S15755; S15755.
DR      InterPro; IPR004001; Actin.
DR      InterPro; IPR004000; Actin-like.
DR      PROSITE; PS00406; ACTINS_1; PARTIAL.
DR      PROSITE; PS00432; ACTINS_2; PARTIAL.
DR      PROSITE; PS01132; ACTINS_ACT LIKE; PARTIAL.
KW      Structural protein; Multigene family.
FT      NON TER 13
FT      SEQUENCE 13 AA; 1420 MW; 8BEFF3C36D4FD05A CRC64;

Query Match 16.7%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 PLV 17
      |||
Db      9 PLV 11

RESULT 14
CRBL VESCR
ID      CRBL VESCR      STANDARD;      PRT;      13 AA.
AC      P01518;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Crabrolin.
OS      Vespa crabro (European hornet).
OC      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC      Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC      Vespidae; Vespinae; Vespa.
OX      NCBI_TaxID=7445;
RN      [1]
RP      SEQUENCE.
RC      TISSUE=Venom;
RX      MEDLINE=84289390; PubMed=6206053;
RA      Argiolas A., Pisano J.J.;
RT      "Isolation and characterization of two new peptides, mastoparan C and
RT      crabrolin, from the venom of the European hornet, Vespa crabro.";
RL      J. Biol. Chem. 259:10106-10111 (1984).
RN      [2]
RP      SYNTHESIS, AND ANTIMICROBIAL ACTIVITY.
RX      MEDLINE=97419326; PubMed=9273892;
RA      Krishnakumari V., Nagaraj R.;
RT      "Antimicrobial and hemolytic activities of crabrolin, a 13-residue
RT      peptide from the venom of the European hornet, Vespa crabro, and its
RT      analogs.";
RL      J. Pept. Res. 50:88-93 (1997).
CC      -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
CC      of neutrophils. Has antimicrobial and hemolytic activity.
DR      PIR; A01781; JZVHP1.
KW      Mast cell degranulation; Chemotaxis; Amidation; Antibiotic.
FT      MOD_RES 13
FT      SEQUENCE 13

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SQ SEQUENCE 13 AA; 1497 MW; 515EF8FCEA8D2407 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 LPL 14  
 ||||  
 DB 2 LPL 4

RESULT 15  
 CRIC\_RANES  
 ID CRIC\_RANES STANDARD; PRT; 13 AA.  
 AC P31832;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Calreticulin (Major microsomal calcium-binding protein) (Fragment).  
 OS Rana esculenta (Edible frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.  
 OX NCBI\_TaxID=8401;  
 RN [1]  
 RP SEQUENCE.

RC TISSUE=Brain;  
 RX MEDLINE=91207333; PubMed=2018493;  
 RA Treves S., Zorzato F., Chiozzi P., Melandri P., Volpe P., Pozzan T.;  
 RT "Frog brain expresses a 60 KDa Ca2+ binding protein similar to  
 RT mammalian calreticulin";  
 RL Biochem. Biophys. Res. Commun. 175:444-450 (1991).  
 CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND  
 CC LOW AFFINITY CALCIUM-BINDING SITES.  
 CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
 CC -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.  
 DR InterPro: IPR001580; Calreticulin.  
 DR PROSITE; PS00803; CALRETICULIN 1; PARTIAL.  
 DR PROSITE; PS00804; CALRETICULIN 2; PARTIAL.  
 DR PROSITE; PS00805; CALRETICULIN REPEAT; PARTIAL.  
 KW Endoplasmic reticulum; Calcium-binding.  
 FT NON\_TER 13  
 SQ SEQUENCE 13 AA; 1510 MW; D0F62AD09EAEE339 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 PLV 17  
 ||||  
 DB 2 PLV 4

RESULT 16  
 FR12\_PEA  
 ID FR12\_PEA STANDARD; PRT; 13 AA.  
 AC P83445;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ferritin 2, chloroplast (Fragment).  
 OS Pisum sativum (Garden pea).  
 CC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 CC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.  
 OX NCBI\_TaxID=3888;  
 RN [1]  
 RP SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.

RC STRAIN=cv. Laxton's Progress; TISSUE=Leaf;  
 RA Shingles R., McCarty R.E.;  
 RL Submitted (SEP-2002) to the SWISS-PROT data bank.  
 CC -!- FUNCTION: Ferritin is an intracellular molecule that stores iron  
 CC in a soluble, nontoxic, readily available form. The functional  
 CC molecule, which is composed of 24 chains, is roughly spherical and

CC contains a central cavity into which the polymeric ferric iron  
 CC core is deposited.  
 CC -!- SUBCELLULAR LOCATION: Chloroplast (inner envelope membrane), and  
 CC other plastids.  
 CC -!- TISSUE SPECIFICITY: Leaves.  
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this protein is:  
 CC 4.74, its MW is: 25.7 kDa.  
 CC -!- SIMILARITY: BELONGS TO THE FERRITIN FAMILY.  
 DR InterPro: IPR001519; Ferritin.  
 DR PROSITE; PS00204; FERRITIN 2; PARTIAL.  
 DR PROSITE; PS00540; FERRITIN 1; PARTIAL.  
 DR PROSITE; PS0905; FERRITIN LIKE; PARTIAL.  
 KW Iron storage; Iron; Metal-binding; Chloroplast.  
 FT NON\_TER 13  
 SQ SEQUENCE 13 AA; 1246 MW; 26C9DC25F334ADC7 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TLT 5  
 ||||  
 DB 8 TLT 10

RESULT 17  
 HPB9\_RANES  
 ID HPB9\_RANES STANDARD; PRT; 13 AA.  
 AC P32416;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-OCT-1993 (Rel. 27, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Hemolytic protein B9 (Fragment).  
 OS Rana esculenta (Edible frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.  
 OX NCBI\_TaxID=8401;  
 RN [1]  
 RP SEQUENCE.

RC TISSUE=Skin secretion;  
 RX MEDLINE=90198965; PubMed=2317508;  
 RA Simmaco M., de Biase D., Severini C., Aita M., Erspamer G.F.,  
 RA Barra D., Bossa F.;  
 RT "Purification and characterization of bioactive peptides from skin  
 RT extracts of Rana esculenta";  
 RL Biochim. Biophys. Acta 1033:318-323 (1990).  
 CC -!- FUNCTION: Shows hemolytic activity.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 DR PIR; S09019; S09019  
 KW Amphibian defense peptide; Amidation; Hemolysis.  
 FT MOD\_RES 13  
 FT NON\_TER 13  
 SQ SEQUENCE 13 AA; 1402 MW; C6B41A765DF9287D CRC64;

Query Match 16.7%; Score 3; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 LPL 14  
 ||||  
 DB 2 LPL 4

RESULT 18  
 IDHP\_RAT  
 ID IDHP\_RAT STANDARD; PRT; 13 AA.  
 AC P56574;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Isocitrate dehydrogenase [NADP], mitochondrial (EC 1.1.1.42)  
 CC (Oxalosuccinate decarboxylase) (IDH) (NADP+-specific IDH) (IDP) (ICD-

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DE M) (Fragment).
GN IDH2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE.
RC STRAIN=Wistar; TISSUE=Heart;
RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
RA Jungblut P.R.;
RL Submitted (SEP-1998) to the SWISS-PROT data bank.
CC -!- FUNCTION: PLAYS A ROLE IN INTERMEDIARY METABOLISM AND ENERGY
CC PRODUCTION. IT MAY TIGHTLY ASSOCIATE OR INTERACT WITH THE PYRUVATE
CC DEHYDROGENASE COMPLEX (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: Isocitrate + NADP(+) = 2-oxoglutarate + CO(2)
CC + NADPH.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN
CC (SPOT P8) IS: 9.0, ITS MW IS: 42 kDa.
CC -!- SIMILARITY: BELONGS TO THE ISOCITRATE AND ISOPROPYLMALATE
CC DEHYDROGENASES FAMILY.
CC InterPro: IPR001804; Isochr.
DR PROSITE; PS00470; IDH_IDH2; PARTIAL.
KW Oxidoreductase; NADP; Glyoxylate bypass; Tricarboxylic acid cycle;
KW Mitochondrion.
FT NON TER 13
FT SEQUENCE 13 AA; 1526 MW; 5FBB1031723E02C3 CRC64;
SQ
Query Match 16.7%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VEK 9
Db 7 VEK 9

RESULT 19
TEMA_RANTE
ID TEMA_RANTE STANDARD; PRT; 13 AA.
AC P56917;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Temporin A.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8407;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Skin secretion;
RX MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Barra D.;
RT "Temporins, antimicrobial peptides from the European red frog Rana
RT temporaria."
RL Eur. J. Biochem. 242:788-792(1996).
CC -!- FUNCTION: Has antibacterial activity against Gram-positive
CC bacteria.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the brevinin family.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD RES 13
FT SEQUENCE 13 AA; 1398 MW; 2653612B9DECD408 CRC64;
SQ
Query Match 16.7%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VEK 9
Db 7 VEK 9

RESULT 20
TEMA_RANTE
ID TEMA_RANTE STANDARD; PRT; 13 AA.
AC P56921;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Temporin F.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8407;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Barra D.;
RT "Temporins, antimicrobial peptides from the European red frog Rana
RT temporaria."
RL Eur. J. Biochem. 242:788-792(1996).
CC -!- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-NEGATIVE AND
CC GRAM-POSITIVE BACTERIA.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the brevinin family.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD RES 13
FT SEQUENCE 13 AA; 1370 MW; 2653612B9DECC338 CRC64;
SQ
Query Match 16.7%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LPL 14
Db 2 LPL 4

RESULT 21
CRBL_VESOR
ID CRBL_VESOR STANDARD; PRT; 14 AA.
AC P17236;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Histamine releasing peptide II (HR-II).
OS Vespa orientalis (Oriental hornet).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=7447;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Mitroshnikov A.I., Snezhkova L.G., Nazimov I.V., Reshetova O.I.,
RA Rosynov B.V., Gushchin I.S.;
RT "Structure and properties of histamine releasing peptides from the
RT venom of Vespa orientalis hornet."
RL Bioorg. Khim. 7:1467-1477(1981).
CC -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
CC of neutrophils.
DR PIR; JN0390; JN0390.
KW Mast cell degranulation; Chemotaxis; Amidation.
FT MOD RES 14
FT SEQUENCE 14 AA; 1524 MW; 22015B4A6CEDFD38 CRC64;
SQ
Query Match 16.7%; Score 3; DB 1; Length 14;

```

Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPL 14  
Db 2 LPL 4

## RESULT 22

ECDC LYMDI STANDARD; PRT; 14 AA.  
AC P80940;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE Testis ecdysiotropin peptide C (TE).  
OS Lymantria dispar (Gypsy moth).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;  
OC Lymantriidae; Lymantria.  
OX NCBI\_TaxID=13123;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Brain;  
RX MEDLINE=97387807; PubMed=9243792;  
RA Loeb M.J., Wagner R.M., Woods C.W., Gelman D.G., Harrison D.,  
RA Bell R.A.;  
RT "Naturally occurring analogs of Lymantria testis ecdysiotropin, a  
RT gonadotropin isolated from brains of Lymantria dispar pupae."  
RL Arch. Insect Biochem. Physiol. 36:37-50(1997)  
CC -!- FUNCTION: STIMULATES SYNTHESIS OF ECDYSTEROID IN THE TESTES  
CC -!- OF LARVAE AND PUPAE.  
SQ SEQUENCE 14 AA; 1553 MW; 17F479531A685CBB CRC64;

Query Match 16.7%; Score 3; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLP 15  
Db 9 PLP 11

## RESULT 23

CYSK CLOPA STANDARD; PRT; 15 AA.  
AC P81340;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Cysteine synthase (EC 4.2.99.8) (O-acetylserine sulphydrylase) (O-acetylserine (thiol)-lyase) (CSase) (CP 27) (Fragment).  
GN CYSK.  
OS Clostridium pasteurianum.  
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
OC Clostridium.  
OX NCBI\_TaxID=1501;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=W5;  
RX MEDLINE=98291870; PubMed=9629918;  
RA Flengsrud R., Skjeldal L.;  
RT "Two-dimensional gel electrophoresis separation and N-terminal  
RT sequence analysis of proteins from Clostridium pasteurianum W5."  
RL Electrophoresis 19:802-806(1998).  
CC -!- CATALYTIC ACTIVITY: O(3)-acetyl-L-serine + H(2)S = L-cysteine +  
CC acetate.  
CC -!- COFACTOR: Pyridoxal phosphate (By similarity).  
CC -!- PATHWAY: Cysteine biosynthesis.  
CC -!- SUBUNIT: Homodimer (By similarity).  
CC -!- SIMILARITY: BELONGS TO THE CYSTEINE SYNTHASE/CYSTATHIONINE BETA-  
CC SYNTHASE FAMILY.  
DR InterPro; IPR001216; Cys\_synthase.

DR PROSITE; PS00901; CYS SYNTHASE; PARTIAL.  
KW Lyase; Cysteine biosynthesis; Pyridoxal phosphate.  
FT NON\_TER 15  
SQ SEQUENCE 15 AA; 1625 MW; 019658289671A352 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PLV 17  
Db 10 PLV 12

## RESULT 24

GTS ASADI STANDARD; PRT; 15 AA.  
AC P83246;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Glutathione S-transferase (EC 2.5.1.18) (GST class-sigma) (adGST) (Fragment).  
DE (Fragment).  
OS Asaphis dichotoma.  
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroidea;  
OC Tellinoidea; Psammobiidae; Asaphis.  
OX NCBI\_TaxID=184428;  
RN [1]  
RP SEQUENCE, FUNCTION, SUBUNIT, MASS SPECTROMETRY, AND CIRCULAR DICHROISM ANALYSIS.  
RC TISSUE=Intestine, and Liver;  
RX MEDLINE=22135252; PubMed=12139969;  
RA Yang H.-L., Nie L.-J., Zhu S.-G., Zhou X.-W.;  
RT "Purification and characterization of a novel glutathione S-  
RT transferase from Asaphis dichotoma."  
RL Arch. Biochem. Biophys. 403:202-208(2002).  
CC -!- FUNCTION: Has a strong specific activity toward 1-chloro-2,4-  
CC dinitrobenzene and ethanynic acid.  
CC -!- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione.  
CC -!- SUBUNIT: Homodimer.  
CC -!- MASS SPECTROMETRY: MW=23138; METHOD=MALDI.  
CC -!- MISCELLANEOUS: In A. dichotoma there are at least two isozymes of  
CC glutathione S-transferase.  
CC -!- MISCELLANEOUS: Optimal pH is 8.5 with 1-chloro-2,4-dinitrobenzene  
CC as the substrate.  
CC -!- MISCELLANEOUS: The Km for 1-chloro-2,4-dinitrobenzene and  
CC glutathione are 0.68 +/-0.05 and 0.106 +/-0.005 mM, and the Vmax  
CC is 0.1446 +/-0.0072 and 0.033 +/-0.002 mmol/min x mg enzyme,  
CC respectively.  
CC -!- SIMILARITY: BELONGS TO THE GST SUPERFAMILY. SIGMA FAMILY.  
DR GO; GO:0004364; P:Glutathione transferase activity; NAS.  
DR GO; GO:0006803; P:Glutathione conjugation reaction; NAS.  
KW Transferase.  
FT NON\_TER 15  
SQ SEQUENCE 15 AA; 1767 MW; CB3E4BF92D3CB0B9 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KIH 11  
Db 4 KIH 6

## RESULT 25

ONCL ONCMY STANDARD; PRT; 15 AA.  
AC P83287;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Oncorhynchus 1 (Fragment).



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OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC TISSUE=Skin;
RA Fernandes J.M.O., Smith V.J., Kemp G.D.;
RT "Purification and N-terminal sequencing of a 3 kDa antibacterial
RT peptide from skin secretions of rainbow trout.";
RL Submitted (MAY-2002) to the SWISS-PROT data bank.
CC -!- FUNCTION: Has antibacterial activity against Gram-positive
CC bacterium P.citreus.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003795; P:antimicrobial peptide activity; NAS.
DR GO: GO:0006805; P:xenobiotic metabolism; NAS.
KW Antibiotic.
FT UNSURE 4 4 OR G.
FT NON_TER 9 9 OR T.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1601 MW; 43C25028DBC12B7C CRC64;

Query Match 16.7%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DVE 8
Db 9 DVE 11

RESULT 26
UC29_MAIZE STANDARD; PRT; 15 AA.
ID UC29_MAIZE
AC P80635;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 45)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.9, ITS MW IS: 37.6 kDa.
DR Maize-2DPAGE; P80635; COLEOPTILE.
DR MaizeDB; 123960; -.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1679 MW; 3D53086B16018BC1 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 PLV 17
Db 8 PLV 10

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RESULT 27
ARCD_PSEPU STANDARD; PRT; 16 AA.
ID ARCD_PSEPU
AC P41147;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Arginine/ornithine antiporter (Fragment).
GN ARCD.
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 4359;
RA Wilson S.D., Wang M., Filpula D.;
RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: CATALYZES AN ELECTRONEUTRAL EXCHANGE BETWEEN ARGININE
CC AND ORNITHINE TO ALLOW HIGH-EFFICIENCY ENERGY CONVERSION IN THE
CC ARGININE DEIMINASE PATHWAY.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (Potential).
CC -!- SIMILARITY: BELONGS TO THE ARCD/CADB/GERAB/LYSI FAMILY OF
CC PERMEASES.
CC -----
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CC -----
DR EMBL; U07185; AAA16963.1; -.
KW Transport; Antiport; Amino-acid transport; Transmembrane;
KW Inner membrane.
FT NON_TER 1 1
SQ SEQUENCE 16 AA; 1644 MW; 90B48A7C8FAA9705 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred.No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LTL 4
Db 14 LTL 16

RESULT 28
FIBA_MELEME STANDARD; PRT; 16 AA.
ID FIBA_MELEME
AC P14456;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Meles meles (Eurasian badger).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Melinae;
OC Meles.
OX NCBI_TaxID=9662;
RN [1]
RP SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.

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CC -|- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY  
CC THROMBIN, WHICH CLAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA  
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES  
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.  
KW Blood coagulation; Plasma. FIBRINOPEPTIDE A.  
FT PEPTIDE 1 16  
FT NON\_TER 16  
SQ SEQUENCE 16 AA; 1708 MW; 09433547919EC7C4 CRC64;  
  
Query Match 16.7%; Score 3; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 TDV 7  
DB 1 TDV 3  
  
RESULT 29  
ID TBP4\_PIG STANDARD; PRT; 16 AA.  
AC P24954;  
DT 01-MAR-1992 (Rel. 21, Created)  
DT 01-MAR-1992 (Rel. 21, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Insulin-like growth factor binding protein 4 (IGFBP-4) (IBP-4)  
DE (IGF-binding protein 4) (Fragment).  
GN IGFBP4.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE  
RX MEDLINE=92109718; PubMed=1722398;  
RA Coleman M.E., Pan Y.-C.E., Scherton T.D.;  
RT "Identification and NH2-terminal amino acid sequence of three  
RT insulin-like growth factor-binding proteins in porcine serum.";  
RL Biochem. Biophys. Res. Commun. 181:1131-1136(1991).  
CC -|- FUNCTION: IGF-BINDING PROTEINS PROLONG THE HALF-LIFE OF THE IGFs  
CC AND HAVE BEEN SHOWN TO EITHER INHIBIT OR STIMULATE THE GROWTH  
CC PROMOTING EFFECTS OF THE IGFs ON CELL CULTURE. THEY ALTER THE  
CC INTERACTION OF IGFs WITH THEIR CELL SURFACE RECEPTORS.  
CC -|- SUBCELLULAR LOCATION: Secreted.  
CC -|- SIMILARITY: Contains 1 IGFBP domain.  
CC -|- SIMILARITY: Contains 1 thyroglobulin type-I domain.  
DR PIR; JH0517; JH0517.  
DR InterPro; IPR000867; Insl\_gro\_fac\_pr.  
DR InterPro; IPR000716; Thyroglobulin\_1.  
DR PROSITE; PS00222; IGF BINDING; PARTIAL.  
DR PROSITE; PS00484; THYROGLOBULIN\_1; PARTIAL.  
KW Growth factor binding.  
FT NON\_TER 16  
SQ SEQUENCE 16 AA; 1799 MW; 40988840096655E2 CRC64;  
  
Query Match 16.7%; Score 3; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 8 EKL 10  
DB 12 EKL 14  
  
RESULT 30  
ID MMFX\_SOLTU STANDARD; PRT; 16 AA.  
AC P80501;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE Unidentified mitochondrial matrix protein (Fragment).  
OS Solanum tuberosum (Potato).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; Lamiales; Solanales; Solanaceae; Solanum.  
OX NCBI\_TaxID=4113;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Tuber;  
RX MEDLINE=97077345; PubMed=8919912;  
RA Jansch L., Kruft V., Schmitz U.K., Braun H.P.;  
RT "New insights into the composition, molecular mass and stoichiometry  
RT of the protein complexes of plant mitochondria.";  
RL Plant J. 9:357-368(1996).  
CC -|- SUBCELLULAR LOCATION: Mitochondrial matrix.  
KW Mitochondrion.  
FT NON\_TER 16  
SQ SEQUENCE 16 AA; 1768 MW; C58D4DB48AA18B8D CRC64;  
  
Query Match 16.7%; Score 3; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 7 VEK 9  
DB 9 VEK 11  
  
RESULT 31  
ID ACT6\_SOYBN STANDARD; PRT; 17 AA.  
AC P15986;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Actin 6 (Fragment).  
GN SACS.  
OS Glycine max (Soybean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosid1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
OX NCBI\_TaxID=3847;  
RN SEQUENCE FROM N.A.  
RC STRAIN=cv. Wayne;  
RX MEDLINE=91346640; PubMed=2102831;  
RA Pearson L., Meagher R.B.;  
RT "Diverse soybean actin transcripts contain a large intron in the 5'  
RT untranslated leader: structural similarity to vertebrate muscle actin  
RT genes.";  
RL Plant Mol. Biol. 14:513-526(1990).  
CC -|- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED  
CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBQUITOUSLY EXPRESSED  
CC IN ALL EUKARYOTIC CELLS.  
CC -|- FUNCTION: ESSENTIAL COMPONENT OF CELL CYTOSKELETON; PLAYS AN  
CC IMPORTANT ROLE IN CYTOPLASMIC STREAMING, CELL SHAPE DETERMINATION,  
CC CELL DIVISION, ORGANELLE MOVEMENT AND EXTENSION GROWTH.  
CC -|- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -|- MISCELLANEOUS: THERE ARE AT LEAST 16 ACTIN GENES IN SOYBEAN.  
CC -|- SIMILARITY: Belongs to the actin family.  
CC -----  
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CC -----  
DR EMBL; X17119; CAA34979.1; -.  
DR PIR; S15754; S15754. Actin.  
DR InterPro; IPR004001; Actin.  
DR Pfam; PF00022; actin; 1.  
DR PROSITE; PS00406; ACTINS\_1; PARTIAL.

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DR PROSITE; PS00432; ACTINS_2; PARTIAL.
DR PROSITE; PS01132; ACTINS_ACT LIKE; PARTIAL.
KW Structural protein; Multigene family.
FT NON_TER 17
SQ SEQUENCE 17 AA; 1749 MW; 38F4970D4BEFF3C3 CRC64;

Query Match
Best Local Similarity 16.7%; Score 3; DB 1; Length 17;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PLV 17
DB 9 PLV 11

RESULT 32
EFG_THEAQ STANDARD; PRT; 17 AA.
AC Q01697;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Elongation factor G (EF-G) (Fragment).
GN FUS1 OR FUS.
OS Thermus aquaticus.
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=271;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EP 00276;
RX MEDLINE=92362620; PubMed=1499561;
RA Voss R.H., Hartmann R.K., Lippmann C., Alexander C., Jahn O.,
RA Erdmann V.;
RT "Sequence of the tufA gene encoding elongation factor EF-Tu from
RT Thermus aquaticus and overproduction of the protein in Escherichia
RT coli.";
RL Eur. J. Biochem. 207:839-846(1992).
CC -!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT TRANSLOCATION
CC OF THE NASCENT PROTEIN CHAIN FROM THE A-SITE TO THE P-SITE OF THE
CC RIBOSOME.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC EF-G/EF-2 SUBFAMILY.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
CC EMBL; X66322; CAA46997.1; -.
CC HAWAP; MF_00054; -.
CC InterPro; IPR000795; EF_GTPbind.
DR PROSITE; PS00301; EFACOR_GTP; PARTIAL.
KW Elongation factor; Protein biosynthesis; GTP-binding.
FT NON_TER 1
SQ SEQUENCE 17 AA; 2094 MW; EA461E1F05F96E1D CRC64;

Query Match
Best Local Similarity 16.7%; Score 3; DB 1; Length 17;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EKL 10
DB 11 EKL 13

RESULT 33
RL23_HALCU STANDARD; PRT; 18 AA.
ID RL23_HALCU

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AC P05975;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 50S ribosomal protein L23P (HL31) (Fragment).
GN RPL23P.
OS Halobacterium cutirubrum.
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxID=2242;
RN [1]
RP SEQUENCE.
RX MEDLINE=84282108; PubMed=6467081;
RA Matheson A.T., Yaguchi M., Christensen P., Rollin C.F., Hasnain S.;
RT "Purification, properties, and N-terminal amino acid sequence of
RT certain 50S ribosomal subunit proteins from the archaeobacterium
RT Halobacterium cutirubrum.";
RL Can. J. Biochem. Cell Biol. 62:426-433(1984).
CC -!- FUNCTION: BINDS TO A SPECIFIC REGION ON THE 23S RRNA
CC (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE L23P FAMILY OF RIBOSOMAL PROTEINS.
DR InterPro; IPR001014; Ribosomal L23.
DR PROSITE; PS00050; RIBOSOMAL L23; PARTIAL.
KW Ribosomal protein; rRNA-binding.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2041 MW; 3E61DC53F9B4DD4C CRC64;

Query Match
Best Local Similarity 16.7%; Score 3; DB 1; Length 18;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PLV 17
DB 7 PLV 9

RESULT 34
UC21_MAIZE STANDARD; PRT; 18 AA.
ID UC21_MAIZE
AC P80627;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 443)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.9, ITS MW IS: 26.5 kDa.
CC -!- SIMILARITY: TO L-ASCORBATE PEROXIDASES.
DR Maize-2DPAGE; P80627; -.
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 1938 MW; F32F6FEF038AB8A CRC64;

Query Match
Best Local Similarity 16.7%; Score 3; DB 1; Length 18;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VEK 9
DB 7 VEK 9

```

Thr, and Ser into dehydrated AA and the formation of thioether bonds with cysteine. The 14-19 beta-methylanthionine thioether bond is oxidized to a sulfoxide. This is followed by membrane translocation and cleavage of the modified precursor.

CC PIR; A58700; A58700.  
CC PDB; 1AJ1; 15-OCT-97.  
CC Antibiotic; Bacteriocin; Lanthibiotic; D-amino acid; Oxidation;  
CC 3D-structure; Thioether bond.  
CC CROSSLNK 1 6 Lanthionine (Ser-Cys).  
CC CROSSLNK 7 12 Beta-methylanthionine (Thr-Cys).  
CC CROSSLNK 9 17 Beta-methylanthionine (Thr-Cys).  
CC CROSSLNK 14 19 Beta-methylanthionine sulfoxide (Cys-Thr).  
CC SEQUENCE 19 AA; 1946 MW; 5C138C7CEB8765B3 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TLT 5  
Db 7 TLT 9

RESULT 37  
LPG\_ECOLI STANDARD; PRT; 19 AA.  
ID LPGE\_ECOLI  
AC P33236;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Gef leader peptide.  
GN GEFL OR B0018.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92048481; PubMed=1943701;  
RA Poulsen L.K., Refn A., Molin S., Andersson P.;  
RT "The gef gene from Escherichia coli is regulated at the level of translation";  
RL Mol. Microbiol. 5:1639-1648 (1991).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX STRAIN=K12 / MG1655;  
RX MEDLINE=97426617; PubMed=9278503;  
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shao Y.;  
RT "The complete genome sequence of Escherichia coli K-12.";  
RL Science 277:1453-1474 (1997).  
CC -----  
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CC -----  
CC EMBL; A8000112; AAC73129.1; ALT\_TERM.  
DR EcoGene; EGI2074; gefl.  
KW Leader peptide; Complete proteome.  
SQ SEQUENCE 19 AA; 2259 MW; 19B3EDF371EB0EB CRC64;

Query Match 16.7%; Score 3; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LTD 6

Thr, and Ser into dehydrated AA and the formation of thioether bonds with cysteine. The 14-19 beta-methylanthionine thioether bond is oxidized to a sulfoxide. This is followed by membrane translocation and cleavage of the modified precursor.

CC PIR; A58700; A58700.  
CC PDB; 1AJ1; 15-OCT-97.  
CC Antibiotic; Bacteriocin; Lanthibiotic; D-amino acid; Oxidation;  
CC 3D-structure; Thioether bond.  
CC CROSSLNK 1 6 Lanthionine (Ser-Cys).  
CC CROSSLNK 7 12 Beta-methylanthionine (Thr-Cys).  
CC CROSSLNK 9 17 Beta-methylanthionine (Thr-Cys).  
CC CROSSLNK 14 19 Beta-methylanthionine sulfoxide (Cys-Thr).  
CC SEQUENCE 19 AA; 1946 MW; 5C138C7CEB8765B3 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TLT 5  
Db 7 TLT 9

RESULT 36  
LANA ACTLG STANDARD; PRT; 19 AA.  
ID LANA ACTLG  
AC P56650;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Lanthibiotic actagardine (Gardimycin).  
OS Actinoplanes liguariae.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Micromonosporineae; Micromonosporaceae; Actinoplanes.  
OX NCBI\_TaxID=69484;  
RN [1]  
RP PRELIMINARY SEQUENCE, AND STRUCTURE BY NMR.  
RX MEDLINE=91008698; PubMed=2211371;  
RA Kettenring J.K., Malabarba A., Vekey K., Cavalleri B.;  
RT "Sequence determination of actagardine, a novel lantibiotic, by homonuclear 2D NMR spectroscopy";  
RL J. Antibiot. 43:1082-1088 (1990).  
RN [2]  
RP SEQUENCE AND STRUCTURE BY NMR.  
RX MEDLINE=95255286; PubMed=7737178;  
RA Zimmermann N., Metzger J.W., Jung G.;  
RT "The tetracyclic lantibiotic actagardine. 1H-NMR and 13C-NMR assignments and revised primary structure.";  
RL Eur. J. Biochem. 228:786-797 (1995).  
RN [3]  
RP STRUCTURE BY NMR.  
RX MEDLINE=97363218; PubMed=9219543;  
RA Zimmermann N., Jung G.;  
RT "The three-dimensional solution structure of the lantibiotic murein-biosynthesis-inhibitor actagardine determined by NMR.";  
RL Eur. J. Biochem. 246:809-819 (1997).  
CC -!- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST SOME GRAM-POSITIVE BACTERIA. HAS GOOD ANTISTREPTOCOCCAL ACTIVITY.  
CC -!- PTM: Maturation of lantibiotics involves the enzymic conversion of

```
Db      |||
        9 LTD 11

RESULT 38
MIFH_TRISP
ID _MIFH_TRISP STANDARD; PRT; 19 AA.
AC P81529;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE L-dopachrome-methyl ester tautomerase (Macrophage migration inhibitory
DE factor homolog) (Fragment).
OS Trichinella spiralis (Trichina worm).
OC Eukaryota; Metazoa; Nematoda; Enoplea; Trichocephalida;
OC Trichinellidae; Trichinella.
OX NCBI_TaxID=6334;
RN [1]
RP SEQUENCE.
RX MEDLINE=99013685; PubMed=9794786;
RA Pennock J.L., Behnke J.M., Bickie Q.D., Devaney E., Grencis R.K.,
RA Isaac R.E., Joshua G.W.P., Selkirk M.E., Zhang Y., Meyer D.J.;
RT "rapid purification and characterization of L-dopamine-methyl-ester
RT tautomerase (macrophage migration inhibitory factor) from Trichinella
RT spiralis, Trichuris muris and Brugia pahangi.";
RL Biochem. J. 335:495-498(1998).
CC -!- FUNCTION: TAUTOMERIZATION OF THE METHYL ESTER OF L-DOPACHROME.
CC -!- INDUCTION: INHIBITED BY FREE FATTY ACIDS AND HAEMATIN.
CC -!- SIMILARITY: BELONGS TO THE MIF FAMILY.
DR InterPro; IP001398; MIF.
DR PROSITE; PS01158; MIF; PARTIAL.
KW Cytokine.
FT NON TER 19
SQ SEQUENCE 19 AA; 2106 MW; F7CAA05F112A628D CRC64;

Query Match 16.7%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TDV 7
    |||
    12 TDV 14

Db

RESULT 39
FIBB_SHEEP
ID _FIBB_SHEEP STANDARD; PRT; 20 AA.
AC P14470;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Ovis aries (Sheep); and
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940, 9925;
RN [1]
RP SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J.;
RA "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.

DR InterPro; IP0002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN AG C DOMAIN; PARTIAL.
KW Blood coagulation; Plasma; Sulfation; SULFATION.
FT PEPTIDE 1 20
FT MOD RES 5 5
FT NON TER 20 20
SQ SEQUENCE 20 AA; 2338 MW; FCF5B6FF0DEC6627 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPL 14
    |||
    15 LPL 17

Db

RESULT 40
FRHA_METBA
ID _FRHA_METBA STANDARD; PRT; 20 AA.
AC P80489;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Coenzyme F420 hydrogenase alpha subunit [EC 1.12.98.1] (8-hydroxy-5-
DE deazaflavin-reducing hydrogenase alpha subunit) (FRH) (Fragment).
GN FRHA.
OS Methanosarcina barkeri.
OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2208;
RN [1]
RP SEQUENCE.
RC STRAIN=Fusaro / DSM 804;
RX MEDLINE=96085134; PubMed=8521835;
RA Michel R., Massanz C., Kostka S., Richter M., Fiebig K.;
RT "Biochemical characterization of the 8-hydroxy-5-deazaflavin-reactive
RT hydrogenase from Methanosarcina barkeri Fusaro.";
RL Eur. J. Biochem. 233:727-735(1995)
CC -!- FUNCTION: REDUCES THE PHYSIOLOGICAL LOW-POTENTIAL TWO-ELECTRON
CC ACCEPTOR COENZYME F420, AND THE ARTIFICIAL ONE-ELECTRON ACCEPTOR
CC METHYLVIOLIGEN.
CC -!- CATALYTIC ACTIVITY: H(2) + coenzyme F420 = reduced coenzyme F420.
CC -!- COFACTOR: FRH CONTAINS NICKEL, IRON-SULFUR, AND FAD COFACTORS.
CC -!- SUBUNIT: PENTAMER OF TWO ALPHA CHAINS, TWO BETA CHAINS AND A
CC GAMMA CHAIN.
CC -!- SUBCELLULAR LOCATION: Membrane-associated.
CC -!- SIMILARITY: BELONGS TO THE [NIFE]/[NIFSE] HYDROGENASE LARGE
CC SUBUNIT FAMILY.
CC PIR; S63483; S63483.
DR InterPro; IP001501; Ni hdl.
DR PROSITE; PS00507; NI_HGENASE_L_1; PARTIAL.
DR PROSITE; PS00508; NI_HGENASE_L_2; PARTIAL.
KW Oxidoreductase; Metal-binding; Nickel; FAD.
FT NON TER 20
SQ SEQUENCE 20 AA; 2233 MW; 0D6597417D776D03 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LTL 4
    |||
    18 LTL 20

Db

RESULT 41
HET1_RADMG
ID _HET1_RADMG STANDARD; PRT; 20 AA.
AC P58689;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
RN [1]
```

DE Cytolysin I (Hmg I) (Magnificolysin I) (Fragment).  
OS Radianthus magnifica (Magnificent sea anemone) (Heteractis magnifica).  
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;  
OC Stichodactylidae; Heteractis.  
OX NCBI\_TaxID=38281;  
RN [1]  
RP SEQUENCE AND CHARACTERIZATION.  
RX MEDLINE=94196594; PubMed=8146870;  
RA Khoo K.S., Kam W.K., Khoo H.B., Gopalakrishnakone P., Chung M.C.;  
RT "Purification and partial characterization of two cytolysins from a  
RT tropical sea anemone, Heteractis magnifica.";  
RL Toxicon 31:1567-1579(1993).  
CC -!- FUNCTION: Has both cytolytic and hemolytic activity. Pore forming  
CC protein.  
CC -!- SUBCELLULAR LOCATION: Secreted; cnidocyst.  
CC -!- SIMILARITY: BELONGS TO THE TENEBROSIN FAMILY.  
KW Cytolysis; Hemolysis; Toxin; Cnidocyst; Transmembrane.  
FT NON TER 20  
SQ SEQUENCE 20 AA; 2003 MW; ED9ABD98AC7C4EBC CRC64;  
Query Match 16.7%; Score 3; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SLT 3  
Db 11 SLT 13  
RESULT 42  
MI17\_BOVIN STANDARD; PRT; 20 AA.  
ID MI17\_BOVIN  
AC P35451;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-JUN-1994 (Rel. 29, Last annotation update)  
DE 17 kDa milk glycoprotein (Fragment).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Milk;  
RX MEDLINE=93308294; PubMed=8320368;  
RA Sorensen E.S., Petersen T.E.;  
RT "Purification and characterization of three proteins isolated from  
RT the protease peptone fraction of bovine milk.";  
RL J. Dairy Res. 60:199-197(1993).  
CC -!- PTM: N-GLYCOSYLATED.  
CC -!- SIMILARITY: TO CAMEL WHEY PROTEIN.  
KW Glycoprotein; Milk.  
FT NON TER 1 1  
FT NON TER 20 20  
SQ SEQUENCE 20 AA; 2233 MW; 4CCA589404C62C27 CRC64;  
Query Match 16.7%; Score 3; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 12 LPL 14  
Db 12 LPL 14  
RESULT 43  
TENA\_ACTTE STANDARD; PRT; 20 AA.  
ID TENA\_ACTTE  
AC P30833;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Tenebrosin A (Fragment).  
OS Actinia tenebrosa (Australian red waratah sea anemone).  
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;  
OC Nynanthae; Actiniidae; Actinia.  
OX NCBI\_TaxID=6105;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=90232538; PubMed=1970442;  
RA Norton R.S., Bobek G., Ivanov J.O., Thomson M., Fiala-Beer E.,  
RA Moritz R.L., Simpson R.J.;  
RT "Purification and characterisation of proteins with cardiac  
RT stimulatory and haemolytic activity from the anemone Actinia  
RT tenebrosa.";  
RL Toxicon 28:29-41(1990).  
CC -!- FUNCTION: This cardiac stimulatory and hemolytic protein is a  
CC channel-forming and/or membrane-penetrating protein.  
CC -!- SUBCELLULAR LOCATION: Secreted; cnidocyst.  
CC -!- SIMILARITY: BELONGS TO THE TENEBROSIN FAMILY.  
DR PIR; A34016; A34016.  
KW Cytolysis; Hemolysis; Toxin; Cnidocyst; Transmembrane.  
FT NON TER 20  
SQ SEQUENCE 20 AA; 1974 MW; FA32AC8BDAFF5FA CRC64;  
Query Match 16.7%; Score 3; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 3 TLT 5  
Db 13 TLT 15  
RESULT 44  
TENB\_ACTTE STANDARD; PRT; 20 AA.  
ID TENB\_ACTTE  
AC P30834;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Tenebrosin B (Fragment).  
OS Actinia tenebrosa (Australian red waratah sea anemone).  
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;  
OC Nynanthae; Actiniidae; Actinia.  
OX NCBI\_TaxID=6105;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=90232538; PubMed=1970442;  
RA Norton R.S., Bobek G., Ivanov J.O., Thomson M., Fiala-Beer E.,  
RA Moritz R.L., Simpson R.J.;  
RT "Purification and characterisation of proteins with cardiac  
RT stimulatory and haemolytic activity from the anemone Actinia  
RT tenebrosa.";  
RL Toxicon 28:29-41(1990).  
CC -!- FUNCTION: This cardiac stimulatory and hemolytic protein is a  
CC channel-forming and/or membrane-penetrating protein.  
CC -!- SUBCELLULAR LOCATION: Secreted; cnidocyst.  
CC -!- SIMILARITY: BELONGS TO THE TENEBROSIN FAMILY.  
DR PIR; B34016; B34016.  
KW Cytolysis; Hemolysis; Toxin; Cnidocyst; Transmembrane.  
FT NON TER 20  
SQ SEQUENCE 20 AA; 1960 MW; FA32B426009FF5FA CRC64;  
Query Match 16.7%; Score 3; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 3 TLT 5  
Db 13 TLT 15  
RESULT 45  
TL22\_SPIOL

ID TL22\_SPIOI STANDARD; PRT; 20 AA.  
AC P82796;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Thylakoid lumenal 22 kDa protein (P22) (Fragment).  
OS Spinacia oleracea (Spinach).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.  
OX NCBI\_TaxID=3562;  
RN [1]  
RP SEQUENCE.  
RA Kieselbach T., Pettersson U., Bystedt M., Schroeder W.P.;  
RL Submitted (SEP-2000) to the SWISS-PROT data bank.  
CC -!- SUBCELLULAR LOCATION: Chloroplast; within the thylakoid lumen.  
KW Chloroplast; Thylakoid.  
FT NON TER 20  
SQ SEQUENCE 20 AA; 2409 MW; 78F5B50699BEB620 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLT 3  
|||  
Db 17 SLT 19

RESULT 46  
YPRB\_SERMA STANDARD; PRT; 20 AA.  
AC P22581;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical protein in prob 5'region (Fragment).  
OS Serratia marcescens.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Serratia.  
OX NCBI\_TaxID=615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sr41;  
RX MEDLINE=91237315; PubMed=1851803;  
RA Omori K., Suzuki S., Inai Y., Komatsubara S.;  
RT "Analysis of the Serratia marcescens probA operon and feedback  
control of proline biosynthesis".  
RL J. Gen. Microbiol. 137:509-517(1991).

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DR EMBL; D90351; BAAL4363.1; -  
DR EMBL; X53086; CAA37253.1; -  
DR FIR; C49753; C49753.  
KW Hypothetical protein.  
FT NON TER 1  
SQ SEQUENCE 20 AA; 2248 MW; 4DD7777735276674 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 EXL 10  
|||  
Db 13 EXL 15

RESULT 47  
BIOA\_CITFR STANDARD; PRT; 5 AA.  
AC P13071;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Adenosylmethionine-8-amino-7-oxononanoate aminotransferase  
DE (EC 2.6.1.62) (7,8-diamino-peilargonic acid aminotransferase) (DAPA  
DE aminotransferase) (Fragment).  
GN BIOA.  
OS Citrobacter freundii.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Citrobacter.  
OX NCBI\_TaxID=546;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89006280; PubMed=2971595;  
RA Shiuan D., Campbell A.;  
RT "Transcriptional regulation and gene arrangement of Escherichia coli,  
RT Citrobacter freundii and Salmonella typhimurium biotin operons.";  
RL Gene 67:203-211(1988).  
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 8-amino-7-oxononanoate = S-adenosyl-4-methylthio-2-oxobutanoate + 7,8-diaminononanoate.  
CC -!- COFACTOR: Pyridoxal phosphate.  
CC -!- PATHWAY: Biotin biosynthesis.  
CC -!- SUBUNIT: Homodimer.  
CC -!- SIMILARITY: Belongs to class-III of pyridoxal-phosphate-dependent aminotransferases.  
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DR EMBL; M21922; -; NOT\_ANNOTATED\_CDS.  
DR FIR; I40697; I40697.  
DR InterPro; IPR005814; Aminotrans\_3.  
DR PROSITE; PS00600; AA\_TRANSFER\_CLASS\_3; PARTIAL.  
KW Biotin biosynthesis; Transferase; Aminotransferase;  
KW Pyridoxal phosphate.  
FT NON TER 5  
SQ SEQUENCE 5 AA; 582 MW; 6AAAB1B1A6F00000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TD 6  
|||  
Db 3 TD 4

RESULT 48  
PRCT\_PERAM STANDARD; PRT; 5 AA.  
AC P01373;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 01-FEB-1995 (Rel. 31, Last annotation update)  
DE Proctolin.  
OS Periplaneta americana (American cockroach).  
OS Limulus polyphemus (Atlantic horseshoe crab), and  
OS Carcinus maenas (Common shore crab) (Green crab).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
OC Blattidae; Periplaneta.  
OX NCBI\_TaxID=6978, 6850, 6759;

RN SEQUENCE.  
 RP SPECIES=P.americana;  
 RX MEDLINE=76074708; PubMed=576;  
 RA Starratt A.N., Brown B.E.;  
 RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter  
 in insects.";  
 RL Life Sci. 17:1253-1256(1975).  
 RN [2]  
 RP BIOLOGICAL SOURCE.  
 RC SPECIES=P.americana;  
 RX MEDLINE=8125865; PubMed=6113690;  
 RA O'Shea M., Adams M.E.;  
 RT "Pentapeptide (proctolin) associated with an identified neuron.";  
 RL Science 213:567-569(1981).  
 RN [3]  
 RP SEQUENCE.  
 RC SPECIES=L.polyphemus;  
 RX MEDLINE=90287800; PubMed=2356151;  
 RA Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,  
 Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,  
 RA Shabanowitz J.;  
 RT "Identification of proctolin in the central nervous system of the  
 horseshoe crab, Limulus polyphemus.";  
 RL Peptides 11:205-211(1990).  
 RN [4]  
 RP SEQUENCE.  
 RC SPECIES=C.maenas;  
 RX MEDLINE=86232789; PubMed=2872661;  
 RA Stangier J., Dirksen H., Keller R.;  
 RT "Identification and immunocytochemical localization of proctolin in  
 pericardial organs of the shore crab, Carcinus maenas.";  
 RL Peptides 7:67-72(1986).  
 CC -!- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY,  
 CC MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.  
 CC -!- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN  
 CC THE CRAB PERICARDIAL ORGANS.  
 DR PIR; A01644; HOROHA.  
 DR PIR; A60411; A60411.  
 KW Neuropeptide.  
 SQ SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;  
 Query Match 11.1%; Score 2; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 12 LP 13  
 DB 3 LP 4  
 RESULT 49  
 TMOF SARBUB  
 ID TMOF SARBUB STANDARD; PRT; 6 AA.  
 AC P41455;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE Trypsin-modulating oostatic factor (TMOF).  
 OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 CC Sarcophagidae; Sarcophaga.  
 CC NCBI\_TaxID=7385;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Ovary.  
 RX MEDLINE=94211930; PubMed=8159807;  
 RA Bylemans D., Borovsky D., Hunt D.F., Shabanowitz J., Grauwels L.,  
 RA de Loof A.;  
 RT "Sequencing and characterization of trypsin modulating oostatic  
 factor (TMOF) from the ovaries of the grey fleshfly, Neobellieria  
 (Sarcophaga) bullata.";

RL Regul. Pept. 50:61-72(1994).  
 CC -!- FUNCTION: HAS AN OOSTATIC ACTIVITY. INHIBITS TRYPSIN BIOSYNTHESIS  
 IN THE MIDGUT WHICH INDIRECTLY REDUCES THE VITELLOGENIN  
 CONCENTRATION IN THE HEMOLYMPH RESULTING IN INHIBITION OF OOCYTE  
 DEVELOPMENT.  
 CC -!- DEVELOPMENTAL STAGE: SYNTHESIZED AND RELEASED FROM FOLLICULAR  
 CC EPITHELIUM AFTER A BLOOD MEAL.  
 KW Hormone.  
 SQ SEQUENCE 6 AA; 695 MW; 61E72451B7642000 CRC64;  
 Query Match 11.1%; Score 2; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 10 LP 11  
 DB 5 LP 6  
 RESULT 50  
 TRPI\_PSEPU  
 ID TRPI\_PSEPU STANDARD; PRT; 6 AA.  
 AC F36414;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-FEB-1995 (Rel. 31, Last annotation update)  
 DE TRPA operon transcriptional activator (Fragment).  
 GN TRPI.  
 OS Pseudomonas putida.  
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 CC Pseudomonadaceae; Pseudomonas.  
 CC NCBI\_TaxID=303;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PPGI C15;  
 RX MEDLINE=89335826; PubMed=2503057;  
 RA Eberly L., Crawford I.P.;  
 RT "DNA sequence of the tryptophan synthase genes of Pseudomonas  
 putida.";  
 RL Biochimie 71:521-531(1989).  
 CC -!- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPA GENES ENCODING  
 THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE  
 INDUCER (INDOLEGLYCEROL PHOSPHATE), TRPI BINDS UPSTREAM OF THE  
 TRPA OPERON, OVERLAPPING ITS OWN PROMOTER REGION.  
 CC -!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL  
 REGULATORS.  
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 CC  
 DR EMBL; X13299; CAA31660.1; -;  
 DR InterPro; IPR000847; HTH\_LysR.  
 DR PROSITE; PS00044; HTH\_LYSR\_FAMILY; PARTIAL.  
 KW Tryptophan biosynthesis; Transcription regulation; Activator;  
 KW DNA-binding.  
 FT NON\_TER 6  
 SQ SEQUENCE 6 AA; 683 MW; 77672AA1EDD6F000 CRC64;  
 Query Match 11.1%; Score 2; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 12 LP 13  
 DB 5 LP 6  
 RESULT 51



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VP19 HSV1K
ID VP19_HSV1K STANDARD; PRT; 6 AA.
AC P23210;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Capsid assembly and DNA maturation protein (Virion protein UL38)
DE (Capsid protein VP19C) (Fragment).
GN UL38.
OS Herpes simplex virus (type 1 / strain KOS).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10306;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91101287; PubMed=1846198;
RA Flanagan W.M., Papavassiliou A.G., Rice M., Hecht L.B.,
RA Silverstein S., Wagner E.K.;
RT "Analysis of the herpes simplex virus type 1 promoter controlling the
RT expression of UL38, a true late gene involved in capsid assembly.";
RL J. Virol. 65:769-786(1991).
CC -!- FUNCTION: COMPONENT OF THE BASAL LAYER IN WHICH THE CAPSIDS ARE
CC EMBEDDED. BINDS DNA.
CC -!- SIMILARITY: TO OTHER HERPESVIRUSES CAPSID PROTEIN VP19C.
CC
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CC
CC EMBL; M57646; AAA5830.1; -
DR Capsid assembly; Coat protein; DNA-binding.
KW NON_TER
FT 6
SQ SEQUENCE 6 AA; 703 MW; 67376451A336F000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PL 14
Db 5 PL 6

RESULT 52
CCFL_ENTFA
ID CCF1_ENTFA STANDARD; PRT; 7 AA.
AC P20104;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Sex pheromone cCF10.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE.
RX MEDLINE=89008313; PubMed=3139658;
RA Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M.,
RA Adsit J.C., Dunny G.M., Suzuki A.;
RT "Structure of cCF10, a peptide sex pheromone which induces
RT conjugative transfer of the Streptococcus faecalis tetracycline
RT resistance plasmid, pCF10.";
RL J. Biol. Chem. 263:14574-14578(1988).
CC -!- FUNCTION: CCF10 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
CC HEMOLYSIN PLASMID PCF10.
DR PIR: A30812; A30812.
KW Pheromone.
SQ SEQUENCE 7 AA; 790 MW; 72C9D2C731B2C740 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PL 14
Db 5 PL 6

RESULT 54
UN06_PINPS
ID UN06_PINPS STANDARD; PRT; 7 AA.
AC P81675;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of needles (N141) (Fragment).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.
RX TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.6, ITS MW IS: 25 kDa.
FT NON_TER 1
FT NON_TER 7

Query Match 11.1%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PL 14
Db 5 PL 6

RESULT 53
MNPI_LEPDE
ID MNPI_LEPDE STANDARD; PRT; 7 AA.
AC P42984;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Myotropic neuropptide 1 (led-MNP-1).
OS Leptinotarsa decemlineata (Colorado potato beetle).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
OC Phytophaga; Chrysomeloidea; Chrysomelidae; Chrysomelinae;
OC Chrysomelini; Leptinotarsa.
OX NCBI_TaxID=7539;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX TISSUE=Head;
RX MEDLINE=95380343; PubMed=7651886;
RA Spittaels K., Vankeerberghen A., Schoofs L., Torrekens S.,
RA Grauwels L., van Leuven F., de Loof A.;
RT "Identification, characterization, and immunological localization of
RT a novel myotropic neuropptide in the Colorado potato beetle,
RT Leptinotarsa decemlineata.";
RL Peptides 16:365-374(1995).
CC -!- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE
CC OVIDUCT.
CC Neuropeptide; Amidation.
KW MOD_RES 7
FT 7
SQ SEQUENCE 7 AA; 705 MW; 6DD73768745B5DB0 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PL 14
Db 5 PL 6

RESULT 55
UN06_PINPS
ID UN06_PINPS STANDARD; PRT; 7 AA.
AC P81675;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of needles (N141) (Fragment).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.
RX TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.6, ITS MW IS: 25 kDa.
FT NON_TER 1
FT NON_TER 7

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SQ SEQUENCE 7 AA; 823 MW; 69D7672448B5740 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LP 13  
 ||  
 Db 5 LP 6

RESULT 55  
 ACT\_CARMA STANDARD; PRT; 8 AA.  
 AC P80709;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUN-1999 (Rel. 38, Last annotation update)  
 DE Actin (Fragment).  
 OS Carinus maenas (Common shore crab) (Green crab).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
 OX NCBI\_TaxID=6759;  
 RN [1]

RP SEQUENCE.  
 RA Lachaise F., Somme G., Carpentier G., Granjeon E., Webster S.,  
 RA Baghdassarian D.;  
 RA "A transaldolase. An enzyme implicated in crab steroidogenesis.";  
 RL Endocrine 5:23-32 (1996).  
 CC -!- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED  
 CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBQUITOUSLY EXPRESSED  
 CC IN ALL EUKARYOTIC CELLS.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:  
 CC 6.8, ITS MW IS: 46 kDa.  
 CC -!- SIMILARITY: Belongs to the actin family.  
 DR InterPro: IPR004001; Actin.  
 DR InterPro: IPR004000; Actin-like.  
 DR PROSITE: PS00406; ACTINS\_1; PARTIAL.  
 DR PROSITE: PS00432; ACTINS\_2; PARTIAL.  
 DR PROSITE: PS01132; ACTINS\_ACT-LIKE; PARTIAL.  
 KW Structural protein.  
 FT NON\_TER 1 1  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 976 MW; 1424005A52CAAB3 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DV 7  
 ||  
 Db 3 DV 4

RESULT 56  
 AKH\_TABAT STANDARD; PRT; 8 AA.  
 AC P14595;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Adipokinetic hormone (AKH) (Dipteran corpora cardiaca factor 1)  
 DE (DCC 1).  
 OS Tabanus atratus (Horse fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae;  
 OC Tabanus.  
 OX NCBI\_TaxID=7207;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Corpora cardiaca;

RX MEDLINE=90046758; PubMed=2813385;  
 RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,  
 RA Vogel V.W., Zhang Y.-S., Hayes D.K.;  
 RT "Primary structure of two neuropeptide hormones with adipokinetic and  
 RT hypotrehalosemic activity isolated from the corpora cardiaca of horse  
 RT flies (Diptera).";  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164 (1989).  
 CC -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA  
 CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF  
 CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT  
 CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.  
 CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.  
 DR PIR; A33995; A33995.  
 DR InterPro: IPR002047; AKH.  
 DR PROSITE: PS00256; AKH; 1.  
 KW Neuropeptide; Amidation; Flight; Pyroglutamate carboxylic acid.  
 FT MOD\_RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 949 MW; 86786771A9D1A736 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LT 3  
 ||  
 Db 2 LT 3

RESULT 57  
 CAD1\_ENTFA STANDARD; PRT; 8 AA.  
 AC P13268;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 01-FEB-1991 (Rel. 17, Last annotation update)  
 DE Sex pheromone CAD1.  
 OS Enterococcus faecalis (Streptococcus faecalis).  
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.  
 OX NCBI\_TaxID=1351;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=85051889; PubMed=6437872;  
 RA Mori M., Sakakami Y., Narita M., Isogai A., Fujino M., Kitada C.,  
 RA Craig R.A., Clewell D.B., Suzuki A.;  
 RT "Isolation and structure of the bacterial sex pheromone, CAD1, that  
 RT induces plasmid transfer in Streptococcus faecalis.";  
 RL FEBS Lett. 178:97-100 (1984).  
 CC -!- FUNCTION: CAD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE  
 CC HEMOLYSIN PLASMID PAD1.  
 KW Pheromone.  
 SQ SEQUENCE 8 AA; 819 MW; 047DD732C735B9C7 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SL 2  
 ||  
 Db 3 SL 4

RESULT 58  
 COW2\_CONFU STANDARD; PRT; 8 AA.  
 AC P58785;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Leu-contryphan-P.  
 OS Conus purpurascens (Purple cone).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;

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OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=41690;
RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC STRAIN=Clipperton Island; TISSUE=Venom;
RX MEDLINE=99368839; PubMed=10461743;
RA Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,
RA Olivera B.M.;
RT "A novel D-leucine-containing Conus peptide: diverse conformational
RT dynamics in the contryphan family.";
RL J. Pept. Res. 54:93-99(1999).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- MASS SPECTROMETRY: MW=888.4; METHOD=LSIMS.
CC -1- SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY.
KW Toxin; Hydroxylation; D-amino acid.
FT DISULFID 2 8
FT MOD RES 4 4 D-LEUCINE.
SQ SEQUENCE 8 AA; 890 MW; 75A367672732CEB8 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LP 13
Db 5 LP 6

RESULT 59
CPD1_ENTFA
ID CPD1_ENTFA STANDARD; PRT; 8 AA.
AC P13269;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Sex pheromone CPD1.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE.
RX MEDLINE=85040388; PubMed=6436978;
RA Suzuki A., Mori M., Sakakami Y., Isogai A., Fujino M., Kitada C.,
RA Craig R.A., Clewell D.B.;
RT "Isolation and structure of bacterial sex pheromone, cPD1.";
RL Science 226:849-850(1984).
CC -1- FUNCTION: CPD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
CC BACTERIOCIIN PLASMID PPD1.
KW Pheromone.
SQ SEQUENCE 8 AA; 913 MW; 8665B729C682C729 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LV 17
Db 2 LV 3

RESULT 60
HTF2_PERAM
ID HTF2_PERAM STANDARD; PRT; 8 AA.
AC P04549;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypertrehalosaeic factor II (Neuropeptide M-II) (Periplanetin CC-2)
DE (Pex-CH-II) (LeD-CC-II) (Hypertrehalosaeic neuropeptide II).
OS Periplaneta americana (American cockroach),
OS Leptinotarsa decemlineata (Colorado potato beetle), and
OS Blatta orientalis (Oriental cockroach).

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OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978, 7539, 6976;
RN [1]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=85046530; PubMed=6548628;
RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
RA Rinehart K.L. Jr.;
RT "structures of two cockroach neuropeptides assigned by fast atom
RT bombardment mass spectrometry.";
RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
RN [2]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=84298179; PubMed=6591205;
RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
RA Miller C.A., Schooley D.A.;
RT "Isolation and primary structure of two peptides with
RT cardioacceleratory and hyperglycemic activity from the corpora
RT cardiaca of Periplaneta americana.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
RN [3]
RP SEQUENCE.
RC SPECIES=L.declineata; TISSUE=Corpora cardiaca;
RX MEDLINE=90160053; PubMed=2576128;
RA Gaede G., Keilner R.;
RT "The metabolic neuropeptides of the corpus cardiaca from the potato
RT beetle and the American cockroach are identical.";
RL Peptides 10:1287-1289(1989).
RN [4]
RP SEQUENCE.
RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
RX MEDLINE=90253659; PubMed=2340112;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structures of hypertrehalosaeic neuropeptides isolated from
RT the corpora cardiaca of the cockroaches Leucophaea maderae,
RT Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
RT and of the stick insect Extatosoma tiaratum assigned by tandem fast
RT atom bombardment mass spectrometry.";
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
CC -1- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR PIR; B4960; B44960.
DR PIR; B49823; B49823.
DR PIR; S08996; S08996.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1006 MW; 86745771A9D1A736 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LT 3
Db 2 LT 3

RESULT 61
PLP_BRANA
ID PLP_BRANA STANDARD; PRT; 8 AA.
AC P81707;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Plastidial lipid-associated protein (Fragment).

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OS Brassica napus (Rape).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Brassica.  
 OX NCBI\_TaxID=3708;  
 [1]  
 RN SEQUENCE.  
 RP STRAIN=CV. TOPAZ; TISSUE=Tapetum;  
 RC MEDLINE=99349136; PubMed=10420651;  
 RX Hernandez-Pinzon I., Ross J.H.E., Barnes K.A., Damant A.P.,  
 RA Murphy D.J.;  
 RT "Composition and role of tapetal lipid bodies in the biogenesis of the  
 RT pollen coat of Brassica napus";  
 RL Planta 208:588-598(1999).  
 CC -!- FUNCTION: MAY PLAY A STRUCTURAL ROLE IN THE ELAIOPLAST, A TAPETUM-  
 CC SPECIFIC PLASTIDIAL LIPID ORGANELLE.  
 CC -!- TISSUE SPECIFICITY: TAPETUM OF ANTHEIRS.  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 989 MW; 9D7B1AA452CAA042 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DV 7  
 ||  
 Db 3 DV 4

RESULT 62  
 ID PPK3 PERAM STANDARD; PRT; 8 AA.  
 AC P82618;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE Pyrokinin-3 (Pea-PK-3) (FXPKL-amide).  
 OS Periplaneta americana (American cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
 OC Blattidae; Periplaneta.  
 OX NCBI\_TaxID=6978;  
 [1]  
 RN SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.

RP TISSUE=Retrocerebral complex;  
 RC MEDLINE=99212469; PubMed=10196736;  
 RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;  
 RX "Differential distribution of pyrokinin-isoforms in cerebral and  
 RT abdominal neurohemal organs of the American cockroach";  
 RL Insect Biochem. Mol. Biol. 29:139-144(1999).  
 RN [2]  
 RP TISSUE SPECIFICITY.  
 RX MEDLINE=20189894; PubMed=10723010;  
 RA Predel R., Eckert M.;  
 RT "Tagma-specific distribution of FXPKLamides in the nervous system of  
 RL the American cockroach";  
 RL J. Comp. Neurol. 419:352-363(2000).  
 CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
 CC (MYOTROPIC ACTIVITY).  
 CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.  
 CC -!- MASS SPECTROMETRY: MW=996.5; METHOD=MALDI.  
 CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
 KW Neuropeptide; Amidation; Pyrokinin.  
 FT MOD\_RES 8  
 SQ SEQUENCE 8 AA; 997 MW; 0B34177409D772C7 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 LV 17  
 ||  
 Db 1 LV 2

RESULT 63  
 ID RT34 BOVIN STANDARD; PRT; 8 AA.  
 AC P82929;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE Mitochondrial 28S ribosomal protein S34 (S34mt) (MRP-S34) (Fragment).  
 GN MRPS34.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Liver;  
 RX MEDLINE=21276436; PubMed=11279123;  
 RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;  
 RT "The small subunit of the mammalian mitochondrial ribosome:  
 RT identification of the full complement of ribosomal proteins present";  
 RL J. Biol. Chem. 276:19363-19374(2001).  
 CC -!- SUBUNIT: Component of the mitochondrial ribosome small subunit  
 CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.  
 CC -!- SUBCELLULAR LOCATION: Mitochondrial.  
 KW Ribosomal protein; Mitochondrion.  
 FT NON\_TER 1  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 935 MW; 9639D1A72058637D CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LT 3  
 ||  
 Db 5 LT 6

RESULT 64  
 ID UPAA HUMAN STANDARD; PRT; 8 AA.  
 AC P30096;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Unknown protein from 2D-page of plasma (Spot 36) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE  
 RC TISSUE=Plasma;  
 RX MEDLINE=93092937; PubMed=1459097;  
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,  
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,  
 RA Hochstrasser D.F.;  
 RT "Plasma protein map: an update by microsequencing";  
 RL Electrophoresis 13:707-714(1992).  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 7, ITS MW IS: 12 kDa.  
 DR SWISS-2DPAGE; P30096; HUMAN.  
 FT NON\_TER 1  
 FT VARIANT 5 5 F -> P  
 FT NON\_TER 8 8 /FTID=VAR\_000004.  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 909 MW; 86677B59D1A72042 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LT 3  
||  
Db 3 LT 4

## RESULT 65

ALC\_CHLRE STANDARD; PRT; 9 AA.  
AC P82678;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Allantoicase (EC 3.5.3.4) (Allantoate amidinohydrolase) (Fragment).  
OS Chlamydomonas reinhardtii.  
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;  
OC Chlamydomonadaceae; Chlamydomonas.  
OX NCBI\_TaxID=3055;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=6145C;  
RX MEDLINE=20318328; PubMed=10860551;  
RA Piedras P., Munoz A., Aguilar M., Pineda M.;  
RT "Allantoate amidinohydrolase (Allantoicase) from Chlamydomonas reinhardtii: its purification and catalytic and molecular characterization."  
RL Arch. Biochem. Biophys. 378:340-348(2000).  
CC -!- FUNCTION: Catalyzes the degradation of allantoate to (-)-ureidoglycolate and (+)-ureidoglycolate to glyoxylate.  
CC -!- CATALYTIC ACTIVITY: Allantoate + H(2)O = (-)-ureidoglycolate + urea.  
CC -!- PATHWAY: Degradation of allantoate (purine catabolism); second step.  
CC -!- SUBUNIT: Homohexamer.  
CC -!- MISCELLANEOUS: Optimum pH is 6.5 and 8 for the reactions with allantoate and ureidoglycolate, respectively.  
CC -!- SIMILARITY: BELONGS TO THE ALLANTOICASE FAMILY.  
KW Hydrolyase; Purine metabolism.  
FT UNSURE 5 5 OR Y.  
FT NON TER 9 9  
SQ SEQUENCE 9 AA; 943 MW; D934ADD9D6D871F2 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TL 4  
||  
Db 8 TL 9

## RESULT 66

BUK\_CLOPA STANDARD; PRT; 9 AA.  
AC P81337;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Butyrate kinase (EC 2.7.2.7) (BK) (CP 38) (Fragment).  
GN BUK.  
OS Clostridium pasteurianum.  
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
OC Clostridium.  
OX NCBI\_TaxID=1501;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=W5;  
RX MEDLINE=98291870; PubMed=9629918;  
RA Flengsrud R., Skjeldal L.;  
RT "Two-dimensional gel electrophoresis separation and N-terminal sequence analysis of proteins from Clostridium pasteurianum W5.";  
RL Electrophoresis 19:802-806(1998).

CC -!- FUNCTION: Catalyzes the conversion of butyryl-CoA through butyryl phosphate to butyrate (By similarity).  
CC -!- CATALYTIC ACTIVITY: ATP + 2-butanolate = ADP + butanoyl phosphate.  
CC -!- PATHWAY: Involved in the acidogenic phase of fermentation.  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -!- SIMILARITY: Belongs to the acetokinase family.

DR HAMAP; MF 00542; -; 1  
DR InterPro; IPR000890; Acetate kin.  
DR PROSITE; PS01075; ACETATE\_KINASE\_1; PARTIAL.  
DR PROSITE; PS01076; ACETATE\_KINASE\_2; PARTIAL.  
KW Transferase; Kinase.  
FT NON TER 9 9  
SQ SEQUENCE 9 AA; 1104 MW; 055D40505727232B CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 KL 10  
||  
Db 3 KL 4

## RESULT 67

FAR5\_PANRE STANDARD; PRT; 9 AA.  
AC P82661;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE FMRFamide-like neuropeptide PF5 (AMRNALVRP-amide).  
DB Panagrellus redivivus.  
OS Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.  
OX NCBI\_TaxID=6233;  
RN [1]  
RP SEQUENCE, FUNCTION, AND AMIDATION.  
RA Moffet C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G., Maule A.G.;  
RT "Isolation, characterization and pharmacology of FMRFamide-related peptides (FARPs) from free-living nematode, Panagrellus redivivus.";  
RL Submitted (JUL-2000) to the SWISS-PROT data bank.  
CC -!- FUNCTION: MYOACTIVE.  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE) FAMILY.  
CC Neuropeptide; Amidation.  
KW MOD RES 9 9 AMIDATION.  
FT SEQUENCE 9 AA; 1077 MW; A0D112C72DD45406 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LV 17  
||  
Db 6 LV 7

## RESULT 68

FAR5\_PENMO STANDARD; PRT; 9 AA.  
AC P83320;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE FMRFamide-like neuropeptide FLP5 (SMPSLRIRF-amide).  
OS Penaeus monodon (Penaeid shrimp).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;  
OC Penaeidae; Penaeus.  
OX NCBI\_TaxID=6687;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.

```

RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sathigornkul P., Pupum J., Krungkarn C., Longyant S.,
RA Chaivithangkul P., Sathigornkul W., Petson A.;
RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Penaeus monodon.";
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1121.1; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 1106 MW; B60B07340735A766 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SL 2
DB 4 SL 5

RESULT 69
FAR9.ASCSU STANDARD; PRT; 9 AA.
AC P43172;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FMRFamide-like neuropeptide AF9.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6255;
RN [1]

SEQUENCE.
RX MEDLINE=95380362; PubMed=7651904;
RA Cowden C., Stretton A.O.W.;
RT "Eight novel FMRFamide-like neuropeptides isolated from the nematode
RT Ascaris suum.";
RL Peptides 16:491-500(1995).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 1012 MW; 524F073774176877 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PL 14
DB 6 PL 7

RESULT 70
FIBB.MACFU STANDARD; PRT; 9 AA.
AC P19345;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain (Contains: Fibrinopeptide B) (Fragment).
GN FGB.
OS Macaca fuscata fuscata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9543;
RN [1]

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RP SEQUENCE.
RA MEDLINE=95289140; PubMed=3928610;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and
RT patas monkey (Erythrocebus patas): their amino acid sequences,
RT restricted mutations, and a molecular phylogeny for macaques,
RT guenons, and baboons.";
RL J. Biochem. 97:1487-1492(1985).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR PIR; C24180; C24180.
DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN AG_C DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON TER 9 9
SQ SEQUENCE 9 AA; 1038 MW; 69FE65B9C735B1B CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SL 2
DB 4 SL 5

RESULT 71
MGMT.BOVIN STANDARD; PRT; 9 AA.
AC P29177;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Methylated-DNA--protein-cysteine methyltransferase (EC 2.1.1.63) (6-O-
DE methylguanine-DNA methyltransferase) (Fragment).
GN MGMT.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]

SEQUENCE.
RX MEDLINE=90174912; PubMed=2308822;
RA Rydberg B., Hall J., Karran P.;
RT "Active site amino acid sequence of the bovine O6-methylguanine-DNA
RT methyltransferase.";
RL Nucleic Acids Res. 18:17-21(1990).
CC -!- FUNCTION: REPAIR OF ALKYLATED GUANINE IN DNA BY STOICHIOMETRICALLY
CC TRANSFERRING THE ALKYL GROUP AT THE O-6 POSITION TO A CYSTEINE IS
CC RESIDUE IN THE ENZYME. THIS IS A SUICIDE REACTION: THE ENZYME IS
CC IRREVERSIBLY INACTIVATED.
CC -!- CATALYTIC ACTIVITY: DNA (containing 6-O-methylguanine) + protein
CC [protein]-L-cysteine = DNA (without 6-O-methylguanine) + protein
CC S-methyl-L-cysteine.
CC -!- SIMILARITY: WITH SEGMENTS OF E. COLI ADA AND OGT METHYLTRANSFERASE
CC WHICH ENCOMPASS THE ALKYL-ACCEPTOR RESIDUES.
DR InterPro; IPR001497; Methyltransf_1.
DR PROSITE; PS00374; MGMT; PARTIAL.
KW DNA repair; Transferase; Methyltransferase.
FT NON TER 1 1
FT ACT SITE 9 9 ALKYL GROUP ACCEPTOR (BY SIMILARITY).
FT NON TER 9 9
SQ SEQUENCE 9 AA; 967 MW; 325171A720476047 CRC64;

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Query Match      11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 LT 3
        |||
Db      6 LT 7.

RESULT 72
MOSH CLYJA      STANDARD;      PRT;      9 AA.
AC P19852;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Sperm-activating peptide SAP-b ([His6]-mosact).
OS Clypeaster japonicus (Sand dollar). Eleutherozoa; Echinozoa;
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Gnathostomata; Clypeasteroidea;
OC Clypeasteridae; Clypeaster.
OX NCBI_TaxID=7644;
RN [1]
RN SEQUENCE.
RC TISSUE=Egg jelly;
RA Suzuki N., Kurita M., Yoshino K.I., Kajiuura H., Nomura K.,
RT Yamaguchi M.;
RT "Purification and structure of mosact and its derivatives from the
RT egg jelly of the sea urchin Clypeaster japonicus.";
RL Zool. Sci. 4:649-656(1987).
RN [2]
RN BROMINATION OF HIS-6.
RX MEDLINE=91167743; PubMed=2076468;
RA Takao T., Yoshino K., Suzuki N., Shimonishi Y.;
RT "Analysis of post-translational modifications of proteins by accurate
RT mass measurement in fast atom bombardment mass spectrometry.";
RL Biomed. Environ. Mass Spectrom. 19:705-712(1990).
CC -!- FUNCTION: Stimulates sperm respiration and motility.
DR PIR; JN0026; JN0026.
KW Bromination.
FT MOD RES      6      BROMINATION (PARTIAL).
SQ SEQUENCE      9 AA; 914 MW; 93245721EDC5B4B5 CRC64;

Query Match      11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      11 HL 12
        |||
Db      6 HL 7

RESULT 73
OXYA_SQUAC      STANDARD;      PRT;      9 AA.
AC P42959;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Aspartocin (Aspartogocin).
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.
OX NCBI_TaxID=7797;
RN [1]
RN SEQUENCE.
RC MEDLINE=73031727; PubMed=5083037;
RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Phylogeny of the neurohypophysial hormones. Two new active peptides
RT isolated from a cartilaginous fish, Squalus acanthias.";
RL Eur. J. Biochem. 29:12-19(1972).
RN [2]

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RP SEQUENCE.
RX MEDLINE=72128038; PubMed=4622083;
RA Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
RT "Identification of 2 new neurohypophysial hormones, valitocin (Val8-
RT oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the
RT spiny dog-fish (Squalus acanthias).";
RL C. R. Acad. Sci., D, Sci. Nat. 274:313-316(1972).
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro; IPR000981; Neurohyp_horm.
DR Pfam; PF00220; hormone4; 1.
KW PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID      1      9      AMIDATION.
FT MOD RES      9 AA; 996 MW; 17F8376EB44404B CRC64;
SQ SEQUENCE      9 AA; 996 MW; 17F8376EB44404B CRC64;

Query Match      11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      13 PL 14
        |||
Db      7 PL 8

RESULT 74
OXYT_RABIT      STANDARD;      PRT;      9 AA.
AC P32878; P01188;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Oxytocin (Oxytocin).
OS Oryctolagus cuniculus (Rabbit),
OS Hippopotamus amphibius (Hippopotamus),
OS Balaenoptera physalus (Finback whale) (Common rorqual), and
OS Tachyglus aculeatus aculeatus (Australian echidna), and
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986, 9833, 9770, 49271, 7873;
RN [1]
RN SEQUENCE.
RC SPECIES=Rabbit;
RX MEDLINE=72215060; PubMed=5150741;
RA Chauvet J., Chauvet M.-T., Acher R.;
RT "Evolution of neurohypophysial hormones: isolation of active
RT principles from rabbits and rats.";
RL Biochimie 53:1099-1104(1971).
RN [2]
RN SEQUENCE.
RC SPECIES=H.amphibius;
RX MEDLINE=71232719; PubMed=5406007;
RA Ferguson D.R., Pickering B.T.;
RT "Arginine and lysine vasopressins in the hippopotamus
RT neurohypophysis.";
RL Gen. Comp. Endocrinol. 13:425-429(1969).
RN [3]
RN SEQUENCE.
RC SPECIES=B.physalus;
RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Isolation of finback whale oxytocin and vasopressin.";
RL Nature 201:191-192(1964).
RN [4]
RN SEQUENCE.
RC SPECIES=A.aculeatus;
RX MEDLINE=73223515; PubMed=4515919;
RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Neurohypophysial hormones and evolution of tetrapods.";
RL Nature New Biol. 244:124-126(1973).
RN [5]
RN SEQUENCE.
RC SPECIES=H.colliiei;

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Wed Nov 26 09:07:12 2003

us-09-641-801-23.oligo.rsp

Db 3 DV 4  
Search completed: November 25, 2003, 19:28:22  
Job time : 6.45515 secs

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RX MEDLINE=70088110; PubMed=5366118;
RA Pickering B.T., Heller H.;
RT "Oxytocin as a neurophysiophysial hormone in the holocephalian
RT elasmobranch fish, Hydroloagus collei.";
RL J. Endocrinol. 45:597-606(1969).
CC -!- FUNCTION: OXYTOCIN CAUSES CONTRACTION OF THE SMOOTH MUSCLE OF THE
CC UTERUS AND OF THE MAMMARY GLAND.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR; A91466; A91466.
DR PIR; A92774; A92774.
DR PIR; A93147; A93147.
DR PIR; A93408; A93408.
DR PIR; B90667; B90667.
DR PDB; 1XY1; 15-OCT-90.
DR PDB; 1XY2; 15-OCT-90.
DR InterPro; IPR000981; Neurhyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Hypothalamus; Amidation; 3D-structure.
FT DISULFID 1
FT MOD_RES 9
FT SEQUENCE 9 AA; 1010 MW; 17F8376EB456D04B CRC64;
SQ AMIDATION
Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 13 PL 14
DB 7 PL 8
RESULT 75
PPH1_LYCES
ID PPH1_LYCES STANDARD; PRT; 9 AA.
AC P83380;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Purple acid phosphatase isozyme LesAP1 (EC 3.1.3.2) (Fragment).
OS Lycopersicon esculentum (tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE, CATALYTIC ACTIVITY, SUBUNIT, SUBCELLULAR LOCATION, AND
RP GLYCOSYLATION.
RC STRAIN=cv. Moneymaker; TISSUE=Seed;
RX MEDLINE=22361242; PubMed=12473124;
RA Bozzo G.G., Raghothama K.G., Plaxton W.C.;
RT "Purification and characterization of two secreted purple acid
RT phosphatase isozymes from phosphate-starved tomato (Lycopersicon
RT esculentum) cell cultures.";
RL Eur. J. Biochem. 269:6278-6286(2002).
CC -!- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an
CC alcohol + phosphate.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: Glycosylated.
CC -!- MISCELLANEOUS: In L.esculentum there are at least two isozymes of
CC purple acid phosphatase.
KW Hydrolase; Glycoprotein.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 1005 MW; 3F17C04B5042CAA8 CRC64;
Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 6 DV 7
||
```



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QM protein - protein search, using sw model

Run on: November 25, 2003, 18:25:50 ; Search time 33.8023 Seconds  
(without alignments)  
137.415 Million cell updates/sec

Title: US-09-641-801-23

Perfect score: 18

Sequence: 1 SLTLTDEKHLPLPLVQ 18

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size: 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database:

SPTREMBL 23:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertibrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5	27.8	17	4	Q96P96
2	5	27.8	19	4	Q9UC6
3	4	22.2	8	8	P93963
4	4	22.2	8	8	P92384
5	4	22.2	8	8	P93973
6	4	22.2	8	8	P92215
7	4	22.2	8	8	P93957
8	4	22.2	8	8	P92222
9	4	22.2	8	8	P92388
10	4	22.2	8	8	P92441
11	4	22.2	8	8	P92404
12	4	22.2	8	8	P93961
13	4	22.2	8	8	P93970
14	4	22.2	8	8	P93955
15	4	22.2	8	8	P93965
16	4	22.2	8	8	P92394

17	4	22.2	8	8	P92382	P92382 hordeum bra
18	4	22.2	8	8	P93966	P93966 aegilops sp
19	4	22.2	8	8	P92227	P92227 crithopsis
20	4	22.2	8	8	P92373	P92373 haynaldia v
21	4	22.2	8	8	P92211	P92211 agropyron c
22	4	22.2	8	8	P92428	P92428 peridictyon
23	4	22.2	8	8	P93959	P93959 hordeum ere
24	4	22.2	8	8	P92219	P92219 australopyr
25	4	22.2	8	8	P93985	P93985 aegilops co
26	4	22.2	8	8	P92443	P92443 taeniatheru
27	4	22.2	8	8	P92391	P92391 heteranthel
28	4	22.2	8	8	P93981	P93981 crithodium
29	4	22.2	8	8	P93992	P93992 pseudoroegn
30	4	22.2	8	8	P92426	P92426 aegilops ta
31	4	22.2	8	8	P92431	P92431 psathyrosta
32	4	22.2	8	8	P92422	P92422 psathyrosta
33	4	22.2	9	4	Q16220	Q16220 homo sapien
34	4	22.2	11	4	Q9UELO	Q9UELO homo sapien
35	4	22.2	13	12	Q9WMG5	Q9WMG5 sigma virus
36	4	22.2	15	8	Q9T2K8	Q9T2K8 spinacia ol
37	4	22.2	15	12	Q66174	Q66174 human coron
38	4	22.2	16	4	Q9NMZ2	Q9NMZ2 homo sapien
39	4	22.2	16	4	O00497	O00497 homo sapien
40	4	22.2	17	8	Q9TDQ2	Q9TDQ2 macaca sylv
41	4	22.2	17	8	Q9T379	Q9T379 macaca sylv
42	4	22.2	18	4	Q16244	Q16244 homo sapien
43	4	22.2	18	6	Q8WN06	Q8WN06 bos taurus
44	4	22.2	19	8	Q31687	Q31687 artemia par
45	4	22.2	19	15	Q905F5	Q905F5 human immun
46	4	22.2	20	2	Q9R9A5	Q9R9A5 nitrosospir
47	4	22.2	20	2	Q9R987	Q9R987 nitrosospir
48	4	22.2	20	4	Q96T45	Q96T45 homo sapien
49	4	22.2	20	10	Q9S900	Q9S900 vigna sinen
50	4	22.2	20	11	Q9QW2	Q9QW2 rattus sp.
51	4	22.2	20	15	Q85636	Q85636 moloney mur
52	3	16.7	5	13	P83308	P83308 gallus gall
53	3	16.7	7	10	P93233	P93233 lycopersico
54	3	16.7	7	12	Q66205	Q66205 transmissib
55	3	16.7	7	13	O42564	O42564 fugu rubrip
56	3	16.7	8	2	Q9R9C2	Q9R9C2 borrelia bu
57	3	16.7	8	6	Q9XSY1	Q9XSY1 canis fami
58	3	16.7	8	6	Q9SM23	Q9SM23 sus scrofa
59	3	16.7	8	9	Q8SBJ0	Q8SBJ0 bacterioph
60	3	16.7	8	9	Q8H9K1	Q8H9K1 bacterioph
61	3	16.7	9	2	Q31363	Q31363 borrelia ga
62	3	16.7	9	2	P83157	P83157 anabaena sp
63	3	16.7	9	4	Q16605	Q16605 homo sapien
64	3	16.7	9	5	Q9TWV0	Q9TWV0 anthopleura
65	3	16.7	9	8	Q94VD8	Q94VD8 varanus nil
66	3	16.7	9	8	Q94VC6	Q94VC6 varanus pil
67	3	16.7	9	8	Q94V61	Q94V61 varanus mer
68	3	16.7	9	10	Q9S8J8	Q9S8J8 oryza sativ
69	3	16.7	9	11	Q61723	Q61723 mus musculu
70	3	16.7	9	15	Q85723	Q85723 simian sarc
71	3	16.7	9	16	Q935G1	Q935G1 salmone
72	3	16.7	10	2	Q9XBH3	Q9XBH3 bacillus ce
73	3	16.7	10	2	Q9R5T2	Q9R5T2 acetobacter
74	3	16.7	10	2	P83154	P83154 anabaena sp
75	3	16.7	10	8	Q9TG86	Q9TG86 diplogloesu
76	3	16.7	10	8	Q94V97	Q94V97 varanus spe
77	3	16.7	10	8	Q94VD5	Q94VD5 varanus oli
78	3	16.7	10	8	Q94VC9	Q94VC9 varanus pan
79	3	16.7	10	8	Q94VF0	Q94VF0 varanus kin
80	3	16.7	10	8	P92771	P92771 xenosaurus
81	3	16.7	10	8	Q94V85	Q94V85 varanus var
82	3	16.7	10	8	Q94PD8	Q94PD8 varanus sca
83	3	16.7	10	8	Q9TG38	Q9TG38 ophisaurus
84	3	16.7	10	8	P92576	P92576 bipes bipor
85	3	16.7	10	8	Q9TG35	Q9TG35 ophisaurus
86	3	16.7	10	8	Q94VD2	Q94VD2 varanus pan
87	3	16.7	10	10	Q9FS93	Q9FS93 silene pent
88	3	16.7	10	11	Q9QVF7	Q9QVF7 rattus sp.
89	3	16.7	10	11	Q9ESU5	Q9ESU5 mus musculu

Q88082 chimpanzee  
 Q47606 escherichia  
 Q9K332 staphylococ  
 Q47569 escherichia  
 Q8HYM4 felis silve  
 Q8TQB3 homo sapien  
 Q94V94 varanus sto  
 Q94V98 varanus gou  
 Q9G616 ceratophora  
 Q9G610 lyriocephal  
 Q9G5V3 phrynoceph

## ALIGNMENTS

## RESULT 1

Q96P96 PRELIMINARY; PRT; 17 AA.  
 ID Q96P96;  
 AC Q96P96;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE NHP2-like protein (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kang H.S., Park Y.J., Jung H.M., Jun D.Y., Huh T.L., Kim Y.H.;  
 RT "Characterization of TPA-responsive genes in U937 cells using ordered  
 RT differential display PCR."  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF401217; AAL02173.1; -;  
 FT NON\_TER 1  
 SQ SEQUENCE 17 AA; 1948 MW; AB699919BD70BCEFF CRC64;

Query Match 27.8%; Score 5; DB 4; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLPL 16  
 |||||  
 DB 13 LPLPL 17

## RESULT 2

Q9UCK6 PRELIMINARY; PRT; 19 AA.  
 ID Q9UCK6;  
 AC Q9UCK6;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
 DE Aspartylglucosaminidase beta 1 subunit (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=93111925; PubMed=1281977;  
 RA Rip J.W., Coulter-Mackie M.B., Rupa C.A., Gordon B.A.;  
 RT "Purification and structure of human liver aspartylglucosaminidase."  
 RL Biochem. J. 288:1005-1010(1992).  
 DR HSP; P20933; IAPY.  
 SQ SEQUENCE 19 AA; 2127 MW; BC2F148525610300 CRC64;

Query Match 27.8%; Score 5; DB 4; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLPLV 17

Db 2 PLPLV 6  
 |||||

## RESULT 3

P93963 PRELIMINARY; PRT; 8 AA.  
 ID P93963;  
 AC P93963;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE PetD protein (Fragment).  
 GN PETD.  
 OS Psathyrostachys stoloniformis.  
 OG Chloroplast  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Psathyrostachys.  
 OX NCBI\_TaxID=58873;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H9182; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 RT sequence data."  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77754; CAB01341.1; -;  
 KW Chloroplast.  
 FT NON\_TER 1  
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4  
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 DB 2 SLTL 5

## RESULT 4

P92384 PRELIMINARY; PRT; 8 AA.  
 ID P92384;  
 AC P92384;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE PetD protein (Fragment).  
 GN PETD.  
 OS Hordeum murinum subsp. glaucum.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Hordeum.  
 OX NCBI\_TaxID=98113;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H801; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 RT sequence data."  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77762; CAB01365.1; -;  
 KW Chloroplast.  
 FT NON\_TER 1  
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTL 4  
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|  
Db 2 SLTL 5

## RESULT 5

P93973 PRELIMINARY; PRT; 8 AA.  
AC P93973;  
DT 01-MAY-1997 (TReMBLrel. 03, Created)  
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE PetD protein (Fragment).  
GN PETD.  
OS Eremopyrum distans.  
OS Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
OC Triticeae; Eremopyrum.  
OX NCBI\_TaxID=58936;  
[1]  
RN SEQUENCE FROM N.A.  
RP STRAIN=H5552; TISSUE=Leaf;  
RC MEDLINE=97271648; PubMed=9126564;  
RX Petersen G.; Seberg O.;  
RA "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
sequence data.";  
RT Mol. Phylogenet. Evol. 7:217-230(1997).  
RL EMBL; Z77745; CAB01314.1; -.  
KW Chloroplast.  
FT NON\_TER 1  
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTL 4  
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|  
Db 2 SLTL 5

## RESULT 6

P92215 PRELIMINARY; PRT; 8 AA.  
AC P92215;  
DT 01-MAY-1997 (TReMBLrel. 03, Created)  
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE PetD protein (Fragment).  
GN PETD.  
OS Amblyopyrum muticum.  
OS Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
OC Triticeae; Amblyopyrum.  
OX NCBI\_TaxID=4595;  
[1]  
RN SEQUENCE FROM N.A.  
RP STRAIN=H5572; TISSUE=Leaf;  
RC MEDLINE=97271648; PubMed=9126564;  
RX Petersen G.; Seberg O.;  
RA "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
sequence data.";  
RT Mol. Phylogenet. Evol. 7:217-230(1997).  
RL EMBL; Z77736; CAB01347.1; -.  
KW Chloroplast.  
FT NON\_TER 1  
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTL 4  
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Db 2 SLTL 5

## RESULT 7

P93957 PRELIMINARY; PRT; 8 AA.  
AC P93957;  
DT 01-MAY-1997 (TReMBLrel. 03, Created)  
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE PetD protein (Fragment).  
GN PETD.  
OS Festucopsis serpentina.  
OS Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
OC Triticeae; Festucopsis.  
OX NCBI\_TaxID=72456;  
[1]  
RN SEQUENCE FROM N.A.  
RP STRAIN=H6511; TISSUE=Leaf;  
RC MEDLINE=97271648; PubMed=9126564;  
RX Petersen G.; Seberg O.;  
RA "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
sequence data.";  
RT Mol. Phylogenet. Evol. 7:217-230(1997).  
RL EMBL; Z79501; CAB01777.1; -.  
KW Chloroplast.  
FT NON\_TER 1  
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTL 4  
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|  
Db 2 SLTL 5

## RESULT 8

P92222 PRELIMINARY; PRT; 8 AA.  
AC P92222;  
DT 01-MAY-1997 (TReMBLrel. 03, Created)  
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE PetD protein (Fragment).  
GN PETD.  
OS Bromus inermis (Smooth brome grass).  
OS Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
OC Bromaeae; Bromus.  
OX NCBI\_TaxID=15371;  
[1]  
RN SEQUENCE FROM N.A.  
RP STRAIN=OSA414; TISSUE=Leaf;  
RC MEDLINE=97271648; PubMed=9126564;  
RX Petersen G.; Seberg O.;  
RA "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
sequence data.";  
RT Mol. Phylogenet. Evol. 7:217-230(1997).  
RL EMBL; Z77759; CAB01356.1; -.  
KW Chloroplast.  
FT NON\_TER 1  
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Wed Nov 26 09:07:12 2003

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTL 4  
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Db 2 SLTL 5

## RESULT 9

ID P92388 PRELIMINARY; PRT; 8 AA.  
AC P92388;  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE PetD protein (Fragment).  
GN PETD.  
OS Henrardia persica.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Triticeae; Henrardia.  
OX NCBI\_TaxID=37678;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H5556; TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G.; Seberg O.;  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
sequence data.";  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; Z77748; CAB01323.1; -.  
KW Chloroplast.  
FT NON\_TER  
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;

Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTL 4  
|||||  
Db 2 SLTL 5

## RESULT 10

ID P92441 PRELIMINARY; PRT; 8 AA.  
AC P92441;  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE PetD protein (Fragment).  
GN PETD.  
OS Thinopyrum bessarabicum.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Triticeae; Thinopyrum.  
OX NCBI\_TaxID=4601;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H6725; TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G.; Seberg O.;  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
sequence data.";  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; Z77769; CAB01386.1; -.  
KW Chloroplast.  
FT NON\_TER  
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;

Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTL 4  
|||||  
Db 2 SLTL 5

## RESULT 11

ID P92404 PRELIMINARY; PRT; 8 AA.  
AC P92404;  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE PetD protein (Fragment).  
GN PETD.  
OS Lophopyrum elongatum (Tall wheatgrass) (Argopyrum elongatum).  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Triticeae; Lophopyrum.  
OX NCBI\_TaxID=4588;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H6592; TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G.; Seberg O.;  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
sequence data.";  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; Z77743; CAB01308.1; -.  
KW Chloroplast.  
FT NON\_TER  
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;

Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTL 4  
|||||  
Db 2 SLTL 5

## RESULT 12

ID P93961 PRELIMINARY; PRT; 8 AA.  
AC P93961;  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE PetD protein (Fragment).  
GN PETD.  
OS Peathrostachys rupestris.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Triticeae; Psathyrostachys.  
OX NCBI\_TaxID=58938;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H6703; TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G.; Seberg O.;  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
sequence data.";  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; Z77755; CAB01344.1; -.  
KW Chloroplast.  
FT NON\_TER  
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4  
 ||||  
 Db 2 SLTL 5

## RESULT 13

P93970 ID P93970 PRELIMINARY; PRT; 8 AA.  
 AC P93970;  
 DT 01-MAY-1997 (TREMBlrel. 03, Created)  
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE PetD protein (Fragment).  
 GN PETD.  
 OS Eremopyrum triticeum.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Eremopyrum.  
 OC NCBI\_TaxID=58937;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H5553; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data.";  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 RL EMBL; Z77746; CAB01315.1; -.  
 DR Eremopyrum triticeum.  
 KW Chloroplast.  
 FT NON TER  
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4  
 ||||  
 Db 2 SLTL 5

## RESULT 14

P93955 ID P93955 PRELIMINARY; PRT; 8 AA.  
 AC P93955;  
 DT 01-MAY-1997 (TREMBlrel. 03, Created)  
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE PetD protein (Fragment).  
 GN PETD.  
 OS Festucopsis festuoides.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Festucopsis.  
 OC NCBI\_TaxID=72455;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H6731; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data.";  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 RL EMBL; Z77770; CAB01389.1; -.  
 DR Festucopsis festuoides.  
 KW Chloroplast.  
 FT NON TER  
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4  
 ||||  
 Db 2 SLTL 5

## RESULT 15

P93965 ID P93965 PRELIMINARY; PRT; 8 AA.  
 AC P93965;  
 DT 01-MAY-1997 (TREMBlrel. 03, Created)  
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE PetD protein (Fragment).  
 GN PETD.  
 OS Secale strictum.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Secale.  
 OC NCBI\_TaxID=58866;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H4342; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data.";  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 RL EMBL; Z77765; CAB01373.1; -.  
 DR Secale strictum.  
 KW Chloroplast.  
 FT NON TER  
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4  
 ||||  
 Db 2 SLTL 5

## RESULT 16

P92394 ID P92394 PRELIMINARY; PRT; 8 AA.  
 AC P92394;  
 DT 01-MAY-1997 (TREMBlrel. 03, Created)  
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE PetD protein (Fragment).  
 GN PETD.  
 OS Hordeum vulgare (Barley).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Hordeum.  
 OC NCBI\_TaxID=4513;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H3139; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data.";  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 RL EMBL; Z77764; CAB01371.1; -.  
 DR Hordeum vulgare (Barley).  
 KW Chloroplast.  
 FT NON TER  
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;  
 Query Match 22.2%; Score 4; DB 8; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4  
 Db 2 SLTL 5

RESULT 17  
 P92382 PRELIMINARY; PRT; 8 AA.  
 ID P92382  
 AC P92382; 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE PetD protein (Fragment).  
 GN PETD.  
 OS Hordeum brachyantherum.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Hordeum.  
 OC NCBI\_TaxID=52712;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data."; Evol. 7:217-230(1997).  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77761; CAB01362.1; -.  
 KW Chloroplast.  
 FT NON TER  
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4  
 Db 2 SLTL 5

RESULT 18  
 P93966 PRELIMINARY; PRT; 8 AA.  
 ID P93966  
 AC P93966; 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE PetD protein (Fragment).  
 GN PETD.  
 OS Aegilops speltoides (Goat grass).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Aegilops.  
 OC NCBI\_TaxID=4573;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H4523; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data."; Evol. 7:217-230(1997).  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77766; CAB01377.1; -.  
 KW Chloroplast.

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KW Chloroplast. 1 1
FT NON_TER 8 AA; 878 MW; 1EC7287731A735B3 CRC64;
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match
Best Local Similarity 22.2%; Score 4; DB 8; Length 8;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
Db 2 SLTL 5

RESULT 21
P92211 ID P92211 PRELIMINARY; PRT; 8 AA.
AC P92211;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Agropyron cristatum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Agropyron.
OX NCBI_TaxID=4593;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H4349; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77771; CAB01392.1; -.
KW Chloroplast.
FT NON_TER 1
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match
Best Local Similarity 22.2%; Score 4; DB 8; Length 8;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
Db 2 SLTL 5

RESULT 22
P92428 ID P92428 PRELIMINARY; PRT; 8 AA.
AC P92428;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Peridictyon sanctum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Peridictyon.
OX NCBI_TaxID=37683;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H5575; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).

DR EMBL; Z77749; CAB01326.1; -.
KW Chloroplast.
FT NON_TER 1
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match
Best Local Similarity 22.2%; Score 4; DB 8; Length 8;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
Db 2 SLTL 5

RESULT 23
P93959 ID P93959 PRELIMINARY; PRT; 8 AA.
AC P93959;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Hordeum erectifolium.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=58926;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H1150; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z79500; CAB01776.1; -.
KW Chloroplast.
FT NON_TER 1
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match
Best Local Similarity 22.2%; Score 4; DB 8; Length 8;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
Db 2 SLTL 5

RESULT 24
P92219 ID P92219 PRELIMINARY; PRT; 8 AA.
AC P92219;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Australopyrum retrofractum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Australopyrum.
OX NCBI_TaxID=4597;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H6723; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).

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RL Mol. Phylogenetic. Evol. 7:217-230(1997).
DR EMBL; Z77767; CAB01380.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 8 AA; 860 MW; BIC7287731A735AA CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
Db 2 SLTL 5

RESULT 25
P93985 PRELIMINARY; PRT; 8 AA.
ID P93985;
AC P93985;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Aegilops comosa.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Aegilops.
OX NCBI_TaxID=4485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H6673; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G.; Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenetic. Evol. 7:217-230(1997).
DR EMBL; Z77742; CAB01305.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
Db 2 SLTL 5

RESULT 26
P92443 PRELIMINARY; PRT; 8 AA.
ID P92443;
AC P92443;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Taeniatherum caput-medusae (Medusahead).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Taeniatherum.
OX NCBI_TaxID=37687;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H10254; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G.; Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenetic. Evol. 7:217-230(1997).
DR EMBL; Z77760; CAB01359.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
Db 2 SLTL 5

RESULT 27
P92391 PRELIMINARY; PRT; 8 AA.
ID P92391;
AC P92391;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Heteranthellium piliferum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Heteranthellium.
OX NCBI_TaxID=37679;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H5557; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G.; Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenetic. Evol. 7:217-230(1997).
DR EMBL; Z77750; CAB01329.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
Db 2 SLTL 5

RESULT 28
P93981 PRELIMINARY; PRT; 8 AA.
ID P93981;
AC P93981;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Crithodium monococcum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Crithodium.
OX NCBI_TaxID=72428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H4547; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G.; Seberg O.;

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RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data."; RA Petersen G.; Seberg O.;  
 RL Mol. Phylogenet. Evol. 7:217-230 (1997). RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data."; RA Petersen G.; Seberg O.;  
 DR EMBL; Z77757; CAB01350.1; -. RL Mol. Phylogenet. Evol. 7:217-230 (1997).  
 KW Chloroplast. DR EMBL; Z77744; CAB01311.1; -.  
 FT NON\_TER 1 1 1 1 1  
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTL 4  
 Db 2 SLTL 5

## RESULT 29

P93992 ID P93992 PRELIMINARY; PRT; 8 AA.  
 AC P93992;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE PetD protein (Fragment).  
 GN PETD.  
 OS Australopyrum velutinum.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Australopyrum.  
 OC NCBI\_TaxID=58935;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H6724; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G.; Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data."; RA Petersen G.; Seberg O.;  
 RL Mol. Phylogenet. Evol. 7:217-230 (1997).  
 DR EMBL; Z77768; CAB01383.1; -.  
 KW Chloroplast.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTL 4  
 Db 2 SLTL 5

## RESULT 30

P92426 ID P92426 PRELIMINARY; PRT; 8 AA.  
 AC P92426;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE PetD protein (Fragment).  
 GN PETD.  
 OS Pseudoroegneria spicata (Bluebunch wheatgrass) (Agropyron spicatum).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Pseudoroegneria.  
 OC NCBI\_TaxID=4604;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H9082; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;

RA Petersen G.; Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data."; RA Petersen G.; Seberg O.;  
 RL Mol. Phylogenet. Evol. 7:217-230 (1997).  
 DR EMBL; Z77744; CAB01311.1; -.  
 KW Chloroplast.  
 FT NON\_TER 1 1 1 1 1  
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTL 4  
 Db 2 SLTL 5

## RESULT 31

P92431 ID P92431 PRELIMINARY; PRT; 8 AA.  
 AC P92431;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE PetD protein (Fragment).  
 GN PETD.  
 OS Aegilops tauschii (Aegilops squarrosa).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Aegilops.  
 OC NCBI\_TaxID=37682;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H6668; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G.; Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data."; RA Petersen G.; Seberg O.;  
 RL Mol. Phylogenet. Evol. 7:217-230 (1997).  
 DR EMBL; Z77758; CAB01353.1; -.  
 KW Chloroplast.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTL 4  
 Db 2 SLTL 5

## RESULT 32

P92422 ID P92422 PRELIMINARY; PRT; 8 AA.  
 AC P92422; P92420;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last annotation update)  
 DE Chloroplast RPOA gene (Fragment).  
 GN PETD.  
 OS Psathyrostachys fragilis.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Psathyrostachys.  
 OC NCBI\_TaxID=37729;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H4372, and H917; TISSUE=Leaf;

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RA Petersen G., Seberg O.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z77753; CAB01338.1; -.
DR EMBL; Z77752; CAB01335.1; -.
FW Chloroplast.
KW NON TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
Db 2 SLTL 5
|||||

RESULT 33
Q16220 PRELIMINARY; PRT; 9 AA.
AC Q16220;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE HGRP protein (Fragment).
GN HGRP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94320083; PubMed=8044796;
RA Nagalla S.R., Spindel E.R.;
RT "Functional analysis of the 5'-flanking region of the human gastrin-
RT releasing peptide gene in small cell lung carcinoma cell lines.";
RT Cancer Res. 54:4461-4467(1994).
DR EMBL; S73265; AAD14116.1; -.
FT NON TER
SQ SEQUENCE 9 AA; 1070 MW; 77FE37672B040864 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 LPLV 17
Db 6 LPLV 9
|||||

RESULT 34
Q9UELO PRELIMINARY; PRT; 11 AA.
AC Q9UELO;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE FAS antigen (CD95 antigen) (Fragment).
GN CD95.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Blood;
MEDLINE=95355401; PubMed=7543095;
RA Wada N., Matsumura M., Ohba Y., Kobayashi N., Takizawa T.,
RA Nakanishi Y.;
RT "Transcription stimulation of the Fas-encoding gene by nuclear factor
RT for interleukin-6 expression upon influenza virus infection.";
RT J. Biol. Chem. 270:18007-18012(1995).
RN [2]

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RP SEQUENCE FROM N.A.
RA Muschen M., Re D., Brauning A., Wolf J., Hansmann M.L., Diehl V.,
RA Kupperts R., Rajewsky K.;
RT "Somatic mutations of the CD95 gene in Hodgkin- and Reed-Sternberg
RT cells.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Muschen M., Re D., Jungnickel B., Diehl V., Rajewsky K., Kupperts R.;
RT "Somatic mutations of the CD95 gene in human B cells as a side-effect
RT of the germinal center reaction.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22404279; PubMed=12516573;
RA Kurth J., Pernio A., Schmitz R., Iking-Konert C., Chiorazzi N.,
RA Thompson K.M., Winkler T., Rajewsky K., Kueppers R.;
RT "Lack of deleterious somatic mutations in the CD95 gene of
RT plasmablasts from systemic lupus erythematosus patients and
RT autoantibody-producing cell lines.";
RL Eur. J. Immunol. 32:3785-3792(2002).
DR EMBL; D31968; BAA20850.1; -.
DR EMBL; AJ279011; CAC35539.1; -.
DR EMBL; AJ279012; CAC35540.1; -.
DR EMBL; AJ279013; CAC35541.1; -.
DR EMBL; AJ509179; CAD48929.1; -.
DR EMBL; AJ509180; CAD48930.1; -.
FT NON TER
SQ SEQUENCE 11 AA; 1256 MW; 0802145E2731B370 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 LPLV 17
Db 8 LPLV 11
|||||

RESULT 35
Q9WMG5 PRELIMINARY; PRT; 13 AA.
AC Q9WMG5;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE 3 protein (Fragment).
GN GENE 3.
OS Sigma virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; unclassified Rhabdoviridae.
OX NCBI_TaxID=11301;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212481; PubMed=8384742;
RA Teninges D., Bras F., Dezelee S.;
RT "Genome organization of the sigma rhabdovirus: six genes and a gene
RT overlap.";
RL Virology 193:1018-1023(1993).
DR EMBL; S57850; AAD40700.1; -.
FT NON TER
SQ SEQUENCE 13 AA; 1456 MW; 9AF4F3FDE75832D5 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 LPLV 17
Db 8 LPLV 11
|||||

RESULT 36

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Q9T2K8
ID Q9T2K8 PRELIMINARY; PRT; 15 AA.
AC Q9T2K8
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE LHCII kinase, 64 kDa kinase (fragment).
OS Spinacia oleracea (Spinach).
CG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE
RX MEDLINE=92183823; PubMed=1544419;
RA Gal A., Herrmann R.G., Lottspeich F., Ohad I.;
RT "Phosphorylation of cytochrome b6 by the LHC II kinase associated with
RL the cytochrome complex.";
RL FEBS Lett. 298:33-35(1992).
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1556 MW; 6E00A4F917DDF33E CRC64;

Query Match 22.2%; Score 4; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DVEK 9
Db 6 DVEK 9

RESULT 37
Q66174
ID Q66174 PRELIMINARY; PRT; 15 AA.
AC Q66174
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Surface protein (fragment).
OS Human coronavirus (strain 229E).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=11137;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=229E;
RX MEDLINE=89366667; PubMed=2701946;
RA Raabe T., Siddell S.;
RT "Nucleotide sequence of the human coronavirus HCV 229E mRNA 4 and mRNA
RT 5 unique regions.";
RL Nucleic Acids Res. 17:6387-6387(1989).
DR EMBL; X15654; CAA33680.1; -.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1834 MW; 8CE369AE77DC4015 CRC64;

Query Match 22.2%; Score 4; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DVEK 9
Db 8 DVEK 11

RESULT 38
Q9NNZ2
ID Q9NNZ2 PRELIMINARY; PRT; 16 AA.
AC Q9NNZ2
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)

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DE Integrin alpha-2 subunit (fragment).
GN ITGA2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98421383; PubMed=9746778;
RA Kritzik M., Savage B., Nugent D.J., Santoso S., Ruggeri Z.M.,
RA Kunicki T.J.;
RT "Nucleotide polymorphisms in the alpha2 gene define multiple alleles
RT that are associated with differences in platelet alpha2 beta1
RT density.";
RL Blood 92:2382-2388(1998).
DR EMBL; AF062039; AAF77577.1; -.
FT NON_TER 16
FT NON_TER 16
SQ SEQUENCE 16 AA; 1635 MW; F6A5FC64F83370A9 CRC64;

Query Match 22.2%; Score 4; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PLPL 16
Db 10 PLPL 13

RESULT 39
O00497
ID O00497 PRELIMINARY; PRT; 16 AA.
AC O00497
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE DNA mismatch repair protein (fragment).
GN HMLH1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Palmitotta R., Veri M.C., Curia M.C., Aceto G., D'Amico F.,
RA Esposito D.L., Mariani-Costantini R., Messerini L., Mori S., Cama A.,
RA Battista P.;
RT "Transcripts with splicings of exons 15 and 16 of the hMLH1 gene in
RT normal lymphocytes: implications in RNA-based mutation screening of
RT hereditary nonpolyposis colorectal cancer.";
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF001359; AAB58936.1; -.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1850 MW; 996602B4FFF583D2 CRC64;

Query Match 22.2%; Score 4; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTL 4
Db 9 SLTL 12

RESULT 40
Q9TDQ2
ID Q9TDQ2 PRELIMINARY; PRT; 17 AA.
AC Q9TDQ2
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NADH dehydrogenase subunit 5 (fragment).
GN NDS.
OS Macaca sylvanus (Barbary ape).

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OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9546;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone;
RX MEDLINE=20028760; PubMed=10563020;
RA Bailey J.F., Henneberg M., Colson I.B., Ciarallo A., Hedges R.E.,
RA Sykes B.;
RT "Monkey business in Pompeii--unique find of a juvenile Barbary macaque
RT skeleton in Pompeii identified using osteology and ancient DNA
RT techniques.";
RL Mol. Biol. Evol. 16:1410-1414(1999).
RW EMBL; AF064450; AAF09257.1; -.
KW Mitochondrion.
FT NON TER 17 17
SQ SEQUENCE 17 AA; 2002 MW; CE16F446963413D2 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
DB 14 SLTL 17

RESULT 41
Q9T379 PRELIMINARY; PRT; 17 AA.
ID Q9T379;
AC Q9T379;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE NADH dehydrogenase subunit 5 (Fragment).
GN ND5.
OS Macaca sylvanus (Barbary ape).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9546;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone;
RX MEDLINE=20028760; PubMed=10563020;
RA Bailey J.F., Henneberg M., Colson I.B., Ciarallo A., Hedges R.E.M.,
RA Sykes B.;
RT "Monkey business in Pompeii - unique find of a juvenile Barbary
RT macaque skeleton in Pompeii identified using osteology and ancient DNA
RT techniques.";
RL Mol. Biol. Evol. 16:1410-1414(1999).
RW EMBL; AF064452; AAF09259.1; -.
DR EMBL; AF064451; AAF09258.1; -.
KW Mitochondrion.
FT NON TER 17 17
SQ SEQUENCE 17 AA; 1974 MW; CE16F45DE01D13D2 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4
DB 14 SLTL 17

RESULT 42
Q16244 PRELIMINARY; PRT; 18 AA.
ID Q16244
AC Q16244;
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DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE STS protein (Fragment).
GN STS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=95038775; PubMed=7951263;
RA Yen P.H., Ferrero G.B., Chinault A.C., Mohandas T., Ballabio A.;
RT "Characterization of the deletion breakpoints in a patient with
RT steroid sulfatase deficiency.";
RL Hum. Mutat. 4:76-78(1994).
RW EMBL; S74383; AAD14153.1; -.
FT NON TER 1 1
SQ SEQUENCE 18 AA; 1958 MW; 3B3072711330CCFA CRC64;

Query Match 22.2%; Score 4; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLPL 16
DB 2 PLPL 5

RESULT 43
Q8WN06 PRELIMINARY; PRT; 18 AA.
ID Q8WN06
AC Q8WN06;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Neuronal nicotinic receptor beta 4 subunit (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Valor L.M., Campos-Caro A., Carrasco-Serrano C., Ortiz J.A.,
RA Ballesta J.J., Criado M.;
RT "Transcription Factors NF-Y and Sp1 are Important Determinants of the
RT Promoter Activity of the Bovine and Human Neuronal Nicotinic Receptor
RT Beta4 Subunit Genes.";
RL J. Biol. Chem. 277:10000-10006(2002).
RW EMBL; AF453876; AAL57839.1; -.
DR Receptor.
KW Receptor.
FT NON TER 18 18
SQ SEQUENCE 18 AA; 1946 MW; 43BB1157148CEB76 CRC64;

Query Match 22.2%; Score 4; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 LPLV 17
DB 5 LPLV 8

RESULT 44
Q31687 PRELIMINARY; PRT; 19 AA.
ID Q31687
AC Q31687;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ATPase subunit 8 (Fragment).
GN ATP8.
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OS Artemia parthenogenetica.
OC Mitochondrion.
OG Eukaryota; Metazoa; Arthropoda; Crustacea; Branchiopoda; Anostraca;
OC Artemiidae; Artemia.
OX NCBI_TaxID=6663;
RN [1]_TaxID=6663;
RP SEQUENCE FROM N.A.
RC STRAIN=La Mata;
RX MEDLINE=94223692; PubMed=8169960;
RA Perez M.I., Valverde J.R., Batuecas B., Amat F., Marco R., Garesse R.;
RT "Speciation in the artemia genus: mitochondrial DNA analysis of
RT bisexual and parthenogenetic brine shrimps.";
RL J. Mol. Evol. 38:156-168(1994).
DR EMBL; X67263; CAA47685.1; -.
KW Mitochondrion.
FT NON TER 1
FT NON TER 19
SQ SEQUENCE 19 AA; 2246 MW; 41922AD313E087E3 CRC64;

Query Match 22.2%; Score 4; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLP 15
DB ||||
5 LPLP 8

RESULT 45
Q905F5 ID Q905F5 PRELIMINARY; PRT; 19 AA.
AC Q905F5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Rev protein (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retroviruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97CG311;
RA Taniguchi Y., Takehsia J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., M'Pandi M., M'Pele P., Harada Y., Hayami M.,
RA Ichimura H., Parra H.-J.;
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RT Republic of Congo-Brazzaville.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF410450; AAL10267.1; -.
FT NON TER 1
FT NON TER 19
SQ SEQUENCE 19 AA; 2221 MW; BE83B262BA711903 CRC64;

Query Match 22.2%; Score 4; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TDVE 8
DB ||||
2 TDVE 5

RESULT 46
Q9R9A5 ID Q9R9A5 PRELIMINARY; PRT; 20 AA.
AC Q9R9A5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Ammonia monooxygenase 1 subunit C (Fragment).
GN AMOCl.
OS Nitrosospira sp. NpAV.
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;

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OC Nitrosomonadaceae; Nitrosospira.
OX NCBI_TaxID=58133;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NpAV;
RX MEDLINE=96001263; PubMed=7557469;
RA Klotz M.G., Norton J.M.;
RT "Sequence of an ammonia monooxygenase subunit A-encoding gene from
RT Nitrosospira sp. NpAV.";
RL Gene 163:159-160(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NpAV;
RX MEDLINE=96275898; PubMed=8674986;
RA Norton J.M., Low J.M., Klotz M.G.;
RT "The gene encoding ammonia monooxygenase subunit A exists in three
RT nearly identical copies in Nitrosospira sp. NpAV.";
RL FEMS Microbiol. Lett. 139:181-188(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=NpAV;
RX MEDLINE=97306641; PubMed=9163908;
RA Klotz M.G., Alzerreca J., Norton J.M.;
RT "A gene encoding a membrane protein exists upstream of the amoA/amoB
RT genes in ammonia oxidizing bacteria: a third member of the amo
RT operon?";
RL FEMS Microbiol. Lett. 150:65-73(1997).
DR EMBL; AF032438; AAB86880.1; -.
KW Monooxygenase.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 20 AA; 2266 MW; A745DC66ACC3E2A9 CRC64;

Query Match 22.2%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LTDV 7
DB ||||
1 LTDV 4

RESULT 47
Q9R987 ID Q9R987 PRELIMINARY; PRT; 20 AA.
AC Q9R987;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Ammonia monooxygenase subunit C1 (Fragment).
GN AMOCl.
OS Nitrosospira sp. Np39-19.
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OX Nitrosomonadaceae; Nitrosospira.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Np39-19;
RA Norton J.M., Alzerreca J.J., Klotz M.G.;
RT "Diversity of the genes encoding ammonia monooxygenase in autotrophic
RT ammonia-oxidizing bacteria.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Np39-19;
RA Shiozawa T.L., Norton J.M., Alzerreca J.J., Klotz M.G.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF042170; AAC25054.1; -.
KW Monooxygenase.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 20 AA; 2266 MW; A745DC66ACC3F2A9 CRC64;

Query Match 22.2%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;

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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LTVL 7  
|||||  
Db 1 LTVL 4

## RESULT 48

Q96T45 ID Q96T45 PRELIMINARY; PRT; 20 AA.  
AC Q96T45;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE MER receptor tyrosine kinase (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20517330; PubMed=11062461;  
RA Gal A., Li Y., Thompson D.A., Weir J., Orth U., Jacobson S.G.,  
RA Apfelstedt-Sylla E., Vollrath D., Vollrath S.G.,  
RT "Mutations in MERK, the human orthologue of the RCS rat retinal  
RT dystrophy gene, cause retinitis pigmentosa."  
RL Nat. Genet. 26:270-271(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Gal A., Li Y., Thompson D.A., Weir J., Orth U., Jacobson S.G.,  
RA Apfelstedt-Sylla E., Vollrath D.,  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF366903; AAK54121.1; --  
KW Kinase; Receptor.  
FT NON\_TER 20  
SQ SEQUENCE 20 AA; 2232 MW; A853BEF7EECE2910 CRC64;

Query Match 22.2%; Score 4; DB 4; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.4e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PLPL 16  
|||||  
Db 5 PLPL 8

## RESULT 49

Q9S900 ID Q9S900 PRELIMINARY; PRT; 20 AA.  
AC Q9S900;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE C7 peptide (Fragment).  
OS Vigna sinensis (Cowpea).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.  
OX NCBI\_TaxID=3920;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92232221; PubMed=1368037;  
RA Hirano H., Kagawa H., Okubo K.,  
RA Phytochemistry 31:731-735(1992).  
RL DR HSP; P02248; IUBI  
DR InterPro; IPR000626; Ubiquitin.  
DR Pfam; PF00240; ubiquitin; 1.  
FT NON\_TER 20  
SQ SEQUENCE 20 AA; 2211 MW; BAA7DDE7501B6B9E CRC64;

Query Match

Best Local Similarity 100.0%; Score 4; DB 10; Length 20;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LTLT 5  
|||||  
Db 6 LTLT 9

## RESULT 50

Q9QUW2 ID Q9QUW2 PRELIMINARY; PRT; 20 AA.  
AC Q9QUW2;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE 22 kDa INTRALYSOSOMAL lipid-transfer protein (Fragment).  
OS Rattus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
OX NCBI\_TaxID=10118;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=97104296; PubMed=8948454;  
RA Kuwana T., Mullock B.M., Luzzio J.P.;  
RT "Identification of a lysosomal protein causing lipid transfer, using a  
RT fluorescence assay designed to monitor membrane fusion between rat  
RT liver endosomes and lysosomes."  
RL Biochem. J. 308:937-946(1995).  
DR HSP; P17900; IGI3.  
SQ SEQUENCE 20 AA; 2211 MW; 3A160591EA5542C5 CRC64;

Query Match 22.2%; Score 4; DB 11; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.4e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTL 4  
|||||  
Db 17 SLTL 20

## RESULT 51

Q85636 ID Q85636 PRELIMINARY; PRT; 20 AA.  
AC Q85636;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE Revertant mutant dl587rev patch region including partial LTR and gag  
DE (fragment).  
OS Moloney murine leukemia virus.  
OC Viruses; Retroid viruses; Retroviridae; Gammaretrovirus.  
OX NCBI\_TaxID=11801;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86089316; PubMed=2416955;  
RA Colicelli J., Goff S.P.;  
RT "Isolation of a recombinant murine leukemia virus utilizing a new  
RT primer tRNA."  
RL J. Virol. 57:37-45(1986).  
RN [2]  
RP SEQUENCE OF 1-5 FROM N.A.  
RX MEDLINE=88019205; PubMed=3660592;  
RA Colicelli J., Goff S.P.;  
RT "Identification of endogenous retroviral sequences as potential donors  
RT for recombinational repair of mutant retroviruses: Positions of  
RT crossover points."  
RL Virology 160:518-522(1987).  
DR EMBL; M12275; AAA46501.1; --  
DR InterPro; IPR000840; Gag\_MA.  
DR Pfam; PF01140; Gag\_MA; 1.  
FT NON\_TER 20  
SQ SEQUENCE 20 AA; 2214 MW; FB14F3F0FB11AC31 CRC64;

Query Match

Best Local Similarity 100.0%; Score 4; DB 15; Length 20;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTL 4  
|||  
Db 10 SLTL 13

## RESULT 52

P83308  
ID P83308 PRELIMINARY; PRT; 5 AA.  
AC P83308;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE FMRamide-like neuropeptide (LPLRF-amide).  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RC TISSUE=Brain;  
RX PubMed=6137771;  
RA Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;  
RT "A novel active pentapeptide from chicken brain identified by  
antibodies to FMRamide."  
RL Nature 305:328-330(1993).  
CC -!- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)  
FAMILY.  
KW Neuropeptide.  
SQ SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;

Query Match 16.7%; Score 3; DB 13; Length 5;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPL 14  
|||  
Db 1 LPL 3

## RESULT 53

P93233  
ID P93233 PRELIMINARY; PRT; 7 AA.  
AC P93233;  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE 1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14)  
DE (Fragment).  
GN LE-ACS1B.  
OS Lycopersicon esculentum (Tomato).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;  
OC Asteridae; Lamiales; Solanales; Solanaceae; Solanum.  
OX NCBI\_TaxID=4081;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97351561; PubMed=9207843;  
RA Oetiker J.H., Olson D.C., Shiu O.Y., Yang S.F.;  
RT "Differential induction of seven 1-aminocyclopropane-1-carboxylate  
synthase genes by elicitor in suspension cultures of tomato  
(Lycopersicon esculentum)."  
RL Plant Mol. Biol. 34:275-286(1997).  
DR EMBL; U75692; AAC49682.1; -.  
KW Lyase.  
FT NON TER 1  
SQ SEQUENCE 7 AA; 828 MW; 71B412C7377415D0 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PLV 17  
|||  
Db 3 PLV 5

## RESULT 54

Q66205  
ID Q66205 PRELIMINARY; PRT; 7 AA.  
AC Q66205;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Membrane protein (1 is 3rd base in codon) (Fragment).  
OS Transmissible gastroenteritis virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
OC Coronaviridae; Coronavirus.  
OX NCBI\_TaxID=11149;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FS772/70;  
RX MEDLINE=88216185; PubMed=2835592;  
RA Britton P., Carmenes R.S., Page K.W., Garwes D.J., Parra F.;  
RT "Sequence of the Nucleoprotein Gene from a Virulent British Field  
Isolate of Transmissible Gastroenteritis Virus and its Expression in  
Saccharomyces Cerevisiae."  
RL Mol. Microbiol. 2:89-99(1988).  
DR EMBL; Y00542; CAA68606.1; -.  
FT NON TER 1  
SQ SEQUENCE 7 AA; 869 MW; 72C691E727233B70 CRC64;

Query Match 16.7%; Score 3; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EKL 10  
|||  
Db 1 EKL 3

## RESULT 55

O42564  
ID O42564 PRELIMINARY; PRT; 7 AA.  
AC O42564;  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
DE Truncated voltage-gated sodium channel alpha subunit (Fragment).  
GN SCN8A.  
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
OC Tetraodontidae; Tetraodontidae; Takifugu.  
OX NCBI\_TaxID=31033;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97442476; PubMed=9295353;  
RA Plummer N.W., McBurney M.W., Meisler M.H.;  
RT "Alternative splicing of the sodium channel SCN8A predicts a truncated  
two-domain protein in fetal brain and non-neuronal cells."  
RL J. Biol. Chem. 272:24008-24015(1997).  
DR EMBL; U97673; AAB80916.1; -.  
KW Ionic channel.  
FT NON TER 1  
SQ SEQUENCE 7 AA; 730 MW; 75B72EA2C73772A0 CRC64;

Query Match 16.7%; Score 3; DB 13; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PLV 17

Qy	11 HLP 13	
Db	2 HLP 4	
RESULT 58		
Q95M23		
ID	Q95M23	PRELIMINARY; PRT; 8 AA.
AC	Q95M23;	
DT	01-DEC-2001 (TrEMBLrel. 19, Created)	
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)	
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)	
DE	Na+/K+ ATPase alpha subunit (EC 3.6.1.37) (Fragment).	
GN	ATP1A1.	
OS	Sus scrofa (Pig).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.	
NCBI_TaxID=9823;		
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=pietrain;	
RA	Blazkova P., Stratil A., Peelman L.J., Van Poucke M., Reiner G.,	
RA	Waldermann H., Kopecky M.;	
RT	"RH mapping of the porcine ATP1A1, ATP1B1, V-ATPase, IVL genes and	
RT	linkage assignments of ATP1a1 and IVL to chromosome 4.";	
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AJ3414138; CAC51422.1; -.	
DR	EMBL; AJ3414138; CAC51422.1; -.	
KW	Hydrolase.	
FT	NON TER	
FT	NON TER	
SQ	SEQUENCE 8 AA; 1117 MW; 604B41AB133B02D3 CRC64;	
Query Match 16.7%; Score 3; DB 6; Length 8;		
Best Local Similarity 100.0%; Pred. No. 8.3e+05;		
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	7 VEK 9	
Db	2 VEK 4	
RESULT 59		
Q8SBJ0		
ID	Q8SBJ0	PRELIMINARY; PRT; 8 AA.
AC	Q8SBJ0;	
DT	01-JUN-2002 (TrEMBLrel. 21, Created)	
DT	01-JUN-2002 (TrEMBLrel. 21, Last sequence update)	
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)	
DE	Gp30.2 (Fragment).	
GN	30.2.	
OS	Bacteriophage RB69.	
OS	Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;	
OC	T4-like viruses.	
OC	NCBI_TaxID=12353;	
EN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Piesinkiene L., Kolesinskiene G., Truncaite L., Zajackauskaite A.,	
RA	Nivinskas R.;	
RT	"Genomic region with genes 30.6-30.3 of T4-related bacteriophages.";	
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AJ439452; CAD28423.1; -.	
FT	NON TER	
FT	NON TER	
SQ	SEQUENCE 8 AA; 918 MW; F3B1A72041B76336 CRC64;	
Query Match 16.7%; Score 3; DB 9; Length 8;		
Best Local Similarity 100.0%; Pred. No. 8.3e+05;		
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	4 LTD 6	
Db	6 LTD 8	
RESULT 60		



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Q8H9K1
ID Q8H9K1 PRELIMINARY; PRT; 8 AA.
AC Q8H9K1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Gp30.2 protein (Fragment).
GN 30.2.
OS Bacteriophage L210.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC T4-like viruses.
OX NCBI_TaxID=192973;
RN [1]
RP SEQUENCE FROM N.A.
RA Kolesinskiene G., Nivinskis R.;
RT "A pair of overlapping genes 30.3 and 30.3' of T4-related
RT bacteriophages."
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ458400; CAD30256.1; -.
FT NON_TER
SQ SEQUENCE 8 AA; 918 MW; F3B1A72041B76336 CRC64;

Query Match 16.7%; Score 3; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LTD 6
Db 6 LTD 8

RESULT 61
O31363
ID O31363 PRELIMINARY; PRT; 9 AA.
AC O31363;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Outer surface protein C (Fragment).
OS OSCP.
GN Borrelia gattinii.
OS Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=29519;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PB1;
RX MEDLINE=97436044; PubMed=9282748;
RA Tilly K., Casjens S., Stevenson B., Bono J.L., Samuels D.S., Hogan D.,
RA Rosa P.;
RT "The Borrelia burgdorferi circular plasmid cp26: conservation of
RT plasmid structure and targeted inactivation of the ospC gene."
RL Mol. Microbiol. 25:361-374(1997).
DR EMBL; U93699; AAC45533.1; -.
FT NON_TER
SQ SEQUENCE 9 AA; 1019 MW; 4864C1A731A44333 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TLT 5
Db 5 TLT 7

RESULT 62
P83157
ID P83157 PRELIMINARY; PRT; 9 AA.
AC P83157;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Superoxide dismutase [Fe] (EC 1.15.1.1) (Fragment).

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OS Anabaena sp. (strain L31).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OX NCBI_TaxID=29412;
RN [1]
RP SEQUENCE.
RA Apte S.K., Uhlemann E., Schmid R., Altendorf K.;
RL Submitted (OCT-2001) to the SWISS-PROT data bank.
CC -!- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
CC CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS.
CC -!- CATALYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) = O(2) + H(2)O(2).
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
CC FAMILY.
DR InterPro; IPR001189; SODismutase.
DR PROSITE; PS00088; SOD_MN; PARTIAL.
KW Oxidoreductase; Iron; Metal-binding.
FT NON_TER
SQ SEQUENCE 9 AA; 1063 MW; C54267376B06C2C9 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLP 15
Db 6 PLP 8

RESULT 63
Q16605
ID Q16605 PRELIMINARY; PRT; 9 AA.
AC Q16605;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Glutathione S-transferase 2 (Fragment).
GN GSTA2 OR GST2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88330756; PubMed=3138230;
RA Chow N.W., Whang-Peng J., Kao-Shan C.S., Tam M.F., Lai H.C., Tu C.P.;
RT "Human glutathione S-transferases. The Ha multigene family encodes
RT products of different but overlapping substrate specificities."
RL J. Biol. Chem. 263:12797-12800(1988).
DR EMBL; M21867; AAA52617.1; -.
DR EMBL; M21866; AAA35938.1; -.
FT NON_TER
SQ SEQUENCE 9 AA; 1116 MW; D168E72327633B1D CRC64;

Query Match 16.7%; Score 3; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KLH 11
Db 6 KLH 8

RESULT 64
Q9TWV0
ID Q9TWV0 PRELIMINARY; PRT; 9 AA.
AC Q9TWV0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Antho-RPAMIDE=NEUROPEPTIDE.
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;

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```
OC Nyantheae; Actiniidae; Anthopleura.
OX NCBI_TaxID=6110;
RN [1]
RP SEQUENCE
RA MEDLINE=93126143; PubMed=1480510;
RX Carlstensen K., Rinehart K.L., McFarlane I.D., Grimmelikhuijzen C.J.;
RT "Isolation of Leu-Pro-Gly-Pro-Leu-Pro-Arg-Pro-NH2 (Antho-RPamide),
an N-terminally protected, biologically active neuropeptide from sea
RT anemones.";
RL Peptides 13:851-857(1992).
SQ SEQUENCE 9 AA; 943 MW; 2908176737686777 CRC64;

Query Match 16.7%; Score 3; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PLP 15
Db 5 PLP 7

RESULT 65
Q94VD8 PRELIMINARY; PRT; 9 AA.
ID Q94VD8;
AC Q94VD8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Varanus niloticus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=62046;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).
DR EMBL; AF407514; AAL10096.1; -.
KW Mitochondrion.
FT NON TER
SQ SEQUENCE 9 AA; 1154 MW; 9E80C7336411A731 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TLT 5
Db 2 TLT 4

RESULT 66
Q94VC6 PRELIMINARY; PRT; 9 AA.
ID Q94VC6;
AC Q94VC6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Varanus pilbarensis.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=62046;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).

OC Nyantheae; Actiniidae; Anthopleura.
OX NCBI_TaxID=6110;
RN [1]
RP SEQUENCE
RA MEDLINE=93126143; PubMed=1480510;
RX Carlstensen K., Rinehart K.L., McFarlane I.D., Grimmelikhuijzen C.J.;
RT "Isolation of Leu-Pro-Gly-Pro-Leu-Pro-Arg-Pro-NH2 (Antho-RPamide),
an N-terminally protected, biologically active neuropeptide from sea
RT anemones.";
RL Peptides 13:851-857(1992).
SQ SEQUENCE 9 AA; 1064 MW; 874CASA36411A735 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLT 3
Db 2 SLT 4

RESULT 67
Q94VE1 PRELIMINARY; PRT; 9 AA.
ID Q94VE1;
AC Q94VE1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Varanus mertensi.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=62044;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).
DR EMBL; AF407512; AAL10090.1; -.
KW Mitochondrion.
FT NON TER
SQ SEQUENCE 9 AA; 1154 MW; 9E80C7336411A731 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TLT 5
Db 2 TLT 4

RESULT 68
Q9S8J8 PRELIMINARY; PRT; 9 AA.
ID Q9S8J8;
AC Q9S8J8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE ORYZATENSIN-BIOACTIVE peptide.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE.
RX MEDLINE=95102521; PubMed=7804141;
RA Takahashi M., Moriguchi S., Yoshikawa M., Sasaki R.;
RT "Isolation and characterization of oryzatensin: a novel bioactive
RT peptide with ileum-contracting and immunomodulating activities derived
RT from rice albumin.";
RL Biochem. Mol. Biol. Int. 33:1151-1158(1994).
DR Gramene; Q9S8J8; -.
SQ SEQUENCE 9 AA; 1093 MW; 0E8C67377B56877B CRC64;

Query Match 16.7%; Score 3; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
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Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLP 15
Db 6 PLP 8

RESULT 69
Q61723 Q61723 PRELIMINARY; PRT; 9 AA.
AC Q61723;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE NF-kappa-B DNA-binding subunit (Fragment).
GN NFKB1 OR NF-KAPPA-B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/cbVJ; TISSUE=Spleen;
RX MEDLINE=90367113; PubMed=2203532;
RA Ghosh S., Gafford A.M., Riviere L.R., Tempet P., Nolan G.P.,
RA Baltimore D.;
RA "Cloning of the p50 DNA binding subunit of NF-kappa-B: Homology to rel
RT and dorsal.";
RL Cell 62:1019-1029(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/cbVJ; TISSUE=Spleen;
RX MEDLINE=94156215; PubMed=8112620;
RA Huo L., Chung W.H., Rothstein T.L.;
RT "C-terminal sequence of the NF-kappa-B p50 precursor from primary
RT murine B-lymphocytes.";
RL Gene 139:287-288(1994).
DR EMBL; L13466; AAC37644.1; -.
DR MGD; MGI:97312; Nfkb1.
KW DNA-binding. 1 1
FT NON TER 1 1 A -> P (IN REF. 1).
FT CONFLICT 5 5
FT NON TER 9 9
SQ SEQUENCE 9 AA; 925 MW; 300821E72DC1B408 CRC64;

Query Match 16.7%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LHL 12
Db 6 LHL 8

RESULT 70
Q85723 Q85723 PRELIMINARY; PRT; 9 AA.
AC Q85723;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE v-sis and p28-sis genes (Fragment).
OS Simian sarcoma virus.
OC Viruses; Retroid viruses; Retroviridae; Gammaretrovirus.
OX NCBI_TaxID=11817;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=84106822; PubMed=6319011;
RX Devare S.G., Shatzman A., Robbins K.C., Rosenberg M., Aaronson S.A.;
RA "Expression of the PDGF-related transforming protein of simian sarcoma
RT virus in E. coli.";
RL Cell 36:43-49(1984).
DR EMBL; K01473; AAA46816.1; -.

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FT NON TER 9 9 1048 MW; 9C53A866C361A731 CRC64;
SQ SEQUENCE 9 AA; 1048 MW; 9C53A866C361A731 CRC64;

Query Match 16.7%; Score 3; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TLT 5
Db 2 TLT 4

RESULT 71
Q935G1 Q935G1 PRELIMINARY; PRT; 9 AA.
AC Q935G1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Putative membrane protein (Fragment).
GN HCM1.01C.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham P., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
DR EMBL; AL513383; CAD09867.1; -.
KW Plasmid; Complete proteome.
FT NON TER 9 9
SQ SEQUENCE 9 AA; 904 MW; 5FDC77776D86767 CRC64;

Query Match 16.7%; Score 3; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLP 15
Db 1 PLP 3

RESULT 72
Q9XBH3 Q9XBH3 PRELIMINARY; PRT; 10 AA.
AC Q9XBH3;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Celf-like protein (Fragment).
GN CBLF.
OS Bacillus cereus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1396;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 10987;
RX MEDLINE=99231848; PubMed=10217496;
RA Okstad O.A., Hegna I., Lindbaeck T., Rishovd A.L., Kolsto A.B.;
RT "Genome organisation is not conserved between Bacillus cereus and

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RT Bacillus subtilis.;
RL Microbiology 145:621-631(1999).
DR EMBL; AJ000394; CAB40625.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1264 MW; D3757EC33339C9D6 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VEK 9
DB 8 VEK 10

RESULT 73
Q9R5T2 PRELIMINARY; PRT; 10 AA.
AC Q9R5T2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE NADP-linked glucose-6-phosphate dehydrogenase (Fragment).
OS Acetobacter hansenii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Acetobacteraceae; Gluconacetobacter.
OX NCBI_TaxID=436;
RN [1]_TaxID=436;
RP SEQUENCE.
RX MEDLINE=92027789; PubMed=1929428;
RA Levy H.R., Cook C.;
RT "Purification and properties of NADP-linked glucose-6-phosphate
RT dehydrogenase from Acetobacter hansenii (Acetobacter xylinum).";
RL Arch. Biochem. Biophys. 291:161-167(1991).
FT NON TER 1
FT NON TER 10
SQ SEQUENCE 10 AA; 1111 MW; 5091D4AAB2D77767 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 HLP 13
DB 2 HLP 4

RESULT 74
P83154 PRELIMINARY; PRT; 10 AA.
AC P83154;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Phycobilisome rod-core linker polypeptide cpcG3 (Fragment).
OS Anabaena sp. (strain L31).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OX NCBI_TaxID=29412;
RN [1]
RP SEQUENCE.
RA Apte S.K., Uhlemann E., Schmid R., Altendorf K.;
RL Submitted (OCT-2001) to the SWISS-PROT data bank.
CC -1- FUNCTION: ROD-CORE LINKER PROTEIN REQUIRED FOR ATTACHMENT OF
CC PHYCOCYANIN TO ALLOPHYCOCYANIN IN CORES OF PHYCOBILISOMES.
CC -1- FUNCTION: LINKER POLYPEPTIDES DETERMINE THE STATE OF AGGREGATION
CC AND THE LOCATION OF THE DISK-SHAPED PHYCOBILIPROTEIN UNITS WITHIN
CC THE PHYCOBILISOME AND MODULATE THEIR SPECTROSCOPIC PROPERTIES IN
CC ORDER TO MEDIATE A DIRECTED AND OPTIMAL ENERGY TRANSFER.
CC -1- SUBUNIT: THE PHYCOBILISOME IS A HEMIDISCAL STRUCTURE THAT IS
CC COMPOSED OF TWO DISTINCT SUBSTRUCTURES: A CORE COMPLEX (THAT
CC CONTAINS PHYCOBILIPROTEINS) AND A NUMBER OF RODS RADIATING FROM
CC THE CORE.
CC -1- SUBCELLULAR LOCATION: THYLAKOID MEMBRANE.
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CC -1- SIMILARITY: TO OTHER PHYCOBILISOME LINKER PROTEINS.
KW Phycobilisome; Photosynthesis; Thylakoid; Membrane.
FT NON TER 10
SQ SEQUENCE 10 AA; 1144 MW; 2F9B662B5B172737 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPL 14
DB 2 LPL 4

RESULT 75
Q9TG86 PRELIMINARY; PRT; 10 AA.
AC Q9TG86;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
OS COI.
OS Diploglossus bilobatus.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scieroglossa; Anguimorpha; Anguillidae;
OC Diploglossus.
OX NCBI_TaxID=102183;
RN [1]_TaxID=102183;
RP SEQUENCE FROM N.A.
RX MEDLINE=99343613; PubMed=10413621;
RA Macey J.R., Schulte J.A. II, Larson A., Tuniyev B.S., Orlov N.,
RA Papenfuss T.J.;
RT "Molecular phylogenetics, tRNA evolution, and historical biogeography
RT in anquid lizards and related taxonomic families.";
RL Mol. Phylogenet. Evol. 12:250-272(1999).
DR EMBL; AF085608; AAD51514.1; -.
FT NON TER 10
SQ SEQUENCE 10 AA; 1255 MW; 5DEB80C7336411A7 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TLT 5
DB 2 TLT 4

Search completed: November 25, 2003, 19:34:02
Job time : 35.8023 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:16:09 ; Search time 45.9419 Seconds  
(without alignments)  
62.189 Million cell updates/sec

Title: US-09-641-801-23

Perfect score: 18

Sequence: 1 SLRLTQVEXLHLPLVQ 18

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : A\_Geneseq\_19Jun03.\*  
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2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*  
4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*  
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20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*  
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22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*  
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	ID	Description
1	18	100.0	18 22 AAB72268	Colostrinin derive
2	18	100.0	18 22 AAB72521	Colostrinin peptid
3	18	100.0	18 22 AAB72533	Colostrinin peptid
4	18	100.0	18 22 AAB59331	Ewe colostrinin pe
5	18	100.0	18 23 AAE20250	Colostrinin consti
6	18	100.0	18 23 AAM51057	Colostrinin consti
7	18	100.0	18 23 AAO14599	Neural cell regula
8	33.3	6	11 AAR03868	Hypotensive peptid
9	6	33.3	6 21 AAY69541	Bioactive peptid

10	6	33.3	8	22	AAB07194	Colostrinin peptid
11	6	33.3	9	11	AAR03874	Hypotensive peptid
12	6	33.3	9	22	AAE07204	Modified colostrin
13	5	27.8	9	22	AAB89809	HIV gp120 protein
14	5	27.8	9	22	AAB89810	HIV gp120 protein
15	5	27.8	9	22	AAB89811	HIV gp120 protein
16	5	27.8	9	22	AAH24855	Human MHC class I
17	5	27.8	9	22	AAH24955	Human MHC class I
18	5	27.8	9	22	AAH25052	Human MHC class I
19	5	27.8	10	22	AAH25004	Human MHC class I
20	5	27.8	10	22	AAH25103	Human MHC class I
21	5	27.8	10	22	AAH25203	Human MHC molecule
22	5	27.8	11	22	AAH20470	Mouse CD166 peptid
23	5	27.8	11	24	ABU03415	Human expressed pr
24	5	27.8	12	22	AAB89415	HIV gp120 protein
25	5	27.8	12	22	AAB89855	HIV gp120 protein
26	5	27.8	12	22	AAB89856	HIV gp120 protein
27	5	27.8	12	22	AAB89857	HIV gp120 protein
28	5	27.8	14	20	AAH30295	Angiopoietin deriv
29	5	27.8	14	22	AAH03935	Human gene 38 enco
30	5	27.8	15	18	AAH39008	Peptide resembling
31	5	27.8	15	18	AAH39898	Peptide resembling
32	5	27.8	15	22	AAB89429	HIV gp120 protein
33	5	27.8	15	22	AAB89430	HIV gp120 protein
34	5	27.8	15	22	AAB89431	HIV gp120 protein
35	5	27.8	15	22	AAB89619	HIV gp120 protein
36	5	27.8	15	22	AAB89620	HIV gp120 protein
37	5	27.8	15	22	AAB89621	HIV gp120 protein
38	5	27.8	15	22	AAB89622	HIV gp120 protein
39	5	27.8	15	22	AAB89623	HIV gp120 protein
40	5	27.8	15	22	AAB90009	HIV gp120 protein
41	5	27.8	15	22	AAB90010	HIV gp120 protein
42	5	27.8	15	22	AAB90011	HIV gp120 protein
43	5	27.8	15	22	AAB90012	HIV gp120 protein
44	5	27.8	15	22	AAB90013	HIV gp120 protein
45	5	27.8	15	22	AAB90014	HIV gp120 protein
46	5	27.8	15	22	AAB90015	HIV gp120 protein
47	5	27.8	15	22	AAB90016	HIV gp120 protein
48	5	27.8	15	22	AAB90022	HIV gp120 protein
49	5	27.8	15	22	AAB90023	HIV gp120 protein
50	5	27.8	15	22	AAB90024	HIV gp120 protein
51	5	27.8	15	22	AAB90025	HIV gp120 protein
52	5	27.8	15	22	AAB90026	HIV gp120 protein
53	5	27.8	15	22	AAB90027	HIV gp120 protein
54	5	27.8	15	22	AAB90028	HIV gp120 protein
55	5	27.8	15	22	AAB90029	HIV gp120 protein
56	5	27.8	15	22	AAB90030	HIV gp120 protein
57	5	27.8	15	22	AAB90031	HIV gp120 protein
58	5	27.8	15	22	AAB90032	HIV gp120 protein
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60	5	27.8	15	22	AAB90039	HIV gp120 protein
61	5	27.8	15	22	AAB90040	HIV gp120 protein
62	5	27.8	15	22	AAB90041	HIV gp120 protein
63	5	27.8	15	22	AAB90042	HIV gp120 protein
64	5	27.8	15	22	AAB90101	HIV gp120 protein
65	5	27.8	15	22	AAB90102	HIV gp120 protein
66	5	27.8	15	22	AAB90103	HIV gp120 protein
67	5	27.8	15	22	AAB90104	HIV gp120 protein
68	5	27.8	15	22	AAB90110	HIV gp120 protein
69	5	27.8	15	22	AAB90111	HIV gp120 protein
70	5	27.8	15	22	AAB90112	HIV gp120 protein
71	5	27.8	15	22	AAB90113	HIV gp120 protein
72	5	27.8	15	22	AAB90114	HIV gp120 protein
73	5	27.8	15	22	AAB90115	HIV gp120 protein
74	5	27.8	15	22	AAB90116	HIV gp120 protein
75	5	27.8	15	22	AAB90118	HIV gp120 protein
76	5	27.8	15	22	AAB90141	HIV gp120 protein
77	5	27.8	15	23	ABH53239	Dentrobacter perm
78	5	27.8	16	23	ABH53243	Bacterial peptid
79	5	27.8	17	20	AAH07455	Mouse TS10q23.3 ge
80	5	27.8	18	20	AAH04173	Human secreted pro
81	5	27.8	18	22	AAB89447	HIV gp120 protein
82	5	27.8	18	22	AAB89448	HIV gp120 protein

83 5 27.8 18 22 AAB89449 HIV gp120 protein  
84 5 27.8 18 22 AAB89663 HIV gp120 protein  
85 5 27.8 18 22 AAB89664 HIV gp120 protein  
86 5 27.8 18 22 AAB89665 HIV gp120 protein  
87 5 27.8 18 22 AAB89666 HIV gp120 protein  
88 5 27.8 18 22 AAB89667 HIV gp120 protein  
89 5 27.8 18 22 AAB89667 HIV gp120 protein  
90 5 27.8 19 23 AAB89667 HIV gp120 protein  
91 5 27.8 19 23 AAB89667 HIV gp120 protein  
92 5 27.8 20 20 AAB89667 HIV gp120 protein  
93 4 22.2 5 15 AAB89667 HIV gp120 protein  
94 4 22.2 5 15 AAB89667 HIV gp120 protein  
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96 4 22.2 5 15 AAB89667 HIV gp120 protein  
97 4 22.2 5 15 AAB89667 HIV gp120 protein  
98 4 22.2 5 15 AAB89667 HIV gp120 protein  
99 4 22.2 5 15 AAB89667 HIV gp120 protein  
100 4 22.2 5 15 AAB89667 HIV gp120 protein

ALIGNMENTS

RESULT 1  
AAB72268  
ID AAB72268 standard; peptide; 18 AA.  
XX  
AC AAB72268;  
XX  
DT 14-MAY-2001 (first entry)  
XX  
DE Colostrinin derived cytokine inducing peptide SEQ ID 23.  
XX  
KW Colostrinin; immune response; cytokine; blood cell proliferation;  
KW central nervous system disorder; neurological disorder; mental disorder;  
KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;  
KW neurosis; infection.  
XX  
OS Synthetic.  
XX  
PN WO20011937-A2.  
XX  
PD 22-FEB-2001.  
XX  
PF 17-AUG-2000; 2000WO-US22818.  
XX  
PR 17-AUG-1999; 99US-0149311.  
XX  
PA (TEXA ) UNIV TEXAS SYSTEM.  
PA (REG- ) REGEN THERAPEUTICS PLC.  
XX  
PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
XX  
PS WPI; 2001-202804/20.  
XX  
PT Inducing a cytokine and modulating an immune response, useful for  
PT treating central nervous system diseases and bacterial and viral  
PT infections, comprises administering colostrinin as an immunological  
PT regulator -  
XX  
PS Claim 1; Page 34; 50pp; English.  
XX  
CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,  
CC a proline rich polypeptide aggregate contained in colostrinum. The  
CC peptides have immune response modulatory activity, and are capable of  
CC inducing cytokines. Colostrinin and its derived peptides are useful for  
CC inducing cytokine production, for modulating an immunological response  
CC and for inducing blood cell proliferation. The peptides are useful in the  
CC treatment of disorders of the central nervous system, neurological  
CC disorders, mental disorders, dementia, neurodegenerative diseases,  
CC Alzheimer's disease, motor neuron disease, psychosis, neurosis, chronic  
CC disorders of the immune system, bacterial and viral infections and  
CC acquired immunological deficiencies.

XX  
SQ Sequence 18 AA;  
Query Match 100.0%; Score 18; DB 22; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.8e-11;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SLTLTDEKHLPLPLVQ 18  
Db 1 SLTLTDEKHLPLPLVQ 18  
RESULT 2  
AAB72521  
ID AAB72521 standard; Peptide; 18 AA.  
XX  
AC AAB72521;  
XX  
DT 09-MAY-2001 (first entry)  
XX  
DE Colostrinin peptide #22.  
XX  
KW Dermatological; oxidative stress regulator; colostrinin.  
XX  
OS Unidentified.  
XX  
PN WO200112650-A2.  
XX  
PD 22-FEB-2001.  
XX  
PF 17-AUG-2000; 2000WO-US22665.  
XX  
PR 17-AUG-1999; 99US-0149310.  
XX  
PA (TEXA ) UNIV TEXAS SYSTEM.  
XX  
PI Stanton GJ, Hughes TK, Boldogh I;  
XX  
PS WPI; 2001-218342/22.  
XX  
PT Modulating oxidative stress level in a cell, involves contacting the  
PT cell with an oxidative stress regulator selected from colostrinin, its  
PT constituent peptide, analog or their combinations -  
XX  
PS Claim 6; Page 26; 48pp; English.  
XX  
CC The present invention relates to a method for modulating the oxidative  
CC stress level in a cell or a patient, comprising contacting the cell with,  
CC or administering to the patient, an oxidative stress regulator selected  
CC from colostrinin, or its constituent peptide (e.g. the present peptide),  
CC to change the level of an oxidizing species in the cell. The method can  
CC be used to treat oxidative damage to skin, by decreasing or preventing an  
CC increase in the level of damage to a biomolecule of the patient.  
XX  
SQ Sequence 18 AA;  
Query Match 100.0%; Score 18; DB 22; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.8e-11;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SLTLTDEKHLPLPLVQ 18  
Db 1 SLTLTDEKHLPLPLVQ 18  
RESULT 3  
AAB72553  
ID AAB72553 standard; Peptide; 18 AA.  
XX  
AC AAB72553;  
XX  
DT 09-MAY-2001 (first entry)  
XX

DE Colostrinin peptide #22.  
XX Neuroprotective; neural cell differentiation regulator; colostrinin;  
KW colostrum.  
XX Unidentified.  
OS  
XX WO200112651-A2.  
PN  
XX 22-FEB-2001.  
XX  
XX 17-AUG-2000; 2000WO-US22774.  
PF  
XX 17-AUG-1999; 99US-0149633.  
XX  
XX (TEXA ) UNIV TEXAS SYSTEM.  
PA  
XX Boldogh I;  
XX  
XX WPI; 2001-226545/23.  
DR  
XX Use of colostrinin, its constituent peptide or analog as a neural cell  
PT regulator, for promoting neural cell differentiation and treating  
PT damaged neural cells in a patient -  
XX  
XX Claim 6; Page 21; 35pp; English.  
XX  
XX The present invention relates to a method for promoting neural cell  
CC differentiation and treating damaged neural cells, using colostrinin and  
CC colostrinin constituent peptides (e.g. the present peptide) as a neural  
CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.  
XX  
XX  
SQ Sequence 18 AA;  
Query Match 100.0%; Score 18; DB 22; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.8e-11;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 SLTLTQVEKHLPLPLVQ 18  
|||||  
Db 1 SLTLTQVEKHLPLPLVQ 18  
|||||  
RESULT 4  
AAB59331  
ID AAB59331 standard; Peptide; 18 AA.  
XX  
AC AAB59331;  
XX  
XX 21-MAR-2001 (first entry)  
DT  
XX  
DE Ewe colostrinin peptide fragment C-6.  
XX  
XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.  
KW  
XX Ovis sp.  
OS  
XX WO200075173-A2.  
XX  
XX 14-DEC-2000.  
PD  
XX 02-JUN-2000; 2000WO-GB02128.  
XX  
XX 02-JUN-1999; 99GB-0012852.  
PR  
XX (REGG-) REGEN THERAPEUTICS PLC.  
PA  
XX Georgiades JA;  
XX  
XX WPI; 2001-071058/08.  
DR  
XX Peptides having an N-terminal amino acid sequence isolated from

PT colostrinin for treating e.g. disorders of the central nervous system  
PT and immune system, viral and bacterial infections, and diseases  
PT characterized by amyloid plaques -  
XX  
XX PS Claim 7; Page 27; 63pp; English.  
XX  
XX The present invention provides the sequences of a number of peptides  
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
CC fragment of colostrum. These peptides can be used in the treatment of  
CC central nervous system disorders such as senile dementia, Parkinson's  
CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
CC disorders such as bacterial and viral infections, to improve the  
CC development of a child's immune system, as a dietary supplement, and to  
CC promote the dissolution of beta-amyloid plaques.  
XX  
XX SQ Sequence 18 AA;  
Query Match 100.0%; Score 18; DB 22; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.8e-11;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 SLTLTQVEKHLPLPLVQ 18  
|||||  
Db 1 SLTLTQVEKHLPLPLVQ 18  
|||||  
RESULT 5  
AAE20250  
ID AAE20250 standard; peptide; 18 AA.  
XX  
AC AAE20250;  
XX  
XX 18-JUN-2002 (first entry)  
DT  
XX  
DE Colostrinin constituent peptide #22.  
XX  
XX Blood cell regulator; colostrinin; constituent peptide; oxidative stress;  
KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;  
KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;  
KW transplantation; implantation; dermatological; vulnary.  
XX  
XX Unidentified.  
OS  
XX  
XX Key Location/Qualifiers  
FH Modified-site 18  
FT /note= "Optionally C-terminal amide"  
FT  
XX WO200213850-A1.  
XX  
XX 21-FEB-2002.  
PD  
XX 17-AUG-2000; 2000WO-US22776.  
XX  
XX 17-AUG-2000; 2000WO-US22776.  
PR  
XX (TEXA ) UNIV TEXAS SYSTEM.  
PA  
XX Stanton GJ, Hughes TK, Boldogh I;  
XX WPI; 2002-269151/31.  
XX  
XX Composition useful for the modulation of blood cell proliferation in a  
PT patient comprises a blood cell regulator selected from colostrinin, its  
PT constituent peptide and/or analog -  
XX  
XX Claim 6; Page 26; 51pp; English.  
PS  
XX The invention relates to a composition which comprises a blood cell  
CC regulator selected from colostrinin, its constituent peptide and/or  
CC analogue. The invention is used for modulating the oxidative stress  
CC level in a cell e.g. mammalian or human cell present in a cell culture,  
CC tissue, organ, or organism; or for treating oxidative damage to the skin  
CC of a patient e.g. animal or human; to modulate oxidative stress during/

CC after a premature birth or normal birth, preventing/delaying aging in a  
 CC patient, enhancing wound healing, and the reduction of side effects of  
 CC cosmetic procedures. The method changes the level of an oxidizing species  
 CC in the cell, such as decreases or prevents increase in the level of  
 CC damage to a biomolecule of the patient selected from DNA, protein and/or  
 CC lipid, compared to the same conditions when the oxidative stress  
 CC regulator is not present. The modulation of oxidative stress results in  
 CC enhanced repair, regeneration, and replacement of cells, tissues and  
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
 CC external organs), as well as enhanced preservation of such organs for  
 CC transplantation, implantation, or scientific research. The present  
 CC sequence is a colostrinin constituent peptide.

XX Sequence 18 AA;

Query Match 100.0%; Score 18; DB 23; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 7.8e-11;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLTQVEKHLPLPLVQ 18  
 |||||  
 Db 1 SLTLTQVEKHLPLPLVQ 18  
 |||||

# RESULT 6

AA051057  
 ID AA051057 standard; Peptide; 18 AA.

XX AC AA051057;

XX DT 30-MAY-2002 (first entry)

XX DE Colostrinin constituent peptide (casein amino acids 139-156).

XX KW Colostrinin; colostrum; immunomodulator; cardiovascular;

XX KW blood cell regulator; cytokine inducer; beta-casein; human.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Modified-site 18 /note= "Optional C-terminal amidation"

XX FT WO200213849-A1.

XX XX 21-FEB-2002.

XX XX 17-AUG-2000; 2000WO-US22775.

XX XX 17-AUG-2000; 2000WO-US22775.

XX XX (TEXA ) UNIV TEXAS SYSTEM.

XX XX (REG- ) REGEN THERAPEUTICS PLC.

XX PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX XX WPI; 2002-269150/31.

XX PT Modulation of blood cell proliferation in a patient involves use of  
 PT blood cell regulator selected from colostrinin, its constituent peptide  
 PT and/or analogue -

XX PS Claim 1; Page 34; 54pp; English.

XX CC The present sequence is that of a colostrinin constituent peptide  
 CC that is used as an immunological regulator and as a blood cell  
 CC regulator in claimed methods of the invention. It is classified  
 CC as having a beta-casein homologue precursor, and corresponds to  
 CC casein amino acids 139-156. Methods are claimed for: inducing a  
 CC cytokine in a cell by contact with an immunological regulator,  
 CC where the cell is present in a cell culture, a tissue, an organ  
 CC or an organism, and the cell is mammalian, including human;  
 CC modulating an immune response in a cell by contact with the

CC immunological regulator under conditions effective to induce a  
 CC cytokine; modulating an immune response in a patient by administering  
 CC an immunological regulator under conditions effective to induce a  
 CC cytokine, where the immunological regulator is administered topically  
 CC or as part of a dietary supplement, and where the immune response is  
 CC specific or non specific, an interferon response or an antibody  
 CC response; modulating blood cell proliferation by contacting blood  
 CC cells with a blood cell regulator, where the blood cells are present  
 CC in a cell culture or an organism, are mammalian or human, and where  
 CC the blood cells are increased in number or differentiated; and a  
 CC method for modulating blood cell proliferation in a patent. A  
 CC claimed cytokine-inducing composition comprises a pharmaceutical  
 CC carrier and an active agent such as the present peptide.

XX Sequence 18 AA;

Query Match 100.0%; Score 18; DB 23; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 7.8e-11;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLTQVEKHLPLPLVQ 18  
 |||||  
 Db 1 SLTLTQVEKHLPLPLVQ 18  
 |||||

# RESULT 7

AA014599

ID AA014599 standard; peptide; 18 AA.

XX AC AA014599;

XX XX 27-MAY-2002 (first entry)

XX XX Neural cell regulatory colostrinin peptide 22.

XX KW Neural cell differentiation; neural cell regulator; colostrinin peptide;

XX KW neural cell formation; proline-rich polypeptide aggregate; colostrum;

XX KW neural cell treatment.

XX OS Unidentified.

XX FH Key Location/Qualifiers

XX FT Modified-site 18 /note= "Optional C-terminal amide"

XX FT WO200213851-A1.

XX XX 21-FEB-2002.

XX XX 17-AUG-2000; 2000WO-US22777.

XX XX 17-AUG-2000; 2000WO-US22777.

XX XX (TEXA ) UNIV TEXAS SYSTEM.

XX XX Boldogh I, Stanton JG, Hughes TK;

XX XX WPI; 2002-269152/31.

XX XX Promoting cell differentiation in a patient involves use of blood cell  
 PT regulator selected from colostrinin, its constituent peptide and/or  
 PT analog -

XX PS Claim 7; Page 21; 37pp; English.

XX CC The invention comprises a method for promoting cell differentiation (e.g.  
 CC neural cell differentiation). The method involves contacting cells with a  
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the  
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich  
 CC polypeptide aggregate that is present in colostrum. The method of the  
 CC invention is useful for promoting the differentiation of cells and for  
 CC treating damaged neural cells in a patient. The present amino acid  
 CC sequence represents a specifically claimed colostrinin peptide used in



```

CC  the method of the invention.
XX
SQ  Sequence 18 AA;

Query Match 100.0%; Score 18; DB 23; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.8e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLTDEKHLPLPLVQ 18
Db 1 SLTLTDEKHLPLPLVQ 18

RESULT 8
AAR03868
ID AAR03868 standard; Protein; 6 AA.
XX
AC AAR03868;
XX
DT 17-FEB-1993 (first entry)
XX
DE Hypotensive peptide (7).
XX
KW Hypotensor; salt.
XX
OS Synthetic.
XX
PN JP02062828-A.
XX
PD 02-MAR-1990.
XX
PF 26-AUG-1988; 88JP-0211696.
XX
PR 26-AUG-1988; 88JP-0211696.
XX
PA (AJIN ) AJINOMOTO KK.
XX
DR WPI; 1990-111933/15.
XX
PT New peptide used as active ingredient of hypotensive agent -
PT which may be prepd. e.g. as tablets, capsules, powder, syrup,
PT injection prepn. etc.
XX
PS Claim; Page 7; 9pp; Japanese.
XX
CC The peptides given in AAR03862-76 and their salts can be used as
CC components of hypotensive agents.
CC The hypotensor may be in the form of tablets, capsules, powder,
CC syrup or injection prepn. contg. 0.001-1000 mg, esp. 0.01-10 mg of
CC the peptide.
XX
SQ Sequence 6 AA;

Query Match 33.3%; Score 6; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LHLPLP 15
Db 1 LHLPLP 6

RESULT 9
AAV69541
ID AAV69541 standard; peptide; 6 AA.
XX
AC AAV69541;
XX
DT 19-APR-2000 (first entry)
XX
DE Bioactive peptide #7 from whey protein hydrolysate.
XX
KW Whey protein hydrolysate; bioactive peptide; non bitter flavour;

KW food product; digestible; hypotensive.
XX
OS Unidentified.
XX
PN WO965326-A1.
XX
PD 23-DEC-1999.
XX
PF 14-JUN-1999; 99WO-NZ00084.
XX
PR 17-JUN-1998; 98NZ-0330710.
XX
PA (NZDA-) NEW ZEALAND DAIRY BOARD.
XX
PI Schlothauer R, Schollum LM, Singh AM, Reid JR;
XX
DR WPI; 2000-116705/10.
XX
PT Preparation of whey protein hydrolysate containing bioactive peptides
PT but does not have bitter flavor -
XX
PS Claim 19; Page 21; 32pp; English.
XX
CC Sequences AAV69535-Y69536 represent bioactive peptides which are
CC components of whey protein hydrolysate. The invention relates to the
CC preparation of whey protein hydrolysate containing such bioactive
CC peptides by treating a whey protein containing substrate with one or more
CC enzymes capable of hydrolysing whey proteins to produce the whey protein
CC hydrolysate containing bioactive peptides, and terminating the hydrolysis
CC before substantial production of unacceptable bitter flavours. The
CC invention also encompasses a non bitter product produced by partial
CC hydrolysis of a substrate containing whey proteins, where the product
CC comprises bioactive peptides and has a degree of hydrolysis of the whey
CC proteins of below 10%, a food product containing the non bitter product,
CC any one or a combination of two or more of the bioactive peptides of the
CC invention, and a method for reducing systolic blood pressure in a patient
CC which comprises administering the non bitter product to the patient. The
CC peptides, products and food products are useful in a method for the
CC reduction of systolic blood pressure. The whey protein products are free
CC from bitter flavours and contain bioactive peptides. The products of the
CC process have high digestibility and good organoleptic properties. The
CC products may have bland or slightly sweet taste and are free of soapy
CC and/or brothy flavours.
XX
SQ Sequence 6 AA;

Query Match 33.3%; Score 6; DB 21; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LHLPLP 15
Db 1 LHLPLP 6

RESULT 10
AAE07194
ID AAE07194 standard; peptide; 8 AA.
XX
AC AAE07194;
XX
DT 06-NOV-2001 (first entry)
XX
DE Colostrin peptide 10.
XX
KW Colostrin; nootropic; neuroprotective; immunomodulatory; antibacterial;
KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;
KW central nervous system disorder; neurodegenerative disorder; weight loss;
KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;
KW acquired immunological deficiency; neurological disorder; dementia;
KW antiviral.
XX
OS Unidentified.

```

XX WO200155199-A1.  
 XX 02-AUG-2001.  
 XX 26-JAN-2001; 2001WO-GB00329.  
 XX 26-JAN-2000; 2000GB-0001825.  
 XX (REGG-) REGEN THERAPEUTICS PLC.  
 XX Georgiades JA;  
 XX WPI; 2001-488775/53.  
 XX Peptide useful as an inter alia in the treatment of e.g. disorders of  
 PT the immune system and the central nervous system comprises ten  
 PT amino-terminal amino acid sequence derived from peptides present in  
 PT colostrinin -  
 XX  
 PS Claim 1; Page 15; 40pp; English.  
 XX  
 CC The invention relates to colostrinin peptide fragments which are useful,  
 CC inter alia, in the treatment of chronic disorders of the immune system  
 CC and the central nervous system. Colostrinin peptides are used as a  
 CC medicament in the treatment of neurological disorders e.g., dementia,  
 CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron  
 CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and  
 CC neurosis, in acquired immunological deficiencies, chronic bacterial and  
 CC viral infections and diseases characterised by the presence of beta-  
 CC amyloid plaques and as a dietary supplement for babies, small children,  
 CC adults and senile persons, who have been subjected to chemotherapy or  
 CC have suffered from cachexia or weight loss due to the chronic disease.  
 CC Colostrinin peptides are also used as food additives and as an auxiliary  
 CC withdrawal treatment for drug addicts, after a period of detoxification  
 CC and in persons dependent on stimulants. Colostrinin peptides are used to  
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional  
 CC disturbances of psychiatric patients in a state of depression. These  
 CC colostrinin peptides improves the development of immune system in a new  
 CC born child and to correct the immunological deficiencies in a child.  
 CC The present sequence is colostrinin peptide 10 related to the invention.  
 CC Colostrinin peptide 10 corresponds to position 150-157 of beta-caesin.  
 XX  
 SX Sequence 8 AA;  
 Query Match 33.3%; Score 6; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 12 LPLPLV 17  
 Db 1 LPLPLV 6  
 XX  
 RESULT 11  
 AAR03874  
 ID AAR03874 standard; Protein; 9 AA.  
 AC AAR03874;  
 XX  
 XX 17-FEB-1993 (first entry)  
 DE  
 DE Hypotensive peptide (13).  
 XX  
 XX Hypotensor; salt.  
 XX  
 XX Synthetic.  
 OS  
 XX Key Location/Qualifiers  
 FH Peptide 4..7  
 FT /note= "claimed peptide"  
 FT Misc-difference 1..2  
 FT /note= "amino acids 1-2 may be serially deleted"

FT Misc-difference 1..4 /note= "amino acids 1-4 may be deleted"  
 FT Misc-difference 1..5 /note= "amino acids 1-5 may be deleted"  
 FT Misc-difference 1..6 /note= "amino acids 1-6 may be deleted"  
 XX JP02062828-A.  
 XX 02-MAR-1990.  
 XX 26-AUG-1988; 88JP-0211696.  
 XX 26-AUG-1988; 88JP-0211696.  
 XX (AJIN ) AJINOMOTO KK.  
 XX WPI; 1990-111933/15.  
 XX New peptide used as active ingredient of hypotensive agent -  
 PT which may be prepd. e.g. as tablets, capsules, powder, syrup,  
 PT injection prepn. etc.  
 PS Claim; Page 2; 9pp; Japanese.  
 XX  
 CC Amino acids (1-2) and (1-4 to 1-6) may be serially deleted.  
 CC The peptides given in AAR03862-76 and their salts can be used as  
 CC components of hypotensive agents.  
 CC The hypotensor may be in the form of tablets, capsules, powder,  
 CC syrup or injection prepn. contg. 0.001-1000 mg, esp. 0.01-10 mg of  
 CC the peptide.  
 XX  
 SX Sequence 9 AA;  
 Query Match 33.3%; Score 6; DB 11; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 10 LHLPLP 15  
 Db 4 LHLPLP 9  
 XX  
 RESULT 12  
 AAE07204  
 ID AAE07204 standard; peptide; 9 AA.  
 XX  
 AC AAE07204;  
 XX  
 XX 06-NOV-2001 (first entry)  
 DT  
 DE Modified colostrinin cyclic peptide #10.  
 XX  
 KW Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;  
 KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;  
 KW central nervous system disorder; neurodegenerative disorder; weight loss;  
 KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;  
 KW acquired immunological deficiency; neurological disorder; dementia;  
 KW antiviral; cyclic.  
 XX  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH Modified-site 1  
 FT /note= "N-terminal acetyl; this residue forms a cyclic  
 FT linkage with Ser found at the C-terminal end"  
 XX  
 XX WO200155199-A1.  
 XX 02-AUG-2001.  
 XX 26-JAN-2001; 2001WO-GB00329.  
 XX

PR 26-JAN-2000; 2000GB-0001825.

PA (REGS-) REGEN THERAPEUTICS PLC.

PI Georgiades JA;

XX WPI; 2001-488775/53.

XX Peptide useful as an inter alia in the treatment of e.g. disorders of  
PT the immune system and the central nervous system comprises ten  
PT amino-terminal amino acid sequence derived from peptides present in  
PT colostrinin -

XX Example 2; Page 9; 40pp; English.

XX The invention relates to colostrinin peptide fragments which are useful,  
CC inter alia, in the treatment of chronic disorders of the immune system  
CC and the central nervous system. Colostrinin peptides are used as a  
CC medicament in the treatment of neurological disorders e.g. dementia,  
CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron  
CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and  
CC neurosis, in acquired immunological deficiencies, chronic bacterial and  
CC viral infections and diseases characterised by the presence of beta-  
CC amyloid plaques and as a dietary supplement for babies, small children,  
CC adults and senile persons, who have been subjected to chemotherapy or  
CC have suffered from cachexia or weight loss due to the chronic disease.  
CC Colostrinin peptides are also used as food additives and as an auxiliary  
CC withdrawal treatment for drug addicts, after a period of detoxification  
CC and in persons dependent on stimulants. Colostrinin peptides are used to  
CC prepare antibodies and to treat emotional disturbances, e.g. emotional  
CC disturbances of psychiatric patients in a state of depression. These  
CC colostrinin peptides improves the development of immune system in a new  
CC born child and to correct the immunological deficiencies in a child.  
CC The present sequence is modified colostrinin cyclic peptide #10 related  
CC to the invention.

XX Sequence 9 AA;

Query Match 33.3%; Score 6; DB 22; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLPLV 17

DB 2 LPLPLV 7

RESULT 13

AAB89809

ID AAB89809 standard; Peptide; 9 AA.

XX AAB89809;

XX 23-MAY-2001 (first entry)

XX HIV gp120 protein binding peptide #902.

XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;  
XX replication; CCR5; CXCR4; CD4; STRL33.

XX Synthetic.

XX WO200116182-A2.

XX 08-MAR-2001.

XX 25-AUG-2000; 2000WO-US23505.

XX 27-AUG-1999; 99US-0151270.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Saxinger C;

XX WPI; 2001-244398/25.

XX Novel polypeptides useful for treating HIV infection, have homology to  
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,  
PT and binds to HIV gp120 under physiological conditions -

XX Example 10; Page 68; 114pp; English.

XX The present invention describes a number of peptides which are able to  
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human  
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are  
CC useful in the treatment of HIV, as they prevent replication of the  
CC virus. The present sequence is an example of a peptide of the invention.

XX Sequence 9 AA;

Query Match 27.8%; Score 5; DB 22; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLT 5

DB 5 SLTLT 9

RESULT 14

AAB89810

ID AAB89810 standard; Peptide; 9 AA.

XX AAB89810;

XX 23-MAY-2001 (first entry)

XX HIV gp120 protein binding peptide #903.

XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;  
XX replication; CCR5; CXCR4; CD4; STRL33.

XX Synthetic.

XX WO200116182-A2.

XX 08-MAR-2001.

XX 25-AUG-2000; 2000WO-US23505.

XX 27-AUG-1999; 99US-0151270.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Saxinger C;

XX WPI; 2001-244398/25.

XX Novel polypeptides useful for treating HIV infection, have homology to  
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,  
PT and binds to HIV gp120 under physiological conditions -

XX Example 10; Page 68; 114pp; English.

XX The present invention describes a number of peptides which are able to  
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human  
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are  
CC useful in the treatment of HIV, as they prevent replication of the  
CC virus. The present sequence is an example of a peptide of the invention.

XX Sequence 9 AA;

Query Match 27.8%; Score 5; DB 22; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLT 5  
 |||||  
 Db 4 SLLT 8

RESULT 15  
 AAB89811  
 ID AAB89811 standard; Peptide; 9 AA.  
 XX  
 AC AAB89811;  
 XX  
 DT 23-MAY-2001 (first entry)  
 XX  
 DE HIV gp120 protein binding peptide #904.  
 XX  
 KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;  
 KW replication; CCR5; CXCR4; CD4; STRL33.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200116182-A2.  
 XX  
 PD 08-MAR-2001.  
 XX  
 PF 25-AUG-2000; 2000WO-US23505.  
 XX  
 PR 27-AUG-1999; 99US-0151270.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Saxinger C;  
 XX  
 DR WPI; 2001-244398/25.  
 XX  
 PT Novel polypeptides useful for treating HIV infection, have homology to  
 PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,  
 PT and binds to HIV gp120 under physiological conditions -  
 XX  
 PS Example 10; Page 68; 114pp; English.  
 XX  
 CC The present invention describes a number of peptides which are able to  
 CC bind to HIV glycoprotein 120 (gp120). These are similar to the human  
 CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are  
 CC useful in the treatment of HIV, as they prevent replication of the  
 CC virus. The present sequence is an example of a peptide of the invention.  
 XX  
 SQ Sequence 9 AA;

Query Match 27.8%; Score 5; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLLT 5  
 |||||  
 Db 3 SLLT 7

RESULT 16  
 AAM24655  
 ID AAM24655 standard; Peptide; 9 AA.  
 XX  
 AC AAM24655;  
 XX  
 DT 04-DEC-2001 (first entry)  
 XX  
 DE Human MHC class I molecule HLA-A2 binding 83P5G4 peptide #32.  
 XX  
 KW 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;  
 KW tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;  
 KW cyrostatic; gene therapy; antibody therapy; ribozyme; blood; cervix;  
 KW single chain monoclonal antibody; urine; uterus; rectum; stomach; human;  
 KW chromosome 1q31-q32.  
 XX

OS Homo sapiens.  
 XX WO200159115-A2.  
 XX  
 PD 16-AUG-2001.  
 XX  
 PF 09-FEB-2001; 2001WO-US04426.  
 XX  
 PR 09-FEB-2000; 2000US-0181261.  
 XX  
 PA (UROG-) UROGENESYS INC.  
 XX  
 PI Hubert RS, Afar DEH, Challita-eid PM, Faris M, Levin E;  
 PI Mitchell SC, Jakobovits A;  
 XX  
 DR WPI; 2001-514669/56.  
 XX  
 PT An isolated 83P5G4-related protein useful as a diagnostic and/or  
 PT therapeutic agent in multiple cancers such as prostate, bladder and  
 PT bone cancer -  
 XX  
 PS Example 15; Page 77; 112pp; English.  
 XX  
 CC The polypeptide sequences represent the 83P5G4-related protein and  
 CC peptide fragments of the protein. 83P5G4 exhibits prostate specific  
 CC expression in normal adult tissue, but it is also aberrantly expressed in  
 CC many cancers including tumours of the prostate, testis, bladder, kidney,  
 CC brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum,  
 CC liver, colon and lung. The 83P5G4 polynucleotide, its related protein and  
 CC peptide fragments and specific PCR primers are therefore useful for  
 CC diagnosing and treating cancer. A vector comprising a polynucleotide  
 CC which encodes a single chain monoclonal antibody, that immunospecifically  
 CC binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a  
 CC polynucleotide having the 83P5G4 coding sequence, are both useful in the  
 CC preparation of a composition for treating a patient with a cancer that  
 CC expresses 83P5G4. The sequences can be used in diagnostic methods to  
 CC monitor the level of 83P5G4 gene products in serum, blood, urine and  
 CC tissue and to thereby detect the presence of cancerous cells.  
 XX  
 SQ Sequence 9 AA;

Query Match 27.8%; Score 5; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLPL 16  
 |||||  
 Db 2 LPLPL 6

RESULT 17  
 AAM24955  
 ID AAM24955 standard; Peptide; 9 AA.  
 XX  
 AC AAM24955;  
 XX  
 DT 04-DEC-2001 (first entry)  
 XX  
 DE Human MHC class I molecule HLA-A24 binding 83P5G4 peptide #32.  
 XX  
 KW 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;  
 KW tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;  
 KW cyrostatic; gene therapy; antibody therapy; ribozyme; blood; cervix;  
 KW single chain monoclonal antibody; urine; uterus; rectum; stomach; human;  
 KW chromosome 1q31-q32.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200159115-A2.  
 XX  
 PD 16-AUG-2001.  
 XX  
 PF 09-FEB-2001; 2001WO-US04426.

```

XX PR 09-FEB-2000; 2000US-0181261.
XX PA (UROG-) UROGENESYS INC.
XX PI Hubert RS, Afar DEH, Challita-eid PM, Faris M, Levin E;
XX PI Mitchell SC, Jakobovits A;
XX WPI; 2001-514669/56.
XX
XX An isolated 83P5G4-related protein useful as a diagnostic and/or
PT therapeutic agent in multiple cancers such as prostate, bladder and
PT bone cancer -
XX
XX Example 15; Page 85; 112pp; English.
XX
XX The polypeptide sequences represent the 83P5G4-related protein and
CC peptide fragments of the protein. 83P5G4 exhibits prostate specific
CC expression in normal adult tissue, but it is also aberrantly expressed in
CC many cancers including tumours of the prostate, testis, bladder, kidney,
CC brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum,
CC liver, colon and lung. The 83P5G4 polynucleotide, its related protein and
CC peptide fragments and specific PCR primers are therefore useful for
CC diagnosing and treating cancer. A vector comprising a polynucleotide
CC which encodes a single chain monoclonal antibody, that immunospecifically
CC binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a
CC polynucleotide having the 83P5G4 coding sequence, are both useful in the
CC preparation of a composition for treating a patient with a cancer that
CC expresses 83P5G4. The sequences can be used in diagnostic methods to
CC monitor the level of 83P5G4 gene products in serum, blood, urine and
CC tissue and to thereby detect the presence of cancerous cells.
XX
XX Sequence 9 AA;
SQ
Query Match 27.8%; Score 5; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLPL 16
DB |||||
5 LPLPL 9

RESULT 18
AAW25052
ID AAW25052 standard; Peptide; 9 AA.
XX AC
XX AAW25052;
XX
XX 04-DEC-2001 (first entry)
XX
XX Human MHC class I molecule HLA-B7 binding 83P5G4 peptide #29.
XX
XX 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;
KW tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;
KW cytostatic; gene therapy; antibody therapy; ribozyme; blood; cervix;
KW single chain monoclonal antibody; urine; uterus; rectum; stomach; human;
KW chromosome 1q31-q32.
XX
XX Homo sapiens.
XX
XX WO200159115-A2.
XX
XX 16-AUG-2001.
XX
XX 09-FEB-2001; 2001WO-US04426.
XX
XX 09-FEB-2000; 2000US-0181261.
XX
XX (UROG-) UROGENESYS INC.
XX
XX Hubert RS, Afar DEH, Challita-eid PM, Faris M, Levin E;
XX PI Mitchell SC, Jakobovits A;
XX
XX An isolated 83P5G4-related protein useful as a diagnostic and/or
PT therapeutic agent in multiple cancers such as prostate, bladder and
PT bone cancer -
PI Mitchell SC, Jakobovits A;

```

```

XX WPI; 2001-514669/56.
XX
XX An isolated 83P5G4-related protein useful as a diagnostic and/or
PT therapeutic agent in multiple cancers such as prostate, bladder and
PT bone cancer -
XX
XX Example 15; Page 87; 112pp; English.
XX
XX The polypeptide sequences represent the 83P5G4-related protein and
CC peptide fragments of the protein. 83P5G4 exhibits prostate specific
CC expression in normal adult tissue, but it is also aberrantly expressed in
CC many cancers including tumours of the prostate, testis, bladder, kidney,
CC brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum,
CC liver, colon and lung. The 83P5G4 polynucleotide, its related protein and
CC peptide fragments and specific PCR primers are therefore useful for
CC diagnosing and treating cancer. A vector comprising a polynucleotide
CC which encodes a single chain monoclonal antibody, that immunospecifically
CC binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a
CC polynucleotide having the 83P5G4 coding sequence, are both useful in the
CC preparation of a composition for treating a patient with a cancer that
CC expresses 83P5G4. The sequences can be used in diagnostic methods to
CC monitor the level of 83P5G4 gene products in serum, blood, urine and
CC tissue and to thereby detect the presence of cancerous cells.
XX
XX Sequence 9 AA;
SQ
Query Match 27.8%; Score 5; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLPL 16
DB |||||
5 LPLPL 9

RESULT 19
AAW25004
ID AAW25004 standard; Peptide; 10 AA.
XX AC
XX AAW25004;
XX
XX 04-DEC-2001 (first entry)
XX
XX Human MHC class I molecule HLA-A24 binding 83P5G4 peptide #81.
XX
XX 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;
KW tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;
KW cytostatic; gene therapy; antibody therapy; ribozyme; blood; cervix;
KW single chain monoclonal antibody; urine; uterus; rectum; stomach; human;
KW chromosome 1q31-q32.
XX
XX Homo sapiens.
XX
XX WO200159115-A2.
XX
XX 16-AUG-2001.
XX
XX 09-FEB-2001; 2001WO-US04426.
XX
XX 09-FEB-2000; 2000US-0181261.
XX
XX (UROG-) UROGENESYS INC.
XX
XX Hubert RS, Afar DEH, Challita-eid PM, Faris M, Levin E;
XX PI Mitchell SC, Jakobovits A;
XX
XX WPI; 2001-514669/56.
XX
XX An isolated 83P5G4-related protein useful as a diagnostic and/or
PT therapeutic agent in multiple cancers such as prostate, bladder and
PT bone cancer -
XX

```

PS Example 15; Page 86; 112pp; English.

XX The polypeptide sequences represent the 83P5G4-related protein and peptide fragments of the protein. 83P5G4 exhibits prostate specific expression in normal adult tissue, but it is also aberrantly expressed in many cancers including tumours of the prostate, testis, bladder, kidney, brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum, liver, colon and lung. The 83P5G4 polynucleotide, its related protein and peptide fragments and specific PCR primers are therefore useful for diagnosing and treating cancer. A vector comprising a polynucleotide which encodes a single chain monoclonal antibody, that immunospecifically binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a polynucleotide having the 83P5G4 coding sequence, are both useful in the preparation of a composition for treating a patient with a cancer that expresses 83P5G4. The sequences can be used in diagnostic methods to monitor the level of 83P5G4 gene products in serum, blood, urine and tissue and to thereby detect the presence of cancerous cells.

XX Sequence 10 AA;

SQ Query Match 27.8%; Score 5; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLPL 16  
|||||  
Db 6 LPLPL 10

RESULT 20  
AAM25103  
ID AAM25103 standard; Peptide; 10 AA.  
XX AC AAM25103;  
XX DT 04-DEC-2001 (first entry)  
XX DE Human MHC class I molecule HLA-B7 binding 83P5G4 peptide #80.  
XX KW 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver; tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum; cytostatic; gene therapy; antibody therapy; ribozyme; blood; cervix;  
XX KW single chain monoclonal antibody; urine; uterus; rectum; stomach; human; chromosome 1q31-q32.  
XX OS Homo sapiens.  
XX PN WO200159115-A2.  
XX PD 16-AUG-2001.  
XX PF 09-FEB-2001; 2001WO-US04426.  
XX PR 09-FEB-2000; 2000US-0181261.  
XX PA (UOOG-) UROGENESYS INC.  
XX PI Hubert RS, Afar DEH, Challita-eid PM, Faris M, Levin E;  
XX PI Mitchell SC, Jakobovits A;  
XX DR WPI; 2001-514669/56.  
XX PT An isolated 83P5G4-related protein useful as a diagnostic and/or therapeutic agent in multiple cancers such as prostate, bladder and bone cancer -  
XX PS Example 15; Page 89; 112pp; English.

XX The polypeptide sequences represent the 83P5G4-related protein and peptide fragments of the protein. 83P5G4 exhibits prostate specific expression in normal adult tissue, but it is also aberrantly expressed in many cancers including tumours of the prostate, testis, bladder, kidney, brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum, liver, colon and lung. The 83P5G4 polynucleotide, its related protein and peptide fragments and specific PCR primers are therefore useful for diagnosing and treating cancer. A vector comprising a polynucleotide which encodes a single chain monoclonal antibody, that immunospecifically binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a polynucleotide having the 83P5G4 coding sequence, are both useful in the preparation of a composition for treating a patient with a cancer that expresses 83P5G4. The sequences can be used in diagnostic methods to monitor the level of 83P5G4 gene products in serum, blood, urine and tissue and to thereby detect the presence of cancerous cells.

CC liver, colon and lung. The 83P5G4 polynucleotide, its related protein and peptide fragments and specific PCR primers are therefore useful for diagnosing and treating cancer. A vector comprising a polynucleotide which encodes a single chain monoclonal antibody, that immunospecifically binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a polynucleotide having the 83P5G4 coding sequence, are both useful in the preparation of a composition for treating a patient with a cancer that expresses 83P5G4. The sequences can be used in diagnostic methods to monitor the level of 83P5G4 gene products in serum, blood, urine and tissue and to thereby detect the presence of cancerous cells.

XX Sequence 10 AA;

SQ Query Match 27.8%; Score 5; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLPL 16  
|||||  
Db 6 LPLPL 10

RESULT 21  
AAM25203  
ID AAM25203 standard; Peptide; 10 AA.  
XX AC AAM25203;  
XX DT 04-DEC-2001 (first entry)  
XX DE Human MHC molecule HLA-B35 binding 83P5G4 peptide #80.  
XX KW 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver; tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum; cytostatic; gene therapy; antibody therapy; ribozyme; blood; cervix;  
XX KW single chain monoclonal antibody; urine; uterus; rectum; stomach; human; chromosome 1q31-q32.  
XX OS Homo sapiens.  
XX PN WO200159115-A2.  
XX PD 16-AUG-2001.  
XX PF 09-FEB-2001; 2001WO-US04426.  
XX PR 09-FEB-2000; 2000US-0181261.  
XX PA (UOOG-) UROGENESYS INC.  
XX PI Hubert RS, Afar DEH, Challita-eid PM, Faris M, Levin E;  
XX PI Mitchell SC, Jakobovits A;  
XX DR WPI; 2001-514669/56.  
XX PT An isolated 83P5G4-related protein useful as a diagnostic and/or therapeutic agent in multiple cancers such as prostate, bladder and bone cancer -  
XX PS Example 15; Page 91; 112pp; English.

XX The polypeptide sequences represent the 83P5G4-related protein and peptide fragments of the protein. 83P5G4 exhibits prostate specific expression in normal adult tissue, but it is also aberrantly expressed in many cancers including tumours of the prostate, testis, bladder, kidney, brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum, liver, colon and lung. The 83P5G4 polynucleotide, its related protein and peptide fragments and specific PCR primers are therefore useful for diagnosing and treating cancer. A vector comprising a polynucleotide which encodes a single chain monoclonal antibody, that immunospecifically binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a polynucleotide having the 83P5G4 coding sequence, are both useful in the preparation of a composition for treating a patient with a cancer that expresses 83P5G4. The sequences can be used in diagnostic methods to monitor the level of 83P5G4 gene products in serum, blood, urine and tissue and to thereby detect the presence of cancerous cells.

CC expresses 83P5G4. The sequences can be used in diagnostic methods to  
CC monitor the level of 83P5G4 gene products in serum, blood, urine and  
CC tissue and to thereby detect the presence of cancerous cells.

XX  
SQ Sequence 10 AA;  
Query Match 27.8%; Score 5; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLPL 16  
|||||  
Db 6 LPLPL 10

RESULT 22  
AAB20470  
ID AAB20470 standard; Peptide; 11 AA.  
XX  
XX  
AC AAB20470;  
XX  
DT 21-JUN-2001 (first entry)  
XX  
DE Mouse CD166 peptide isolated in database screening.  
XX  
XX  
KW CD166; AlCAM; mouse; PSK; seizure related protein; epilepsy;  
KW neurological disorder; diagnosis; therapy.  
XX  
OS Mus sp.  
XX  
XX WO200125268-A1.  
XX  
XX  
PD 12-APR-2001.  
XX  
XX  
PF 04-OCT-2000; 2000WO-DK00556.  
XX  
XX  
PR 04-OCT-1999; 99DK-0001420.  
XX  
XX (SCHR/) SCHROTZ-KING P.  
PA (KING/) KING A.  
PA (MANN/) MANN M.  
PA (ANDE/) ANDERSEN J.  
PA (KUES/) KUESTER B.  
XX  
XX  
PI Schrotz-King P, King A, Mann M, Andersen J, Kuester B;  
XX  
XX  
DR WPI; 2001-290605/30.  
XX  
XX  
PT Novel human seizure related proteins useful for controlling epileptic  
PT seizures and neurological disorders, and for identifying potential drug  
PT targets for use in diagnosis and/or prognosis of neurological disorders

XX  
XX  
PS Disclosure; Page 59; 150pp; English.  
XX  
XX  
CC The present sequence is that of a mouse CD166 (ALCAM) peptide  
CC identified during a proteomics screening approach for membrane  
CC receptors in the brain. 9 Proteins from an RP-HPLC preparation  
CC from the mouse E16 brain plasma membrane were analyzed by  
CC nano-electrospray tandem mass spectrometry. Peptide sequences were  
CC found by searching NRDB or EST databases with peptide sequence tags.  
CC Sample 8 was identified as CD166. Sample 7 was novel, and named  
CC PSK-1. Human PSKs (see AAB2046-48) were subsequently identified.  
CC These are novel transmembrane receptor or secreted proteins that  
CC are potentially involved in the control or generation of seizures  
CC such as epileptic seizures or other neurological disorders.  
CC PSK-1, -2 and -3 polynucleotides and polypeptides can be used to  
CC identify potential drug targets. They can also be used in the  
CC diagnosis of seizure related conditions or other neurodegeneration  
CC such as Alzheimer, Rasmussen's Encephalitis, Parkinson's disease,  
CC multiple sclerosis, cerebrovascular disorders (stroke syndromes)  
CC like ischaemia, Huntington's disease or schizophrenia (claimed),  
CC and in the treatment of conditions caused by PSK upregulation,

CC deficiency or impaired function.  
XX  
SQ Sequence 11 AA;  
Query Match 27.8%; Score 5; DB 22; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TLTDV 7  
|||||  
Db 6 TLTDV 10

RESULT 23  
ABU03415  
ID ABU03415 standard; Protein; 11 AA.  
XX  
XX  
AC ABU03415;  
XX  
DT 29-JAN-2003 (first entry)  
XX  
DE Human expressed protein tag (EPT) #195.  
XX  
KW Translational profiling; expressed protein tag; EPT; kinase;  
KW phosphatase; protease; protease inhibitor; transporter;  
KW cytoskeletal protein; receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer;  
KW gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma;  
KW leukaemia.  
XX  
XX Homo sapiens.  
XX  
XX WO200278524-A2.  
XX  
XX  
PD 10-OCT-2002.  
XX  
XX  
PF 28-MAR-2002; 2002WO-US09671.  
XX  
XX  
PR 28-MAR-2001; 2001US-279495P.  
PR 21-MAY-2001; 2001US-292544P.  
PR 08-AUG-2001; 2001US-310801P.  
PR 01-OCT-2001; 2001US-326370P.  
PR 04-DEC-2001; 2001US-336780P.  
PR 20-FEB-2002; 2002US-358985P.  
XX  
XX (ZYCO-) ZYCOS INC.  
XX  
XX  
PI Chicz RM, Tomlinson AJ, Urban RG;  
XX  
XX  
DR WPI; 2003-040607/03.  
XX  
XX  
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma  
PT or leukemia

XX  
XX  
PS Claim 10; SEQ ID No 195; 134pp; English.  
XX  
XX  
CC The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor.  
CC The polypeptide is useful as an immunogenic composition for eliciting  
CC in a mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to  
CC this polypeptide, is useful for treating cancer. The polypeptide is  
CC also useful for identifying compounds that binds to a naturally  
CC processed class I or class II MHC-binding polypeptide. The polypeptides  
CC and polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational  
CC profiling.

CC Note: This sequence does not appear in the printed specification but was  
 CC obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

SQ Sequence 11 AA;  
 Query Match 27.8%; Score 5; DB 24; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TLTDV 7  
 |||||  
 Db 6 TLTDV 10

RESULT 24  
 AAB89415  
 ID AAB89415 standard; Peptide; 12 AA.  
 XX AC AAB89415;  
 XX DT 23-MAY-2001 (first entry)  
 XX DE HIV gp120 protein binding peptide #508.  
 XX KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;  
 XX KW replication; CCR5; CXCR4; CD4; STRL33.  
 XX OS Synthetic.  
 XX PN WO200116182-A2.  
 XX PD 08-MAR-2001.  
 XX PF 25-AUG-2000; 2000WO-US23505.  
 XX PR 27-AUG-1999; 99US-0151270.  
 XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX PI Saxinger C;  
 XX DR WPI; 2001-244398/25.  
 XX PT Novel polypeptides useful for treating HIV infection, have homology to  
 XX PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,  
 XX PS and binds to HIV gp120 under physiological conditions -  
 XX PS Example 9; Page 57; 114pp; English.  
 XX CC The present invention describes a number of peptides which are able to  
 XX CC bind to HIV glycoprotein 120 (gp120). These are similar to the human  
 XX CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are  
 XX CC useful in the treatment of HIV, as they prevent replication of the  
 XX CC virus. The present sequence is an example of a peptide of the invention.

SQ Sequence 12 AA;  
 Query Match 27.8%; Score 5; DB 22; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLT 5  
 |||||  
 Db 6 SLTLT 10

RESULT 25  
 AAB89855  
 ID AAB89855 standard; Peptide; 12 AA.  
 XX AC AAB89855;  
 XX DT 23-MAY-2001 (first entry)  
 XX DE HIV gp120 protein binding peptide #949.  
 XX KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;  
 XX KW replication; CCR5; CXCR4; CD4; STRL33.  
 XX OS Synthetic.  
 XX PN WO200116182-A2.  
 XX PD 08-MAR-2001.  
 XX PF 25-AUG-2000; 2000WO-US23505.  
 XX PR 27-AUG-1999; 99US-0151270.  
 XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX PI Saxinger C;

DT 23-MAY-2001 (first entry)  
 XX HIV gp120 protein binding peptide #948.  
 XX KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;  
 XX KW replication; CCR5; CXCR4; CD4; STRL33.  
 XX OS Synthetic.  
 XX PN WO200116182-A2.  
 XX PD 08-MAR-2001.  
 XX PF 25-AUG-2000; 2000WO-US23505.  
 XX PR 27-AUG-1999; 99US-0151270.  
 XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX PI Saxinger C;  
 XX DR WPI; 2001-244398/25.  
 XX PT Novel polypeptides useful for treating HIV infection, have homology to  
 XX PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,  
 XX PS and binds to HIV gp120 under physiological conditions -  
 XX PS Example 10; Page 69; 114pp; English.  
 XX CC The present invention describes a number of peptides which are able to  
 XX CC bind to HIV glycoprotein 120 (gp120). These are similar to the human  
 XX CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are  
 XX CC useful in the treatment of HIV, as they prevent replication of the  
 XX CC virus. The present sequence is an example of a peptide of the invention.

SQ Sequence 12 AA;  
 Query Match 27.8%; Score 5; DB 22; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLT 5  
 |||||  
 Db 8 SLTLT 12

RESULT 26  
 AAB89856  
 ID AAB89856 standard; Peptide; 12 AA.  
 XX AC AAB89856;  
 XX DT 23-MAY-2001 (first entry)  
 XX DE HIV gp120 protein binding peptide #949.  
 XX KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;  
 XX KW replication; CCR5; CXCR4; CD4; STRL33.  
 XX OS Synthetic.  
 XX PN WO200116182-A2.  
 XX PD 08-MAR-2001.  
 XX PF 25-AUG-2000; 2000WO-US23505.  
 XX PR 27-AUG-1999; 99US-0151270.  
 XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX PI Saxinger C;





```
XX AAE03935;
XX 09-AUG-2001 (first entry)
XX Human gene 38 encoded secreted protein fragment HBJFJ14, SEQ ID NO:98.
XX
XX Human; secreted protein; proliferative disorder; cancer; tumour;
XX foetal abnormality; developmental abnormality; haematopoietic disorder;
XX immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
XX inflammation; allergy; neurological disorder; Alzheimer's disease;
XX Parkinson's disease; cognitive disorder; schizophrenia; asthma;
XX skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
XX cardiovascular disorder; angogenic disorder; kidney disorder;
XX gastrointestinal disorder; pregnancy-related disorder;
XX endocrine disorder; infection; wound healing; vulnerary;
XX cell culture; chemotaxis; food additive; gene therapy;
XX binding partner identification.
XX
XX Homo sapiens.
XX
XX WO200077022-A1.
XX
XX 21-DEC-2000.
XX
XX 01-JUN-2000; 2000WO-US15136.
XX
XX 11-JUN-1999; 99US-0138629.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM, Komatsoulis GA;
XX WPI; 2001-367020/38.
XX N-PSDB; AAD08382.
XX
XX Nucleic acids encoding 50 human secreted polypeptides, useful for
XX preventing, diagnosing and/or treating diseases, e.g. Parkinson's
XX disease, botulism, cancers and Scimitar syndrome -
XX
XX Claim 11; Page 546; 614pp; English.
XX
XX RAD08345-AAD08394 represent cDNAs corresponding to 50 human secreted
XX protein genes and AAE03898-AAE03947 represent the proteins they encode.
XX AAE03948-AAE03996 represent human secreted protein fragments or variants.
XX The genes and their secreted proteins are useful for preventing,
XX treating or ameliorating medical conditions, e.g., by protein or gene
XX therapy. Pathological conditions can be diagnosed by determining the
XX amount of the new protein in a sample or by determining the presence of
XX mutations in the new genes. Specific uses are described for each of the
XX 50 genes, based on the tissues in which they are most highly expressed,
XX and include developing products for the diagnosis or treatment of
XX proliferative disorders, cancer, tumours, foetal and developmental
XX abnormalities, haematopoietic disorders, diseases of the immune system,
XX AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
XX allergies, neurological disorders (e.g., Alzheimer's disease,
XX Parkinson's disease), cognitive disorders, schizophrenia, asthma,
XX skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
XX cardiovascular disorders, angogenic disorders, kidney disorders,
XX gastrointestinal disorders, pregnancy-related disorders, endocrine
XX disorders, and infections. The proteins can also be used to aid wound
XX healing and epithelial cell proliferation, to prevent skin aging due to
XX sunburn, to maintain organs before transplantation, for supporting cell
XX culture of primary tissues, to regenerate tissues, to identify their
XX cognate ligands or binding partners, and in chemotaxis, and can be used
XX as a food additive or preservative to modify storage properties.
XX Antibodies specific for a protein of the invention can be used in
XX alleviating symptoms associated with the disorders mentioned above, and
XX in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked
XX immunosorbent assay (ELISA). The present sequence represents a human
XX secreted protein fragment of the invention.
XX
XX Sequence 14 AA;

Query Match 27.8%; Score 5; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Mismatches 0; Gaps 0;
Matches 5; Conservative 0; Indels 0;

QY 10 LHLPL 14
Db 5 LHLPL 9

RESULT 30
AAW39008
ID AAW39008 standard; peptide; 15 AA.
XX AAW39008;
XX
XX 27-MAR-1998 (first entry)
XX
XX Peptide resembling an SH3 domain binding peptide SEQ ID NO:407.
XX
XX Cortactin; SH3 domain; binding peptide; Src homology region 3;
XX tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
XX Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
XX
XX Synthetic.
XX
XX WO9730074-A1.
XX
XX 21-AUG-1997.
XX
XX 14-FEB-1997; 97WO-US02298.
XX
XX 16-FEB-1996; 96US-0602999.
XX
XX (CYTO-) CYTOGEN CORP.
XX (UYNC-) UNIV NORTH CAROLINA.
XX
XX Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
XX Sparks AB, Thorn JM;
XX
XX WPI; 1997-424972/39.
XX
XX Src homology region 3 binding peptide - used to activate Src
XX tyrosine kinase(s) and to stimulate immune response by increasing
XX production of certain lymphokine(s), e.g. interleukin-1
XX
XX Claim 22; Page 93; 131pp; English.
XX
XX The present sequence represents a peptide which resembles a Src homology
XX region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
XX (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
XX bind the middle SH3 domain of Nck; (c) peptides which bind the SH3
XX domain of Abl; (d) peptides which bind the SH3 domain of PLC gamma; (e)
XX peptides which bind the SH3 domain of p53bp2; (f) peptides which bind
XX the SH3 domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)
XX peptides which bind the amino-terminal SH3 domain of Grb2. The purified
XX binding peptides can be used in the method to identify inhibitors of
XX their binding to their respective SH3 domains, which could be used to
XX modulate the pharmacological activity of proteins or polypeptide
XX containing the SH3 domain. The peptides can also be used to activate
XX Src or Src-related protein tyrosine kinases, to stimulate the immune
XX response by increasing the production of certain lymphokines, e.g.
XX tumour necrosis factor-alpha and interleukin-1, or to deliver a
XX Src related proteins.
XX
XX Sequence 15 AA;

Query Match 27.8%; Score 5; DB 18; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QV      12 LPLPL 16
        |||||
Db      3 LPLPL 7

RESULT 31
ID AAW38988
XX AAW38988 standard; peptide; 15 AA.
AC AAW38988;
XX
XX
XX 27-MAR-1998 (first entry)
XX
XX Peptide resembling an SH3 domain binding peptide SEQ ID NO:395.
XX
XX Cortactin; SH3 domain; binding peptide; Src homology region 3;
XX tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
XX Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
XX
XX Synthetic.
XX
XX WO9730074-A1.
XX
XX 21-AUG-1997.
XX
XX 14-FEB-1997; 97WO-US02298.
XX
XX 16-FEB-1996; 96US-0602999.
XX
XX (CYTO-) CYTOGEN CORP.
XX (UYNC-) UNIV NORTH CAROLINA.
XX
XX Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
XX Sparks AB, Thorn JM;
XX
XX WPI; 1997-424972/39.
XX
XX Src homology region 3 binding peptide - used to activate Src
XX tyrosine kinase(s) and to stimulate immune response by increasing
XX production of certain lymphokine(s), e.g. interleukin-1
XX
XX Claim 22; Page 92; 131pp; English.
XX
XX The present sequence represents a peptide which resembles a Src homology
XX region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
XX (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
XX bind the middle SH3 domain of Nck; (c) peptides which bind the SH3
XX domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)
XX peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind
XX the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3
XX domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)
XX peptides which bind the amino-terminal SH3 domain of Grb2. The purified
XX binding peptides can be used in the method to identify inhibitors of
XX their binding to their respective SH3 domains, which could be used to
XX modulate the pharmacological activity of proteins or polypeptide
XX containing the SH3 domain. The peptides can also be used to activate
XX Src or Src-related protein tyrosine kinases, to stimulate the immune
XX response by increasing the production of certain lymphokines, e.g.
XX tumour necrosis factor-alpha and interleukin-1, or to deliver a
XX conjugated molecule to certain cellular compartments containing Src or
XX Src related proteins.
XX
XX Sequence 15 AA;
XX
XX Query Match 27.8%; Score 5; DB 18; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QV      12 LPLPL 16
XX        |||||
XX Db      10 LPLPL 14

RESULT 32
ID AAB89429
XX AAB89429 standard; Peptide; 15 AA.
XX
XX AC AAB89429;
XX
XX 23-MAY-2001 (first entry)
XX
XX HIV gp120 protein binding peptide #522.
XX
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX replication; CCR5; CXCR4; CD4; STRL33.
XX
XX Synthetic.
XX
XX WO200116182-A2.
XX
XX 08-MAR-2001.
XX
XX 25-AUG-2000; 2000WO-US23505.
XX
XX 27-AUG-1999; 99US-0151270.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Saxinger C;
XX
XX WPI; 2001-244398/25.
XX
XX Novel polypeptides useful for treating HIV infection, have homology to
XX regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX and binds to HIV gp120 under physiological conditions -
XX
XX Example 9; Page 58; 114pp; English.
XX
XX The present invention describes a number of peptides which are able to
XX bind to HIV glycoprotein 120 (gp120). These are similar to the human
XX chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
XX useful in the treatment of HIV, as they prevent replication of the
XX virus. The present sequence is an example of a peptide of the invention.
XX
XX Sequence 15 AA;
XX
XX Query Match 27.8%; Score 5; DB 22; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QV      1 SLTTLT 5
XX        |||||
XX Db      9 SLTTLT 13

RESULT 33
ID AAB89430
XX AAB89430 standard; Peptide; 15 AA.
XX
XX AC AAB89430;
XX
XX 23-MAY-2001 (first entry)
XX
XX HIV gp120 protein binding peptide #523.
XX
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX replication; CCR5; CXCR4; CD4; STRL33.
XX
XX Synthetic.
XX
XX WO200116182-A2.
XX
XX 08-MAR-2001.
XX
XX 25-AUG-2000; 2000WO-US23505.
XX

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PR 27-AUG-1999; 99US-0151270.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Saxinger C;
XX
XX WPI; 2001-244398/25.
XX
XX Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions -
XX
XX Example 9; Page 58; 114pp; English.
XX
XX The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the
CC virus. The present sequence is an example of a peptide of the invention.
XX
XX Sequence 15 AA;
SQ Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTTLT 5
Db 8 SLTTLT 12

RESULT 34
AAB89431
ID AAB89431 standard; Peptide; 15 AA.
XX
XX AC AAB89431;
XX
XX 23-MAY-2001 (first entry)
XX
XX HIV gp120 protein binding peptide #524.
XX
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX
XX Synthetic.
XX
XX WO200116182-A2.
XX
XX 08-MAR-2001.
XX
XX 25-AUG-2000; 2000WO-US23505.
XX
XX 27-AUG-1999; 99US-0151270.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Saxinger C;
XX
XX WPI; 2001-244398/25.
XX
XX Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions -
XX
XX Example 9; Page 58; 114pp; English.
XX
XX The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the
CC virus. The present sequence is an example of a peptide of the invention.
XX
XX Sequence 15 AA;
SQ Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTTLT 5
Db 8 SLTTLT 12

RESULT 34
AAB89431
ID AAB89431 standard; Peptide; 15 AA.
XX
XX AC AAB89431;
XX
XX 23-MAY-2001 (first entry)
XX
XX HIV gp120 protein binding peptide #524.
XX
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX
XX Synthetic.
XX
XX WO200116182-A2.
XX
XX 08-MAR-2001.
XX
XX 25-AUG-2000; 2000WO-US23505.
XX
XX 27-AUG-1999; 99US-0151270.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Saxinger C;
XX
XX WPI; 2001-244398/25.
XX
XX Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions -
XX
XX Example 9; Page 58; 114pp; English.
XX
XX The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the
CC virus. The present sequence is an example of a peptide of the invention.
XX
XX Sequence 15 AA;
SQ Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTTLT 5
Db 11 SLTTLT 15

RESULT 36
AAB89620
ID AAB89620 standard; Peptide; 15 AA.
XX
XX AC AAB89620;
XX
XX 23-MAY-2001 (first entry)
XX
XX HIV gp120 protein binding peptide #713.
XX
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW
```







PS Example 10; Page 73; 114pp; English.  
XX  
CC The present invention describes a number of peptides which are able to  
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human  
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are  
CC useful in the treatment of HIV, as they prevent replication of the  
CC virus. The present sequence is an example of a peptide of the invention.  
XX  
SQ Sequence 15 AA;  
  
Query Match 27.8%; Score 5; DB 22; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SLTLT 5  
Db 8 SLTLT 12  
  
RESULT 45  
AAB90014  
ID AAB90014 standard; Peptide; 15 AA.  
XX  
AC AAB90014;  
XX  
DT 23-MAY-2001 (first entry)  
XX  
DE HIV gp120 protein binding peptide #1107.  
XX  
KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;  
KW replication; CCR5; CXCR4; CD4; STRL33.  
XX  
OS Synthetic.  
XX  
PN WO200116182-A2.  
XX  
PD 08-MAR-2001.  
XX  
PF 25-AUG-2000; 2000WO-US23505.  
XX  
PR 27-AUG-1999; 99US-0151270.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Saxinger C;  
XX  
DR WPI; 2001-244398/25.  
XX  
PT Novel polypeptides useful for treating HIV infection, have homology to  
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,  
PT and binds to HIV gp120 under physiological conditions -  
XX  
OS Synthetic.  
XX  
PN WO200116182-A2.  
XX  
PD 08-MAR-2001.  
XX  
PF 25-AUG-2000; 2000WO-US23505.  
XX  
PR 27-AUG-1999; 99US-0151270.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Saxinger C;  
XX  
DR WPI; 2001-244398/25.  
XX  
PT Novel polypeptides useful for treating HIV infection, have homology to  
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,  
PT and binds to HIV gp120 under physiological conditions -  
XX  
PS Example 10; Page 73; 114pp; English.  
XX  
CC The present invention describes a number of peptides which are able to  
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human  
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are  
CC useful in the treatment of HIV, as they prevent replication of the  
CC virus. The present sequence is an example of a peptide of the invention.  
XX  
SQ Sequence 15 AA;  
  
Query Match 27.8%; Score 5; DB 22; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SLTLT 5  
Db 8 SLTLT 12  
  
RESULT 46  
AAB90015

ID AAB90015 standard; Peptide; 15 AA.  
XX  
AC AAB90015;  
XX  
DT 23-MAY-2001 (first entry)  
XX  
DE HIV gp120 protein binding peptide #1108.  
XX  
KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;  
KW replication; CCR5; CXCR4; CD4; STRL33.  
XX  
OS Synthetic.  
XX  
PN WO200116182-A2.  
XX  
PD 08-MAR-2001.  
XX  
PF 25-AUG-2000; 2000WO-US23505.  
XX  
PR 27-AUG-1999; 99US-0151270.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Saxinger C;  
XX  
DR WPI; 2001-244398/25.  
XX  
PT Novel polypeptides useful for treating HIV infection, have homology to  
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,  
PT and binds to HIV gp120 under physiological conditions -  
XX  
PS Example 10; Page 73; 114pp; English.  
XX  
CC The present invention describes a number of peptides which are able to  
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human  
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are  
CC useful in the treatment of HIV, as they prevent replication of the  
CC virus. The present sequence is an example of a peptide of the invention.  
XX  
SQ Sequence 15 AA;  
  
Query Match 27.8%; Score 5; DB 22; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SLTLT 5  
Db 8 SLTLT 12  
  
RESULT 47  
AAB90016  
ID AAB90016 standard; Peptide; 15 AA.  
XX  
AC AAB90016;  
XX  
DT 23-MAY-2001 (first entry)  
XX  
DE HIV gp120 protein binding peptide #1109.  
XX  
KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;  
KW replication; CCR5; CXCR4; CD4; STRL33.  
XX  
OS Synthetic.  
XX  
PN WO200116182-A2.  
XX  
PD 08-MAR-2001.  
XX  
PF 25-AUG-2000; 2000WO-US23505.  
XX  
PR 27-AUG-1999; 99US-0151270.  
XX



PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Saxinger C;

XX WPI; 2001-244398/25.

XX Novel polypeptides useful for treating HIV infection, have homology to  
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,  
PT and binds to HIV gp120 under physiological conditions -

XX Example 10; Page 73; 114pp; English.

XX The present invention describes a number of peptides which are able to  
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human  
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are  
CC useful in the treatment of HIV, as they prevent replication of the  
CC virus. The present sequence is an example of a peptide of the invention.

XX SQ Sequence 15 AA;

Query Match 27.8%; Score 5; DB 22; Length 15;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 S L T L T 5

Db 8 S L T L T 12

RESULT 48

AAB90022

ID AAB90022 standard; Peptide; 15 AA.

XX AC AAB90022;

XX DT 23-MAY-2001 (first entry)

XX HIV gp120 protein binding peptide #1115.

XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;  
KW replication; CCR5; CXCR4; CD4; STRL33.

XX OS Synthetic.

XX PN WO200116182-A2.

XX PD 08-MAR-2001.

XX PF 25-AUG-2000; 2000WO-US23505.

XX PR 27-AUG-1999; 99US-0151270.

XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Saxinger C;

XX WPI; 2001-244398/25.

XX Novel polypeptides useful for treating HIV infection, have homology to  
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,  
PT and binds to HIV gp120 under physiological conditions -

XX Example 10; Page 73; 114pp; English.

XX The present invention describes a number of peptides which are able to  
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human  
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are  
CC useful in the treatment of HIV, as they prevent replication of the  
CC virus. The present sequence is an example of a peptide of the invention.

XX SQ Sequence 15 AA;

Query Match 27.8%; Score 5; DB 22; Length 15;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 S L T L T 5

Db 8 S L T L T 12

RESULT 49

AAB90023

ID AAB90023 standard; Peptide; 15 AA.

XX AC AAB90023;

XX DT 23-MAY-2001 (first entry)

XX HIV gp120 protein binding peptide #1116.

XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;  
KW replication; CCR5; CXCR4; CD4; STRL33.

XX OS Synthetic.

XX PN WO200116182-A2.

XX PD 08-MAR-2001.

XX PF 25-AUG-2000; 2000WO-US23505.

XX PR 27-AUG-1999; 99US-0151270.

XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Saxinger C;

XX WPI; 2001-244398/25.

XX Novel polypeptides useful for treating HIV infection, have homology to  
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,  
PT and binds to HIV gp120 under physiological conditions -

XX Example 10; Page 73; 114pp; English.

XX The present invention describes a number of peptides which are able to  
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human  
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are  
CC useful in the treatment of HIV, as they prevent replication of the  
CC virus. The present sequence is an example of a peptide of the invention.

XX SQ Sequence 15 AA;

Query Match 27.8%; Score 5; DB 22; Length 15;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 S L T L T 5

Db 8 S L T L T 12

RESULT 50

AAB90024

ID AAB90024 standard; Peptide; 15 AA.

XX AC AAB90024;

XX DT 23-MAY-2001 (first entry)

XX HIV gp120 protein binding peptide #1117.

XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;  
KW replication; CCR5; CXCR4; CD4; STRL33.

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OS Synthetic.
XX WO200116182-A2.
XX
XX
XX 08-MAR-2001.
XX
XX PF 25-AUG-2000; 2000WO-US23505.
XX
XX PR 27-AUG-1999; 99US-0151270.
XX
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX PI Saxinger C;
XX
XX WPI; 2001-244398/25.
XX
XX PT Novel polypeptides useful for treating HIV infection, have homology to
XX PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX PT and binds to HIV gp120 under physiological conditions
XX
XX PS Example 10; Page 73; 114pp; English.
XX
XX CC The present invention describes a number of peptides which are able to
XX CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
XX CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
XX CC useful in the treatment of HIV, as they prevent replication of the
XX CC virus. The present sequence is an example of a peptide of the invention.
XX
XX SQ Sequence 15 AA;

Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTTLT 5
DB 8 SLTTLT 12

RESULT 51
AAB90025
ID AAB90025 standard; Peptide; 15 AA.
XX
XX AC AAB90025;
XX
XX DT 23-MAY-2001 (first entry)
XX
XX DE HIV gp120 protein binding peptide #1118.
XX
XX KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX KW replication; CCR5; CXCR4; CD4; STRL33.
XX
XX OS Synthetic.
XX
XX PN WO200116182-A2.
XX
XX PD 08-MAR-2001.
XX
XX PF 25-AUG-2000; 2000WO-US23505.
XX
XX PR 27-AUG-1999; 99US-0151270.
XX
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX PI Saxinger C;
XX
XX DR WPI; 2001-244398/25.
XX
XX PT Novel polypeptides useful for treating HIV infection, have homology to
XX PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX PT and binds to HIV gp120 under physiological conditions
XX
XX PS Example 10; Page 73; 114pp; English.
XX
XX CC The present invention describes a number of peptides which are able to
XX CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
XX CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
XX CC useful in the treatment of HIV, as they prevent replication of the
XX CC virus. The present sequence is an example of a peptide of the invention.
XX
XX SQ Sequence 15 AA;

Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTTLT 5
DB 8 SLTTLT 12

RESULT 51
AAB90025
ID AAB90025 standard; Peptide; 15 AA.
XX
XX AC AAB90025;
XX
XX DT 23-MAY-2001 (first entry)
XX
XX DE HIV gp120 protein binding peptide #1118.
XX
XX KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX KW replication; CCR5; CXCR4; CD4; STRL33.
XX
XX OS Synthetic.
XX
XX PN WO200116182-A2.
XX
XX PD 08-MAR-2001.
XX
XX PF 25-AUG-2000; 2000WO-US23505.
XX
XX PR 27-AUG-1999; 99US-0151270.
XX
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX PI Saxinger C;
XX
XX DR WPI; 2001-244398/25.
XX
XX PT Novel polypeptides useful for treating HIV infection, have homology to
XX PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX PT and binds to HIV gp120 under physiological conditions
XX
XX PS Example 10; Page 73; 114pp; English.

```

```

XX
XX The present invention describes a number of peptides which are able to
XX CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
XX CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
XX CC useful in the treatment of HIV, as they prevent replication of the
XX CC virus. The present sequence is an example of a peptide of the invention.
XX
XX SQ Sequence 15 AA;

Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTTLT 5
DB 8 SLTTLT 12

RESULT 52
AAB90026
ID AAB90026 standard; Peptide; 15 AA.
XX
XX AC AAB90026;
XX
XX DT 23-MAY-2001 (first entry)
XX
XX DE HIV gp120 protein binding peptide #1119.
XX
XX KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX KW replication; CCR5; CXCR4; CD4; STRL33.
XX
XX OS Synthetic.
XX
XX PN WO200116182-A2.
XX
XX PD 08-MAR-2001.
XX
XX PF 25-AUG-2000; 2000WO-US23505.
XX
XX PR 27-AUG-1999; 99US-0151270.
XX
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX PI Saxinger C;
XX
XX DR WPI; 2001-244398/25.
XX
XX PT Novel polypeptides useful for treating HIV infection, have homology to
XX PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX PT and binds to HIV gp120 under physiological conditions
XX
XX PS Example 10; Page 73; 114pp; English.
XX
XX CC The present invention describes a number of peptides which are able to
XX CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
XX CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
XX CC useful in the treatment of HIV, as they prevent replication of the
XX CC virus. The present sequence is an example of a peptide of the invention.
XX
XX SQ Sequence 15 AA;

Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTTLT 5
DB 8 SLTTLT 12

RESULT 53
AAB90027
ID AAB90027 standard; Peptide; 15 AA.

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```

XX AAB90027;
AC
XX 23-MAY-2001 (first entry)
DT
XX
XX HIV gp120 protein binding peptide #1120.
DE
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW KW replication; CCR5; CXCR4; CD4; STRL33.
XX
XX Synthetic.
OS
XX WO200116182-A2.
XX PN
XX 08-MAR-2001.
XX PD
XX 25-AUG-2000; 2000WO-US23505.
XX PF
XX 27-AUG-1999; 99US-0151270.
XX PR
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PA
XX Saxinger C;
XX PI
XX WPI; 2001-244398/25.
XX DR
XX Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions -
XX
XX Example 10; Page 73; 114pp; English.
XX PS
XX The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the
CC virus. The present sequence is an example of a peptide of the invention.
XX CC
XX Sequence 15 AA;
XX SQ
XX
XX Query Match 27.8%; Score 5; DB 22; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SLTLT 5
XX Db |||||
XX 8 SLTLT 12
XX
XX RESULT 54
XX AAB90028
XX ID AAB90028 standard; Peptide; 15 AA.
XX AC
XX AAB90028;
XX XX
XX 23-MAY-2001 (first entry)
XX DT
XX HIV gp120 protein binding peptide #1121.
XX DE
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX KW KW replication; CCR5; CXCR4; CD4; STRL33.
XX XX
XX Synthetic.
XX OS
XX WO200116182-A2.
XX PN
XX 08-MAR-2001.
XX PD
XX 25-AUG-2000; 2000WO-US23505.
XX PF
XX 27-AUG-1999; 99US-0151270.
XX PR
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PA
XX Saxinger C;
XX PI
XX WPI; 2001-244398/25.
XX DR
XX Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions -
XX
XX Example 10; Page 73; 114pp; English.
XX PS
XX The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the
CC virus. The present sequence is an example of a peptide of the invention.
XX CC
XX Sequence 15 AA;
XX SQ
XX
XX Query Match 27.8%; Score 5; DB 22; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SLTLT 5
XX Db |||||
XX 8 SLTLT 12
XX
XX RESULT 54
XX AAB90028
XX ID AAB90028 standard; Peptide; 15 AA.
XX AC
XX AAB90028;
XX XX
XX 23-MAY-2001 (first entry)
XX DT
XX HIV gp120 protein binding peptide #1121.
XX DE
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX KW KW replication; CCR5; CXCR4; CD4; STRL33.
XX XX
XX Synthetic.
XX OS
XX WO200116182-A2.
XX PN
XX 08-MAR-2001.
XX PD
XX 25-AUG-2000; 2000WO-US23505.
XX PF
XX 27-AUG-1999; 99US-0151270.
XX PR
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PA

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XX Saxinger C;
PI
XX WPI; 2001-244398/25.
XX DR
XX Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions -
XX
XX Example 10; Page 73; 114pp; English.
XX PS
XX The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the
CC virus. The present sequence is an example of a peptide of the invention.
XX CC
XX Sequence 15 AA;
XX SQ
XX
XX Query Match 27.8%; Score 5; DB 22; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SLTLT 5
XX Db |||||
XX 8 SLTLT 12
XX
XX RESULT 55
XX AAB90029
XX ID AAB90029 standard; Peptide; 15 AA.
XX AC
XX AAB90029;
XX XX
XX 23-MAY-2001 (first entry)
XX DT
XX HIV gp120 protein binding peptide #1122.
XX DE
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX KW KW replication; CCR5; CXCR4; CD4; STRL33.
XX XX
XX Synthetic.
XX OS
XX WO200116182-A2.
XX PN
XX 08-MAR-2001.
XX PD
XX 25-AUG-2000; 2000WO-US23505.
XX PF
XX 27-AUG-1999; 99US-0151270.
XX PR
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PA
XX Saxinger C;
XX PI
XX WPI; 2001-244398/25.
XX DR
XX Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions -
XX
XX Example 10; Page 73; 114pp; English.
XX PS
XX The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the
CC virus. The present sequence is an example of a peptide of the invention.
XX CC
XX Sequence 15 AA;
XX SQ
XX
XX Query Match 27.8%; Score 5; DB 22; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SLTLT 5
XX Db |||||
XX 8 SLTLT 12
XX
XX RESULT 55
XX AAB90029
XX ID AAB90029 standard; Peptide; 15 AA.
XX AC
XX AAB90029;
XX XX
XX 23-MAY-2001 (first entry)
XX DT
XX HIV gp120 protein binding peptide #1122.
XX DE
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX KW KW replication; CCR5; CXCR4; CD4; STRL33.
XX XX
XX Synthetic.
XX OS
XX WO200116182-A2.
XX PN
XX 08-MAR-2001.
XX PD
XX 25-AUG-2000; 2000WO-US23505.
XX PF
XX 27-AUG-1999; 99US-0151270.
XX PR
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PA
XX Saxinger C;
XX PI
XX WPI; 2001-244398/25.
XX DR
XX Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions -
XX
XX Example 10; Page 73; 114pp; English.
XX PS
XX The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the
CC virus. The present sequence is an example of a peptide of the invention.
XX CC
XX Sequence 15 AA;
XX SQ
XX
XX Query Match 27.8%; Score 5; DB 22; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SLTLT 5
XX Db |||||
XX 8 SLTLT 12
XX
XX RESULT 55
XX AAB90029
XX ID AAB90029 standard; Peptide; 15 AA.
XX AC
XX AAB90029;
XX XX
XX 23-MAY-2001 (first entry)
XX DT
XX HIV gp120 protein binding peptide #1122.
XX DE
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX KW KW replication; CCR5; CXCR4; CD4; STRL33.
XX XX
XX Synthetic.
XX OS
XX WO200116182-A2.
XX PN
XX 08-MAR-2001.
XX PD
XX 25-AUG-2000; 2000WO-US23505.
XX PF
XX 27-AUG-1999; 99US-0151270.
XX PR
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PA
XX Saxinger C;
XX PI
XX WPI; 2001-244398/25.
XX DR
XX Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions -
XX
XX Example 10; Page 73; 114pp; English.
XX PS
XX The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the
CC virus. The present sequence is an example of a peptide of the invention.
XX CC
XX Sequence 15 AA;
XX SQ
XX
XX Query Match 27.8%; Score 5; DB 22; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SLTLT 5
XX Db |||||
XX 8 SLTLT 12
XX
XX RESULT 55
XX AAB90029
XX ID AAB90029 standard; Peptide; 15 AA.
XX AC
XX AAB90029;
XX XX
XX 23-MAY-2001 (first entry)
XX DT
XX HIV gp120 protein binding peptide #1122.
XX DE
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX KW KW replication; CCR5; CXCR4; CD4; STRL33.
XX XX
XX Synthetic.
XX OS
XX WO200116182-A2.
XX PN
XX 08-MAR-2001.
XX PD
XX 25-AUG-2000; 2000WO-US23505.
XX PF
XX 27-AUG-1999; 99US-0151270.
XX PR
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PA

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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLT 5  
Db 8 SLTLT 12

RESULT 56  
AAB90030  
ID AAB90030 standard; Peptide; 15 AA.  
XX AC  
XX AAB90030;  
XX 23-MAY-2001 (first entry)  
XX DE HIV gp120 protein binding peptide #1123.  
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;  
KW replication; CCR5; CXCR4; CD4; STRL33.  
XX Synthetic.  
XX WO200116182-A2.  
XX 08-MAR-2001.  
XX 25-AUG-2000; 2000WO-US23505.  
XX 27-AUG-1999; 99US-0151270.  
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.  
XX Saxinger C;  
XX WPI; 2001-244398/25.  
XX Novel polypeptides useful for treating HIV infection, have homology to regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33, and binds to HIV gp120 under physiological conditions -  
PT Example 10; Page 73; 114pp; English.  
XX The present invention describes a number of peptides which are able to bind to HIV glycoprotein 120 (gp120). These are similar to the human chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are useful in the treatment of HIV, as they prevent replication of the virus. The present sequence is an example of a peptide of the invention.  
XX Sequence 15 AA;  
SQ

Query Match 27.8%; Score 5; DB 22; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLT 5  
Db 8 SLTLT 12

RESULT 57  
AAB90031  
ID AAB90031 standard; Peptide; 15 AA.  
XX AC  
XX AAB90031;  
XX 23-MAY-2001 (first entry)  
XX DE HIV gp120 protein binding peptide #1124.  
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;  
KW replication; CCR5; CXCR4; CD4; STRL33.  
XX Synthetic.

XX WO200116182-A2.  
XX 08-MAR-2001.  
XX 25-AUG-2000; 2000WO-US23505.  
XX 27-AUG-1999; 99US-0151270.  
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.  
XX Saxinger C;  
XX WPI; 2001-244398/25.  
XX Novel polypeptides useful for treating HIV infection, have homology to regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33, and binds to HIV gp120 under physiological conditions -  
PT Example 10; Page 73; 114pp; English.  
XX The present invention describes a number of peptides which are able to bind to HIV glycoprotein 120 (gp120). These are similar to the human chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are useful in the treatment of HIV, as they prevent replication of the virus. The present sequence is an example of a peptide of the invention.  
XX Sequence 15 AA;  
SQ

Query Match 27.8%; Score 5; DB 22; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLT 5  
Db 8 SLTLT 12

RESULT 58  
AAB90032  
ID AAB90032 standard; Peptide; 15 AA.  
XX AC AAB90032;  
XX 23-MAY-2001 (first entry)  
XX DE HIV gp120 protein binding peptide #1125.  
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;  
KW replication; CCR5; CXCR4; CD4; STRL33.  
XX Synthetic.  
XX WO200116182-A2.  
XX 08-MAR-2001.  
XX 25-AUG-2000; 2000WO-US23505.  
XX 27-AUG-1999; 99US-0151270.  
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.  
XX Saxinger C;  
XX WPI; 2001-244398/25.  
XX Novel polypeptides useful for treating HIV infection, have homology to regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33, and binds to HIV gp120 under physiological conditions -  
PT Example 10; Page 74; 114pp; English.  
XX

The present invention describes a number of peptides which are able to bind to HIV glycoprotein 120 (gp120). These are similar to the human chemokine receptors CCR5, CXCR4, and STRL33, as well as CD4. These are useful in the treatment of HIV, as they prevent replication of the virus. The present sequence is an example of a peptide of the invention.

Sequence	15 AA;
SQ	

Query Match	27.8%;	Score 5;	DB 22;	Length 15;
Best Local Similarity	100.0%;	Pred. No. 2e+02;		

Qy	1	SLTLT	5
Db	8	SLTLT	12

RESULT 59  
AAB90033  
ID AAB90033 standard; Peptide; 15 AA.

AC AAB90033:

23-MAY-2001 (first entry)

DE HIV gp120 protein binding peptide #1126.

Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;  
replication; CCR5; CXCR4; CD4; STRL33.

OS Synthetic.

PN WO200116182-A2.

AA  
PD  
08-MAR-2007

25-AUG-2000: 2000WO-US23505.

XX  
PR 27-AUG-1999: 99US-0151270.XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

PI Saxinger C:

WPI; 2001-244398/25.

Novel polypeptides useful for treating HIV infection, have homology to regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33, and binds to HIV gp120 under physiological conditions

PS Example 10; Page 74; 114pp; English.

The present invention describes a number of peptides which are able to bind to HIV glycoprotein 120 (gp120). These are similar to the human chemokine receptors CCR5, CXCR4 and SSTR133, as well as CD4. These are useful in the treatment of HIV, as they prevent replication of the virus. The present sequence is an example of a peptide of the invention.

SQ	Sequence	15 AA;
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Query Match 27.8%; Score 5; DB 22; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels

Qy	1	SLTLT	5
Db	8	SLTLT	12

RESULT 60  
AAB90039  
ID AAB90039 standard; Peptide; 15 AA.

XX

AC	AAE90039;
XX	
XX	23-MAY-2001 (first entry)
DT	
XX	
XX	
DE	HIV gp120 protein binding peptide #1132.
XX	
XX	
KW	Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW	replication; CCR5; CXCR4; CD4; STRL33.

PS Example 10; Page 74; 114pp; English.

The present invention describes a number of peptides which are able to bind to HIV glycoprotein 120 (gp120). These are similar to the human chemokine receptors CCR5, CXCR4 and SFR33, as well as CD4. These are useful in the treatment of HIV, as they prevent replication of the virus. The present sequence is an example of a peptide of the invention.

Sequence	15 AA;
SQ	

Query Match 27.8%; Score 5; DB 22; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels

Qy	1	SLTLT	5
Db	8	SLTLT	12

RESULT 61  
AAB90040  
ID AAB90040 standard; Peptide; 15 AA.

AC AAB90040;

DT 23-MAY-2001 (first entry)

DE HIV gp120 protein binding peptide #1133.

Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;  
KW  
replication; CCR5; CXCR4; CD4; STRL33.  
KW

OS Synthetic.

PN WO200116182-A2.

PD 08-MAR-2001.

PF 25-AUG-2000; 2000WO-US23505.

PR 27-AUG-1999; 99US-0151270.

(USSH ) US DEPT HEALTH & HUMAN SERVICES

XX

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PI Saxinger C;
XX WPI; 2001-244398/25.
XX Novel polypeptides useful for treating HIV infection, have homology to
XX regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX and binds to HIV gp120 under physiological conditions
XX Example 10; Page 74; 114pp; English.
XX The present invention describes a number of peptides which are able to
XX bind to HIV glycoprotein 120 (gp120). These are similar to the human
XX chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
XX useful in the treatment of HIV, as they prevent replication of the
XX virus. The present sequence is an example of a peptide of the invention.
XX Sequence 15 AA;
SQ Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTTLT 5
Db 8 SLTTLT 12
|||||

RESULT 62
AAB90041
ID AAB90041 standard; Peptide; 15 AA.
AC AAB90041;
XX 23-MAY-2001 (first entry)
XX HIV gp120 protein binding peptide #1134.
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX replication; CCR5; CXCR4; CD4; STRL33.
XX Synthetic.
XX WO200116182-A2.
XX 08-MAR-2001.
XX 25-AUG-2000; 2000WO-US23505.
XX 27-AUG-1999; 99US-0151270.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX Saxinger C;
XX WPI; 2001-244398/25.
XX Novel polypeptides useful for treating HIV infection, have homology to
XX regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX and binds to HIV gp120 under physiological conditions
XX Example 10; Page 74; 114pp; English.
XX The present invention describes a number of peptides which are able to
XX bind to HIV glycoprotein 120 (gp120). These are similar to the human
XX chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
XX useful in the treatment of HIV, as they prevent replication of the
XX virus. The present sequence is an example of a peptide of the invention.
XX Sequence 15 AA;
SQ Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTTLT 5
Db 8 SLTTLT 12
|||||

RESULT 63
AAB90042
ID AAB90042 standard; Peptide; 15 AA.
XX AAB90042;
XX 23-MAY-2001 (first entry)
XX HIV gp120 protein binding peptide #1135.
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX replication; CCR5; CXCR4; CD4; STRL33.
XX Synthetic.
XX WO200116182-A2.
XX 08-MAR-2001.
XX 25-AUG-2000; 2000WO-US23505.
XX 27-AUG-1999; 99US-0151270.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX Saxinger C;
XX WPI; 2001-244398/25.
XX Novel polypeptides useful for treating HIV infection, have homology to
XX regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX and binds to HIV gp120 under physiological conditions
XX Example 10; Page 74; 114pp; English.
XX The present invention describes a number of peptides which are able to
XX bind to HIV glycoprotein 120 (gp120). These are similar to the human
XX chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
XX useful in the treatment of HIV, as they prevent replication of the
XX virus. The present sequence is an example of a peptide of the invention.
XX Sequence 15 AA;
SQ Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTTLT 5
Db 8 SLTTLT 12
|||||

RESULT 64
AAB90101
ID AAB90101 standard; Peptide; 15 AA.
XX AAB90101;
XX 23-MAY-2001 (first entry)
XX HIV gp120 protein binding peptide #1194.
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX replication; CCR5; CXCR4; CD4; STRL33.
XX Synthetic.
XX

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PN WO200116182-A2.
XX
PD 08-MAR-2001.
XX
PF 25-AUG-2000; 2000WO-US233505.
XX
PR 27-AUG-1999; 99US-0151270.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Saxinger C;
XX
DR WPI; 2001-244398/25.
XX
PT Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions -
XX
PS Example 10; Page 75; 114pp; English.
XX
CC The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the
CC virus. The present sequence is an example of a peptide of the invention.
XX
SQ Sequence 15 AA;
XX
Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 SLTTLT 5
Db 8 SLTTLT 12
XX
RESULT 66
AAB90103
ID AAB90103 standard; Peptide; 15 AA.
XX
AC AAB90103;
XX
DT 23-MAY-2001 (first entry)
XX
DE HIV gp120 protein binding peptide #1196.
XX
KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX
OS Synthetic.
XX
PN WO200116182-A2.
XX
PD 08-MAR-2001.
XX
PF 25-AUG-2000; 2000WO-US233505.
XX
PR 27-AUG-1999; 99US-0151270.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Saxinger C;
XX
DR WPI; 2001-244398/25.
XX
PT Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions -
XX
PS Example 10; Page 75; 114pp; English.
XX
CC The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the
CC virus. The present sequence is an example of a peptide of the invention.
XX
SQ Sequence 15 AA;
XX
Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 SLTTLT 5
Db 8 SLTTLT 12
XX
RESULT 65
AAB90102
ID AAB90102 standard; Peptide; 15 AA.
XX
AC AAB90102;
XX
DT 23-MAY-2001 (first entry)
XX
DE HIV gp120 protein binding peptide #1195.
XX
KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX
OS Synthetic.
XX
PN WO200116182-A2.
XX
PD 08-MAR-2001.
XX
PF 25-AUG-2000; 2000WO-US233505.
XX
PR 27-AUG-1999; 99US-0151270.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Saxinger C;
XX
DR WPI; 2001-244398/25.
XX
PT Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions -
XX
PS Example 10; Page 75; 114pp; English.
XX
CC The present invention describes a number of peptides which are able to

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XX 23-MAY-2001 (first entry)
XX DT
XX DR WPI; 2001-244398/25.
XX PT
XX DE HIV gp120 protein binding peptide #1197.
XX KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX KW replication; CCR5; CXCR4; CD4; STRL33.
XX OS Synthetic.
XX CC
XX PN WO200116182-A2.
XX PD
XX PD 08-MAR-2001.
XX PF 25-AUG-2000; 2000WO-US23505.
XX PR
XX PR 27-AUG-1999; 99US-0151270.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Saxinger C;
XX QY WPI; 2001-244398/25.
XX DR
XX PT Novel polypeptides useful for treating HIV infection, have homology to
XX PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX KW and binds to HIV gp120 under physiological conditions -
XX OS
XX CC The present invention describes a number of peptides which are able to
XX CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
XX CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
XX CC useful in the treatment of HIV, as they prevent replication of the
XX CC virus. The present sequence is an example of a peptide of the invention.
XX SQ Sequence 15 AA;
XX
XX Query Match 27.8%; Score 5; DB 22; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SLTTLT 5
XX DB |||||
XX 8 SLTTLT 12
XX
XX RESULT 69
XX AAB90111
XX ID AAB90111 standard; Peptide; 15 AA.
XX AC AAB90111;
XX DT 23-MAY-2001 (first entry)
XX DE HIV gp120 protein binding peptide #1204.
XX KW
XX KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX KW replication; CCR5; CXCR4; CD4; STRL33.
XX OS Synthetic.
XX PN WO200116182-A2.
XX PD
XX PD 08-MAR-2001.
XX PF 25-AUG-2000; 2000WO-US23505.
XX PR
XX PR 27-AUG-1999; 99US-0151270.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Saxinger C;
XX DR WPI; 2001-244398/25.
XX PT
XX PT Novel polypeptides useful for treating HIV infection, have homology to
XX PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX KW and binds to HIV gp120 under physiological conditions -
XX OS
XX CC The present invention describes a number of peptides which are able to
XX CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
XX CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
XX CC useful in the treatment of HIV, as they prevent replication of the
XX CC virus. The present sequence is an example of a peptide of the invention.
XX SQ Sequence 15 AA;
XX
XX Query Match 27.8%; Score 5; DB 22; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SLTTLT 5
XX DB |||||
XX 8 SLTTLT 12
XX
XX RESULT 68
XX AAB90110
XX ID AAB90110 standard; Peptide; 15 AA.
XX AC AAB90110;
XX DT 23-MAY-2001 (first entry)
XX DE HIV gp120 protein binding peptide #1203.
XX KW
XX KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX KW replication; CCR5; CXCR4; CD4; STRL33.
XX OS Synthetic.
XX PN WO200116182-A2.
XX PD
XX PD 08-MAR-2001.
XX PF 25-AUG-2000; 2000WO-US23505.
XX PR
XX PR 27-AUG-1999; 99US-0151270.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Saxinger C;

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QY      1 SLTTLT 5
Db      |||||
        8 SLTTLT 12

RESULT 70
ID      AAB90112 standard; Peptide; 15 AA.
XX
AC      AAB90112;
XX
DT      23-MAY-2001 (first entry)
XX
DE      HIV gp120 protein binding peptide #1205.
XX
KW      Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW      replication; CCR5; CXCR4; CD4; STRL33.
XX
OS      Synthetic.
XX
PN      WO200116182-A2.
XX
PD      08-MAR-2001.
XX
PF      25-AUG-2000; 2000WO-US233505.
XX
PR      27-AUG-1999; 99US-0151270.
XX
PA      (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI      Saxinger C;
XX
DR      WPI; 2001-244398/25.
XX
PT      Novel polypeptides useful for treating HIV infection, have homology to
PT      regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT      and binds to HIV gp120 under physiological conditions -
XX
PS      Example 10; Page 75; 114pp; English.
XX
CC      The present invention describes a number of peptides which are able to
CC      bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC      chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC      useful in the treatment of HIV, as they prevent replication of the
CC      virus. The present sequence is an example of a peptide of the invention.
XX
SQ      Sequence 15 AA;

Query Match      27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTTLT 5
Db      |||||
        8 SLTTLT 12

RESULT 72
ID      AAB90114 standard; Peptide; 15 AA.
XX
AC      AAB90114;
XX
DT      23-MAY-2001 (first entry)
XX
DE      HIV gp120 protein binding peptide #1207.
XX
KW      Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW      replication; CCR5; CXCR4; CD4; STRL33.
XX
OS      Synthetic.
XX
PN      WO200116182-A2.
XX
PD      08-MAR-2001.
XX
PF      25-AUG-2000; 2000WO-US233505.
XX
PR      27-AUG-1999; 99US-0151270.
XX
PA      (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI      Saxinger C;
XX
DR      WPI; 2001-244398/25.
XX
PT      Novel polypeptides useful for treating HIV infection, have homology to
PT      regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT      and binds to HIV gp120 under physiological conditions -
XX
PS      Example 10; Page 75; 114pp; English.
XX
CC      The present invention describes a number of peptides which are able to
CC      bind to HIV glycoprotein 120 (gp120). These are similar to the human

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CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the
CC virus. The present sequence is an example of a peptide of the invention.
SQ Sequence 15 AA;
Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;
QY 1 SLTLT 5
DB 8 SLTLT 12

RESULT 73
AAB90115
ID AAB90115 standard; Peptide; 15 AA.
XX AAB90115;
XX
XX 23-MAY-2001 (first entry)
XX HIV gp120 protein binding peptide #1208.
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX Synthetic.
XX WO200116182-A2.
XX
XX 08-MAR-2001.
XX
XX 25-AUG-2000; 2000WO-US23505.
XX
XX 27-AUG-1999; 99US-0151270.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX Saxinger C;
XX WPI; 2001-244398/25.
XX
XX Novel polypeptides useful for treating HIV infection, have homology to
XX regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX and binds to HIV gp120 under physiological conditions -
XX Example 10; Page 75; 114pp; English.
XX
XX The present invention describes a number of peptides which are able to
XX bind to HIV glycoprotein 120 (gp120). These are similar to the human
XX chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
XX useful in the treatment of HIV, as they prevent replication of the
XX virus. The present sequence is an example of a peptide of the invention.
XX Sequence 15 AA;
SQ Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;
QY 1 SLTLT 5
DB 8 SLTLT 12

RESULT 74
AAB90116
ID AAB90116 standard; Peptide; 15 AA.
XX AAB90116;
XX
XX 23-MAY-2001 (first entry)
XX HIV gp120 protein binding peptide #1211.
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX Synthetic.
XX WO200116182-A2.
XX
XX 08-MAR-2001.
XX
XX 25-AUG-2000; 2000WO-US23505.
XX
XX 27-AUG-1999; 99US-0151270.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX Saxinger C;
XX

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DT 23-MAY-2001 (first entry)
XX HIV gp120 protein binding peptide #1209.
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX Synthetic.
XX WO200116182-A2.
XX
XX 08-MAR-2001.
XX
XX 25-AUG-2000; 2000WO-US23505.
XX
XX 27-AUG-1999; 99US-0151270.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX Saxinger C;
XX WPI; 2001-244398/25.
XX
XX Novel polypeptides useful for treating HIV infection, have homology to
XX regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX and binds to HIV gp120 under physiological conditions -
XX Example 10; Page 76; 114pp; English.
XX
XX The present invention describes a number of peptides which are able to
XX bind to HIV glycoprotein 120 (gp120). These are similar to the human
XX chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
XX useful in the treatment of HIV, as they prevent replication of the
XX virus. The present sequence is an example of a peptide of the invention.
XX Sequence 15 AA;
SQ Query Match 27.8%; Score 5; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;
QY 1 SLTLT 5
DB 8 SLTLT 12

RESULT 75
AAB90118
ID AAB90118 standard; Peptide; 15 AA.
XX AAB90118;
XX
XX 23-MAY-2001 (first entry)
XX HIV gp120 protein binding peptide #1211.
XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX Synthetic.
XX WO200116182-A2.
XX
XX 08-MAR-2001.
XX
XX 25-AUG-2000; 2000WO-US23505.
XX
XX 27-AUG-1999; 99US-0151270.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX Saxinger C;
XX

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DR WPI; 2001-244398/25.  
XX  
PT Novel polypeptides useful for treating HIV infection, have homology to  
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,  
PT and binds to HIV gp120 under physiological conditions -  
XX  
PS Example 10; Page 76; 114pp; English.  
XX  
CC The present invention describes a number of peptides which are able to  
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human  
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are  
CC useful in the treatment of HIV, as they prevent replication of the  
CC virus. The present sequence is an example of a peptide of the invention.  
XX  
SQ Sequence 15 AA;  
  
Query Match 27.8%; Score 5; DB 22; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SLTLT 5  
|  
|  
|  
|  
Db 8 SLTLT 12

Search completed: November 25, 2003, 19:27:10  
Job time : 46.9419 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:25:48 ; Search time 28.8837 Seconds  
(without alignments)  
114.943 Million cell updates/sec

Title: US-09-641-801-23

Perfect score: 18

Sequence: 1 SLTLTDEKHLPLPLVQ 18

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Searched: 673684 seqs, 18443283 residues

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Total number of hits satisfying chosen parameters: 139996

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Published Applications AA:\*

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- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*
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- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*
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- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*
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- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	5	27.8	9	10	US-09-780-053-448
5	5	27.8	9	10	US-09-780-053-545
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7	5	27.8	9	15	US-10-084-813-917
8	5	27.8	9	15	US-10-084-813-918
9	5	27.8	10	10	US-09-780-053-497
10	5	27.8	10	10	US-09-780-053-596
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14	5	27.8	12	15	US-10-084-813-962
15	5	27.8	12	15	US-10-084-813-963

5	27.8	12	15	US-10-084-813-964	Sequence 964, App
5	27.8	15	9	US-09-829-855-223	Sequence 223, App
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5	27.8	15	12	US-10-161-791-407	Sequence 407, App
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5	27.8	15	15	US-10-084-813-521	Sequence 521, App
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5	27.8	15	15	US-10-084-813-1209	Sequence 1209, Ap
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5	27.8	15	15	US-10-084-813-1224	Sequence 1224, Ap
5	27.8	16	9	US-09-829-855-227	Sequence 227, App
5	27.8	17	12	US-10-299-003-14	Sequence 14, Appl
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5	27.8	18	15	US-10-084-813-774	Sequence 774, App
5	27.8	19	9	US-09-829-855-225	Sequence 225, App
5	27.8	20	11	US-09-983-802-664	Sequence 664, App
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4	22.2	7	9	US-09-739-254-132	Sequence 132, App
4	22.2	7	9	US-09-904-615-132	Sequence 132, App
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4	22.2	8	9	US-09-358-423-23	Sequence 23, Appl
4	22.2	8	9	US-09-358-423-24	Sequence 24, Appl
4	22.2	8	12	US-10-224-125-32	Sequence 32, Appl
4	22.2	8	14	US-10-047-881-23	Sequence 23, Appl
4	22.2	8	14	US-10-047-881-24	Sequence 24, Appl
4	22.2	9	10	US-09-780-053-566	Sequence 566, App

89 4 22.2 9 10 US-09-894-018-312 Sequence 312, App  
90 4 22.2 9 10 US-09-821-831-68 Sequence 68, Appl  
91 4 22.2 9 10 US-09-519-048-84 Sequence 84, Appl  
92 4 22.2 9 10 US-09-919-048-126 Sequence 126, App  
93 4 22.2 9 10 US-09-919-048-170 Sequence 170, App  
94 4 22.2 9 10 US-09-017-743C-16 Sequence 16, Appl  
95 4 22.2 9 10 US-09-909-460-91 Sequence 91, Appl  
96 4 22.2 9 12 US-10-155-883B-53 Sequence 53, Appl  
97 4 22.2 9 12 US-09-793-451-122 Sequence 122, App  
98 4 22.2 9 12 US-09-793-451-131 Sequence 131, App  
99 4 22.2 9 12 US-09-793-451-142 Sequence 142, App  
100 4 22.2 9 12 US-09-793-451-236 Sequence 236, App

## ALIGNMENTS

RESULT 1  
US-10-281-652-23  
; Sequence 23, Application US/10281652  
; Publication No. US20030091606A1  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/10/281,652  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US/09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-10-281-652-23

Query Match 100.0%; Score 18; DB 15; Length 18;  
Best Local Similarity 100.0%; Pred. No. 8.3e-11;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLTDVEKHLPLPLVQ 18  
Db 1 SLTLTDVEKHLPLPLVQ 18

RESULT 2  
US-10-148-936-8  
; Sequence 8, Application US/10148936  
; Publication No. US20030113819A1  
; GENERAL INFORMATION:  
; APPLICANT: Horton, Jeffrey  
; APPLICANT: Smith, John  
; APPLICANT: Teear, Michelle  
; APPLICANT: Kendall, Jonathan  
; APPLICANT: Michael, Nigel  
; TITLE OF INVENTION: Reagent and Method for Delivery of Molecules into Cells  
; FILE REFERENCE: PA9963  
; CURRENT APPLICATION NUMBER: US/10/148,936  
; CURRENT FILING DATE: 2000-12-04  
; PRIOR APPLICATION NUMBER: PCT/GB00/04593  
; PRIOR FILING DATE: 2000-12-04  
; PRIOR APPLICATION NUMBER: GB 9928674.2  
; PRIOR FILING DATE: 1999-12-06  
; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic oligomer  
US-10-148-936-8

Query Match 33.3%; Score 6; DB 15; Length 14;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLPLV 17  
Db 5 LPLPLV 10

RESULT 3  
US-09-780-053-148  
; Sequence 148, Application US/09780053  
; Patent No. US20020102640A1  
; GENERAL INFORMATION:  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Mary Farris  
; APPLICANT: Elana Levin  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN  
; FILE REFERENCE: 129.5USU1  
; CURRENT APPLICATION NUMBER: US/09/780,053  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/181,261  
; PRIOR FILING DATE: 2000-02-09  
; NUMBER OF SEQ ID NOS: 716  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 148  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-09-780-053-148

Query Match 27.8%; Score 5; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLPL 16  
Db 2 LPLPL 6

RESULT 4  
US-09-780-053-448  
; Sequence 448, Application US/09780053  
; Patent No. US20020102640A1  
; GENERAL INFORMATION:  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Mary Farris  
; APPLICANT: Elana Levin  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN  
; FILE REFERENCE: 129.5USU1  
; CURRENT APPLICATION NUMBER: US/09/780,053  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/181,261  
; PRIOR FILING DATE: 2000-02-09

; NUMBER OF SEQ ID NOS: 716  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 448  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-09-780-053-448

Query Match 27.8%; Score 5; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LPLPL 16  
|  
|  
|  
|  
Db 5 LPLPL 9

RESULT 5  
US-09-780-053-545  
; Sequence 545, Application US/09780053  
; Patent No. US20020102640A1  
; GENERAL INFORMATION:  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Pia M. Challita-Bid  
; APPLICANT: Mary Faris  
; APPLICANT: Elana Levin  
; APPLICANT: Steve Chapell Mitchell  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN  
; FILE REFERENCE: 129.5USU1  
; CURRENT APPLICATION NUMBER: US/09/780,053  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR FILING DATE: 2000-02-09  
; PRIOR FILING DATE: 2000-02-09  
; NUMBER OF SEQ ID NOS: 716  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 545  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-09-780-053-545

Query Match 27.8%; Score 5; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LPLPL 16  
|  
|  
|  
|  
Db 5 LPLPL 9

RESULT 6  
US-10-084-813-916  
; Sequence 916, Application US/10084813  
; Publication No. US20030068615A1  
; GENERAL INFORMATION:  
; APPLICANT: SAXINGER, CARL  
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC  
; FILE REFERENCE: 215875  
; CURRENT APPLICATION NUMBER: US/10/084,813  
; CURRENT FILING DATE: 2002-02-27  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR FILING DATE: 1999-08-27  
; NUMBER OF SEQ ID NOS: 1242  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 916  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-084-813-916

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide  
US-10-084-813-916

Query Match 27.8%; Score 5; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5  
|  
|  
|  
|  
Db 5 SLTLT 9

RESULT 7  
US-10-084-813-917  
; Sequence 917, Application US/10084813  
; Publication No. US20030068615A1  
; GENERAL INFORMATION:  
; APPLICANT: SAXINGER, CARL  
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC  
; FILE REFERENCE: 215875  
; CURRENT APPLICATION NUMBER: US/10/084,813  
; CURRENT FILING DATE: 2002-02-27  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR FILING DATE: 1999-08-27  
; NUMBER OF SEQ ID NOS: 1242  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 917  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide  
US-10-084-813-917

Query Match 27.8%; Score 5; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5  
|  
|  
|  
|  
Db 4 SLTLT 8

RESULT 8  
US-10-084-813-918  
; Sequence 918, Application US/10084813  
; Publication No. US20030068615A1  
; GENERAL INFORMATION:  
; APPLICANT: SAXINGER, CARL  
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC  
; FILE REFERENCE: 215875  
; CURRENT APPLICATION NUMBER: US/10/084,813  
; CURRENT FILING DATE: 2002-02-27  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR FILING DATE: 1999-08-27  
; NUMBER OF SEQ ID NOS: 1242  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 918  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide  
US-10-084-813-918

Query Match 27.8%; Score 5; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTILT 5  
Db 3 SLTILT 7

RESULT 9  
US-09-780-053-497  
; Sequence 497, Application US/09780053  
; Patent No. US20020102840A1  
; GENERAL INFORMATION:  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Mary Faris  
; APPLICANT: Elana Levin  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN  
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER  
; FILE REFERENCE: 129.5USU1  
; CURRENT APPLICATION NUMBER: US/09/780,053  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/181,261  
; PRIOR FILING DATE: 2000-02-09  
; NUMBER OF SEQ ID NOS: 716  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 497  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-09-780-053-497

Query Match 27.8%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLPL 16  
Db 6 LPLPL 10

RESULT 10  
US-09-780-053-596  
; Sequence 596, Application US/09780053  
; Patent No. US20020102640A1  
; GENERAL INFORMATION:  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Mary Faris  
; APPLICANT: Elana Levin  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN  
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER  
; FILE REFERENCE: 129.5USU1  
; CURRENT APPLICATION NUMBER: US/09/780,053  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/181,261  
; PRIOR FILING DATE: 2000-02-09  
; NUMBER OF SEQ ID NOS: 716  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 596  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-09-780-053-596

Query Match 27.8%; Score 5; DB 10; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLPL 16  
Db 6 LPLPL 10

RESULT 11  
US-09-780-053-696  
; Sequence 696, Application US/09780053  
; Patent No. US20020102640A1  
; GENERAL INFORMATION:  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Mary Faris  
; APPLICANT: Elana Levin  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN  
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER  
; FILE REFERENCE: 129.5USU1  
; CURRENT APPLICATION NUMBER: US/09/780,053  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/181,261  
; PRIOR FILING DATE: 2000-02-09  
; NUMBER OF SEQ ID NOS: 716  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 696  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-09-780-053-696

Query Match 27.8%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLPL 16  
Db 6 LPLPL 10

RESULT 12  
US-10-286-457-346  
; Sequence 346, Application US/10286457  
; Publication No. US20030166004A1  
; GENERAL INFORMATION:  
; APPLICANT: JENO GYURIS et al.  
; TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY  
; FILE REFERENCE: GPCI-P01-178  
; CURRENT APPLICATION NUMBER: US/10/286,457  
; CURRENT FILING DATE: 2002-11-01  
; PRIOR APPLICATION NUMBER: 60/334822  
; PRIOR FILING DATE: 2001-11-01  
; NUMBER OF SEQ ID NOS: 684  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 346  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: artificial sequence isolated from random peptide libraries, b  
; OTHER INFORMATION: ability to selectively bind to endothelial cells  
US-10-286-457-346

Query Match 27.8%; Score 5; DB 12; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KLHLP 13  
Db 9 KLHLP 13

Db 6 KLHLP 10

## RESULT 13

US-10-084-813-537  
; Sequence 537, Application US/10084813  
; Publication No. US20030068615A1  
; GENERAL INFORMATION:

; APPLICANT: SAXINGER, CARL  
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GPI20 AND RELATED NUCLEIC  
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE  
; FILE REFERENCE: 215875  
; CURRENT APPLICATION NUMBER: US/10/084,813  
; PRIOR FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: PCT/US00/23505  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR APPLICATION NUMBER: US 60/151,270  
; PRIOR FILING DATE: 1999-08-27  
; NUMBER OF SEQ ID NOS: 1242  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 537  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide  
US-10-084-813-537

Query Match 27.8%; Score 5; DB 15; Length 12;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5

Db 6 SLTLT 10

## RESULT 14

US-10-084-813-962  
; Sequence 962, Application US/10084813  
; Publication No. US20030068615A1  
; GENERAL INFORMATION:

; APPLICANT: SAXINGER, CARL  
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GPI20 AND RELATED NUCLEIC  
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE  
; FILE REFERENCE: 215875  
; CURRENT APPLICATION NUMBER: US/10/084,813  
; PRIOR FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: PCT/US00/23505  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR APPLICATION NUMBER: US 60/151,270  
; PRIOR FILING DATE: 1999-08-27  
; NUMBER OF SEQ ID NOS: 1242  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 962  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide  
US-10-084-813-962

Query Match 27.8%; Score 5; DB 15; Length 12;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5

Db 8 SLTLT 12

## RESULT 15

US-10-084-813-963

; Sequence 963, Application US/10084813  
; Publication No. US20030068615A1  
; GENERAL INFORMATION:

; APPLICANT: SAXINGER, CARL  
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GPI20 AND RELATED NUCLEIC  
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE  
; FILE REFERENCE: 215875  
; CURRENT APPLICATION NUMBER: US/10/084,813  
; PRIOR FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: PCT/US00/23505  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR APPLICATION NUMBER: US 60/151,270  
; PRIOR FILING DATE: 1999-08-27  
; NUMBER OF SEQ ID NOS: 1242  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 963  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide  
US-10-084-813-963

Query Match 27.8%; Score 5; DB 15; Length 12;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5

Db 7 SLTLT 11

## RESULT 16

US-10-084-813-964  
; Sequence 964, Application US/10084813  
; Publication No. US20030068615A1  
; GENERAL INFORMATION:

; APPLICANT: SAXINGER, CARL  
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GPI20 AND RELATED NUCLEIC  
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE  
; FILE REFERENCE: 215875  
; CURRENT APPLICATION NUMBER: US/10/084,813  
; PRIOR FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: PCT/US00/23505  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR APPLICATION NUMBER: US 60/151,270  
; PRIOR FILING DATE: 1999-08-27  
; NUMBER OF SEQ ID NOS: 1242  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 964  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide  
US-10-084-813-964

Query Match 27.8%; Score 5; DB 15; Length 12;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5

Db 6 SLTLT 10

## RESULT 17

US-09-829-855-223  
; Sequence 223, Application US/09829855  
; Patent No. US20020065609A1  
; GENERAL INFORMATION:

; APPLICANT: Matthew, Ashby N.  
; TITLE OF INVENTION: Methods for the Survey and Genetic Analysis of Populations



; FILE REFERENCE: ASHBY-1  
; CURRENT APPLICATION NUMBER: US/09/829,855  
; CURRENT FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: US 60/196063  
; PRIOR FILING DATE: 2000-04-10  
; PRIOR APPLICATION NUMBER: US 60/196258  
; PRIOR FILING DATE: 2000-04-11  
; NUMBER OF SEQ ID NOS: 244  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 223  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Denitrobacter permanens  
US-09-829-855-223

Query Match 27.8%; Score 5; DB 9; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLPLV 17  
Db 4 PLPLV 8

RESULT 18  
US-10-161-791-385  
; Sequence 385, Application US/10161791  
; Publication No. US20030186863A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/161,791  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 990-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 385:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-10-161-791-385

Query Match 27.8%; Score 5; DB 12; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLPL 16  
Db 10 LPLPL 14

RESULT 19  
US-10-161-791-407  
; Sequence 407, Application US/10161791  
; Publication No. US20030186863A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/161,791  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 990-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 407:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-10-161-791-407

Query Match 27.8%; Score 5; DB 12; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLPL 16  
Db 3 LPLPL 7

RESULT 20  
US-10-084-813-29  
; Sequence 29, Application US/10084813  
; Publication No. US20030068615A1

```

; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR FILING DATE: 2000-08-25
; PRIOR FILING DATE: 1999-08-27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-29

Query Match          27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SLTLT 5
Db      8 SLTLT 12

RESULT 21
US-10-084-813-521
; Sequence 521, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR FILING DATE: 1999-08-27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 521
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-521

Query Match          27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SLTLT 5
Db      9 SLTLT 13

RESULT 22
US-10-084-813-522
; Sequence 522, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875

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; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 522
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-522

Query Match          27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SLTLT 5
Db      8 SLTLT 12

RESULT 23
US-10-084-813-523
; Sequence 523, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 523
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-523

Query Match          27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SLTLT 5
Db      7 SLTLT 11

RESULT 24
US-10-084-813-726
; Sequence 726, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270

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; PRIOR FILING DATE: 1999-08-27  
; NUMBER OF SEQ ID NOS: 1242  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 726  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide  
US-10-084-813-726

Query Match 27.8%; Score 5; DB 15; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLT 5  
|  
|  
|  
|  
|  
Db 11 SLTLT 15

RESULT 25  
US-10-084-813-727  
; Sequence 727, Application US/10084813  
; Publication No. US20030068615A1  
; GENERAL INFORMATION:  
; APPLICANT: SAXINGER, CARL  
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC  
; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE  
; FILE REFERENCE: 215875  
; CURRENT APPLICATION NUMBER: US/10/084,813  
; CURRENT FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: PCT/US00/23505  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR FILING DATE: 1999-08-27  
; NUMBER OF SEQ ID NOS: 1242  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 727  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide  
US-10-084-813-727

Query Match 27.8%; Score 5; DB 15; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLT 5  
|  
|  
|  
|  
|  
Db 10 SLTLT 14

RESULT 26  
US-10-084-813-728  
; Sequence 728, Application US/10084813  
; Publication No. US20030068615A1  
; GENERAL INFORMATION:  
; APPLICANT: SAXINGER, CARL  
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC  
; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE  
; FILE REFERENCE: 215875  
; CURRENT APPLICATION NUMBER: US/10/084,813  
; CURRENT FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: PCT/US00/23505  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR FILING DATE: 1999-08-27  
; NUMBER OF SEQ ID NOS: 1242  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 728  
; LENGTH: 15

; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide  
US-10-084-813-728

Query Match 27.8%; Score 5; DB 15; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLT 5  
|  
|  
|  
|  
|  
Db 9 SLTLT 13

RESULT 27  
US-10-084-813-729  
; Sequence 729, Application US/10084813  
; Publication No. US20030068615A1  
; GENERAL INFORMATION:  
; APPLICANT: SAXINGER, CARL  
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC  
; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE  
; FILE REFERENCE: 215875  
; CURRENT APPLICATION NUMBER: US/10/084,813  
; CURRENT FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: PCT/US00/23505  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR FILING DATE: 1999-08-27  
; NUMBER OF SEQ ID NOS: 1242  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 729  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide  
US-10-084-813-729

Query Match 27.8%; Score 5; DB 15; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLT 5  
|  
|  
|  
|  
|  
Db 8 SLTLT 12

RESULT 28  
US-10-084-813-730  
; Sequence 730, Application US/10084813  
; Publication No. US20030068615A1  
; GENERAL INFORMATION:  
; APPLICANT: SAXINGER, CARL  
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC  
; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE  
; FILE REFERENCE: 215875  
; CURRENT APPLICATION NUMBER: US/10/084,813  
; CURRENT FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: PCT/US00/23505  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR FILING DATE: 1999-08-27  
; NUMBER OF SEQ ID NOS: 1242  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 730  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide  
US-10-084-813-730

Query Match 27.8%; Score 5; DB 15; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLT 5  
| | | | |  
Db 7 SLTLT 11

RESULT 29  
US-10-084-813-1115  
; Sequence 1115, Application US/10084813  
; Publication No. US20030068615A1  
; GENERAL INFORMATION:  
; APPLICANT: SAXINGER, CARL  
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC  
; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE  
; FILE REFERENCE: 215875  
; CURRENT APPLICATION NUMBER: US/10/084,813  
; PRIOR FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: PCT/US00/23505  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR APPLICATION NUMBER: US 60/151,270  
; PRIOR FILING DATE: 1999-08-27  
; NUMBER OF SEQ ID NOS: 1242  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1115  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide  
US-10-084-813-1115

Query Match 27.8%; Score 5; DB 15; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLT 5  
| | | | |  
Db 8 SLTLT 12

RESULT 30  
US-10-084-813-1116  
; Sequence 1116, Application US/10084813  
; Publication No. US20030068615A1  
; GENERAL INFORMATION:  
; APPLICANT: SAXINGER, CARL  
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC  
; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE  
; FILE REFERENCE: 215875  
; CURRENT APPLICATION NUMBER: US/10/084,813  
; PRIOR FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: PCT/US00/23505  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR APPLICATION NUMBER: US 60/151,270  
; PRIOR FILING DATE: 1999-08-27  
; NUMBER OF SEQ ID NOS: 1242  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1116  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide  
US-10-084-813-1116

Query Match 27.8%; Score 5; DB 15; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLT 5  
| | | | |  
Db 8 SLTLT 12

RESULT 31  
US-10-084-813-1117  
; Sequence 1117, Application US/10084813  
; Publication No. US20030068615A1  
; GENERAL INFORMATION:  
; APPLICANT: SAXINGER, CARL  
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC  
; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE  
; FILE REFERENCE: 215875  
; CURRENT APPLICATION NUMBER: US/10/084,813  
; CURRENT FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: PCT/US00/23505  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR APPLICATION NUMBER: US 60/151,270  
; PRIOR FILING DATE: 1999-08-27  
; NUMBER OF SEQ ID NOS: 1242  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1117  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide  
US-10-084-813-1117

Query Match 27.8%; Score 5; DB 15; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLT 5  
| | | | |  
Db 8 SLTLT 12

RESULT 32  
US-10-084-813-1118  
; Sequence 1118, Application US/10084813  
; Publication No. US20030068615A1  
; GENERAL INFORMATION:  
; APPLICANT: SAXINGER, CARL  
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC  
; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE  
; FILE REFERENCE: 215875  
; CURRENT APPLICATION NUMBER: US/10/084,813  
; CURRENT FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: PCT/US00/23505  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR APPLICATION NUMBER: US 60/151,270  
; PRIOR FILING DATE: 1999-08-27  
; NUMBER OF SEQ ID NOS: 1242  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1118  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide  
US-10-084-813-1118

Query Match 27.8%; Score 5; DB 15; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLT 5  
| | | | |  
Db 8 SLTLT 12

```
RESULT 33
US-10-084-813-1119
; Sequence 1119, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1119
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1119
Query Match          27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTLT 5
Db      8 SLTLT 12

RESULT 34
US-10-084-813-1120
; Sequence 1120, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1120
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1120
Query Match          27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTLT 5
Db      8 SLTLT 12

RESULT 35
US-10-084-813-1121
; Sequence 1121, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1121
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1121
Query Match          27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTLT 5
Db      8 SLTLT 12
```

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; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1121
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1121
Query Match          27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTLT 5
Db      8 SLTLT 12

RESULT 36
US-10-084-813-1128
; Sequence 1128, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1128
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1128
Query Match          27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTLT 5
Db      8 SLTLT 12

RESULT 37
US-10-084-813-1129
; Sequence 1129, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1129
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1129
Query Match          27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTLT 5
Db      8 SLTLT 12
```

; CURRENT FILING DATE: 2002-02-27  
 ; PRIOR APPLICATION NUMBER: PCT/US00/23505  
 ; PRIOR FILING DATE: 2000-08-25  
 ; PRIOR APPLICATION NUMBER: US 60/151,270  
 ; PRIOR FILING DATE: 1999-08-27  
 ; NUMBER OF SEQ ID NOS: 1242  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 1129  
 ; LENGTH: 15  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: binding peptide  
 US-10-084-813-1129

Query Match 27.8%; Score 5; DB 15; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTTLT 5  
 Db 8 SLTTLT 12

## RESULT 38

US-10-084-813-1130  
 ; Sequence 1130, Application US/10084813  
 ; Publication No. US20030068615A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SAXINGER, CARL  
 ; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC  
 ; FILE REFERENCE: 215875  
 ; CURRENT APPLICATION NUMBER: US/10/084,813  
 ; PRIOR FILING DATE: 2002-02-27  
 ; PRIOR APPLICATION NUMBER: PCT/US00/23505  
 ; PRIOR FILING DATE: 2000-08-25  
 ; PRIOR APPLICATION NUMBER: US 60/151,270  
 ; PRIOR FILING DATE: 1999-08-27  
 ; NUMBER OF SEQ ID NOS: 1242  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 1130  
 ; LENGTH: 15  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: binding peptide  
 US-10-084-813-1130

Query Match 27.8%; Score 5; DB 15; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTTLT 5  
 Db 8 SLTTLT 12

## RESULT 39

US-10-084-813-1131  
 ; Sequence 1131, Application US/10084813  
 ; Publication No. US20030068615A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SAXINGER, CARL  
 ; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC  
 ; FILE REFERENCE: 215875  
 ; CURRENT APPLICATION NUMBER: US/10/084,813  
 ; PRIOR FILING DATE: 2002-02-27  
 ; PRIOR APPLICATION NUMBER: PCT/US00/23505  
 ; PRIOR FILING DATE: 2000-08-25  
 ; PRIOR APPLICATION NUMBER: US 60/151,270  
 ; PRIOR FILING DATE: 1999-08-27

; NUMBER OF SEQ ID NOS: 1242  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 1131  
 ; LENGTH: 15  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: binding peptide  
 US-10-084-813-1131

Query Match 27.8%; Score 5; DB 15; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTTLT 5  
 Db 8 SLTTLT 12

## RESULT 40

US-10-084-813-1132  
 ; Sequence 1132, Application US/10084813  
 ; Publication No. US20030068615A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SAXINGER, CARL  
 ; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC  
 ; FILE REFERENCE: 215875  
 ; CURRENT APPLICATION NUMBER: US/10/084,813  
 ; PRIOR FILING DATE: 2002-02-27  
 ; PRIOR APPLICATION NUMBER: PCT/US00/23505  
 ; PRIOR FILING DATE: 2000-08-25  
 ; PRIOR APPLICATION NUMBER: US 60/151,270  
 ; PRIOR FILING DATE: 1999-08-27  
 ; NUMBER OF SEQ ID NOS: 1242  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 1132  
 ; LENGTH: 15  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: binding peptide  
 US-10-084-813-1132

Query Match 27.8%; Score 5; DB 15; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTTLT 5  
 Db 8 SLTTLT 12

## RESULT 41

US-10-084-813-1133  
 ; Sequence 1133, Application US/10084813  
 ; Publication No. US20030068615A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SAXINGER, CARL  
 ; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC  
 ; FILE REFERENCE: 215875  
 ; CURRENT APPLICATION NUMBER: US/10/084,813  
 ; PRIOR FILING DATE: 2002-02-27  
 ; PRIOR APPLICATION NUMBER: PCT/US00/23505  
 ; PRIOR FILING DATE: 2000-08-25  
 ; PRIOR APPLICATION NUMBER: US 60/151,270  
 ; PRIOR FILING DATE: 1999-08-27  
 ; NUMBER OF SEQ ID NOS: 1242  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 1133  
 ; LENGTH: 15  
 ; TYPE: PRT

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1133

Query Match      27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTLT 5
        |||||
Db       8 SLTLT 12

RESULT 42
US-10-084-813-1134
; Sequence 1134, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1134
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1134

Query Match      27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTLT 5
        |||||
Db       8 SLTLT 12

RESULT 43
US-10-084-813-1135
; Sequence 1135, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1135
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1135

Query Match      27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTLT 5
        |||||
Db       8 SLTLT 12

RESULT 44
US-10-084-813-1136
; Sequence 1136, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1136
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1136

Query Match      27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTLT 5
        |||||
Db       8 SLTLT 12

RESULT 45
US-10-084-813-1137
; Sequence 1137, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1137
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1137

Query Match      27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTLT 5
        |||||
Db       8 SLTLT 12
```

```
Db      8 SLTLT 12
|||||
RESULT 46
US-10-084-813-1138
; Sequence 1138, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1138
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1138
Query Match      27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTLT 5
Db      8 SLTLT 12
|||||
RESULT 47
US-10-084-813-1139
; Sequence 1139, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1139
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1139
Query Match      27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTLT 5
Db      8 SLTLT 12
|||||
RESULT 48
US-10-084-813-1140
; Sequence 1140, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1140
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1140
Query Match      27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTLT 5
Db      8 SLTLT 12
|||||
RESULT 49
US-10-084-813-1146
; Sequence 1146, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1146
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1146
Query Match      27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTLT 5
Db      8 SLTLT 12
|||||
RESULT 50
US-10-084-813-1147
; Sequence 1147, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
```



; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC  
; FILE REFERENCE: 215875  
; CURRENT APPLICATION NUMBER: US/10/084,813  
; PRIOR FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: PCT/US00/23505  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR APPLICATION NUMBER: US 60/151,270  
; PRIOR FILING DATE: 1999-08-27  
; NUMBER OF SEQ ID NOS: 1242  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1147  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide  
US-10-084-813-1147

Query Match 27.8%; Score 5; DB 15; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5  
|  
|  
|  
|  
|  
Db 8 SLTLT 12

RESULT 51  
US-10-084-813-1148  
; Sequence 1148, Application US/10084813  
; Publication No. US20030068615A1  
; GENERAL INFORMATION:  
; APPLICANT: SAXINGER, CARL  
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC  
; FILE REFERENCE: 215875  
; CURRENT APPLICATION NUMBER: US/10/084,813  
; CURRENT FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: PCT/US00/23505  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR APPLICATION NUMBER: US 60/151,270  
; PRIOR FILING DATE: 1999-08-27  
; NUMBER OF SEQ ID NOS: 1242  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1148  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide  
US-10-084-813-1148

Query Match 27.8%; Score 5; DB 15; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5  
|  
|  
|  
|  
|  
Db 8 SLTLT 12

RESULT 52  
US-10-084-813-1207  
; Sequence 1207, Application US/10084813  
; Publication No. US20030068615A1  
; GENERAL INFORMATION:  
; APPLICANT: SAXINGER, CARL  
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC  
; FILE REFERENCE: 215875  
; CURRENT APPLICATION NUMBER: US/10/084,813  
; CURRENT FILING DATE: 2002-02-27

; PRIOR APPLICATION NUMBER: PCT/US00/23505  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR APPLICATION NUMBER: US 60/151,270  
; PRIOR FILING DATE: 1999-08-27  
; NUMBER OF SEQ ID NOS: 1242  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1207  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide  
US-10-084-813-1207

Query Match 27.8%; Score 5; DB 15; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5  
|  
|  
|  
|  
|  
Db 8 SLTLT 12

RESULT 53  
US-10-084-813-1208  
; Sequence 1208, Application US/10084813  
; Publication No. US20030068615A1  
; GENERAL INFORMATION:  
; APPLICANT: SAXINGER, CARL  
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC  
; FILE REFERENCE: 215875  
; CURRENT APPLICATION NUMBER: US/10/084,813  
; CURRENT FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: PCT/US00/23505  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR APPLICATION NUMBER: US 60/151,270  
; PRIOR FILING DATE: 1999-08-27  
; NUMBER OF SEQ ID NOS: 1242  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1208  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide  
US-10-084-813-1208

Query Match 27.8%; Score 5; DB 15; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLT 5  
|  
|  
|  
|  
|  
Db 8 SLTLT 12

RESULT 54  
US-10-084-813-1209  
; Sequence 1209, Application US/10084813  
; Publication No. US20030068615A1  
; GENERAL INFORMATION:  
; APPLICANT: SAXINGER, CARL  
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC  
; FILE REFERENCE: 215875  
; CURRENT APPLICATION NUMBER: US/10/084,813  
; CURRENT FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: PCT/US00/23505  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR APPLICATION NUMBER: US 60/151,270  
; PRIOR FILING DATE: 1999-08-27  
; NUMBER OF SEQ ID NOS: 1242

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1209
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1209

Query Match      27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTLT 5
Db      8 SLTLT 12

RESULT 55
US-10-084-813-1210
; Sequence 1210, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: US 60/151,270
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1210
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1210

Query Match      27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTLT 5
Db      8 SLTLT 12

RESULT 56
US-10-084-813-1216
; Sequence 1216, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: US 60/151,270
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1216
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1216

Query Match      27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTLT 5
Db      8 SLTLT 12

RESULT 57
US-10-084-813-1217
; Sequence 1217, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1217
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1217

Query Match      27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTLT 5
Db      8 SLTLT 12

RESULT 58
US-10-084-813-1218
; Sequence 1218, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1218
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1218

Query Match      27.8%; Score 5; DB 15; Length 15;
```

Best Local Similarity 100.0%; Pred. No. 1.7e+02; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTTLT 5  
|||||  
Db 8 SLTTLT 12

RESULT 59  
US-10-084-813-1219  
; Sequence 1219, Application US/10084813  
; Publication No. US20030068615A1  
; GENERAL INFORMATION:  
; APPLICANT: SAXINGER, CARL  
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC  
; FILE REFERENCE: 215875  
; CURRENT APPLICATION NUMBER: US/10/084,813  
; PRIOR FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: PCT/US00/23505  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR FILING DATE: 1999-08-27  
; NUMBER OF SEQ ID NOS: 1242  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1219  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide  
US-10-084-813-1219

Query Match 27.8%; Score 5; DB 15; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTTLT 5  
|||||  
Db 8 SLTTLT 12

RESULT 60  
US-10-084-813-1220  
; Sequence 1220, Application US/10084813  
; Publication No. US20030068615A1  
; GENERAL INFORMATION:  
; APPLICANT: SAXINGER, CARL  
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC  
; FILE REFERENCE: 215875  
; CURRENT APPLICATION NUMBER: US/10/084,813  
; PRIOR FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: PCT/US00/23505  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR FILING DATE: 1999-08-27  
; NUMBER OF SEQ ID NOS: 1242  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1220  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide  
US-10-084-813-1220

Query Match 27.8%; Score 5; DB 15; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTTLT 5  
|||||

Db 8 SLTTLT 12

RESULT 61  
US-10-084-813-1221  
; Sequence 1221, Application US/10084813  
; Publication No. US20030068615A1  
; GENERAL INFORMATION:  
; APPLICANT: SAXINGER, CARL  
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC  
; FILE REFERENCE: 215875  
; CURRENT APPLICATION NUMBER: US/10/084,813  
; PRIOR FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: PCT/US00/23505  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR FILING DATE: 1999-08-27  
; NUMBER OF SEQ ID NOS: 1242  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1221  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide  
US-10-084-813-1221

Query Match 27.8%; Score 5; DB 15; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTTLT 5  
|||||  
Db 8 SLTTLT 12

RESULT 62  
US-10-084-813-1222  
; Sequence 1222, Application US/10084813  
; Publication No. US20030068615A1  
; GENERAL INFORMATION:  
; APPLICANT: SAXINGER, CARL  
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC  
; FILE REFERENCE: 215875  
; CURRENT APPLICATION NUMBER: US/10/084,813  
; PRIOR FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: PCT/US00/23505  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR FILING DATE: 1999-08-27  
; NUMBER OF SEQ ID NOS: 1242  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1222  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide  
US-10-084-813-1222

Query Match 27.8%; Score 5; DB 15; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTTLT 5  
|||||  
Db 8 SLTTLT 12

RESULT 63  
US-10-084-813-1224

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; Sequence 1224, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1224
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1224

Query Match      27.8%; Score 5; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLT 5
Db 8 SLTLT 12

RESULT 64
US-09-829-855-227
; Sequence 227, Application US/09829855
; Patent No. US20020065609A1
; GENERAL INFORMATION:
; APPLICANT: Matthew, Ashby N.
; TITLE OF INVENTION: Methods for the Survey and Genetic Analysis of Populations
; FILE REFERENCE: ASHY-1
; CURRENT APPLICATION NUMBER: US/09/829,855
; CURRENT FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US 60/196063
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 60/196258
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 244
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 227
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Benzene mineralizing clone SB-1
US-09-829-855-227

Query Match      27.8%; Score 5; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLPLV 17
Db 4 PLPLV 8

RESULT 65
US-10-299-003-14
; Sequence 14, Application US/10299003
; Publication No. US2003013924A1
; GENERAL INFORMATION:
; APPLICANT: Steck, Peter
; APPLICANT: Pershouse, Mark A.
; APPLICANT: Jasser, Samar

```

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; APPLICANT: Yung, Alfred W.K.
; APPLICANT: Tavcigian, Sean V.
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
; FILE REFERENCE: 2318-385
; CURRENT APPLICATION NUMBER: US/10/299,003
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: U.S. 09/140,749
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: U.S. 08/791,115
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: U.S. 60/057,750
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: U.S. 60/083,563
; PRIOR FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-299-003-14

Query Match      27.8%; Score 5; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LHLPL 14
Db 3 LHLPL 7

RESULT 66
US-10-084-813-552
; Sequence 552, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 552
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-552

Query Match      27.8%; Score 5; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTLT 5
Db 12 SLTLT 16

RESULT 67
US-10-084-813-553
; Sequence 553, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 553
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-553

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; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 553
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-553

Query Match      27.8%; Score 5; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTLT 5
Db      11 SLTLT 15

RESULT 68
US-10-084-813-554
; Sequence 554, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 554
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-554

Query Match      27.8%; Score 5; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTLT 5
Db      10 SLTLT 14

RESULT 69
US-10-084-813-770
; Sequence 770, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 772
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; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 770
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-770

Query Match      27.8%; Score 5; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTLT 5
Db      14 SLTLT 18

RESULT 70
US-10-084-813-771
; Sequence 771, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 771
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-771

Query Match      27.8%; Score 5; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLTLT 5
Db      13 SLTLT 17

RESULT 71
US-10-084-813-772
; Sequence 772, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 772
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/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-772

Query Match      27.8%; Score 5; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTTLT 5
Db 12 SLTTLT 16

RESULT 72
US-10-084-813-773
/ Sequence 773, Application US/10084813
/ Publication No. US20030068615A1
/ GENERAL INFORMATION:
/ APPLICANT: SAXINGER, CARL
/ TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
/ FILE REFERENCE: 215875
/ CURRENT APPLICATION NUMBER: US/10/084,813
/ PRIOR FILING DATE: 2002-02-27
/ PRIOR APPLICATION NUMBER: PCT/US00/23505
/ PRIOR FILING DATE: 2000-08-25
/ PRIOR APPLICATION NUMBER: US 60/151,270
/ PRIOR FILING DATE: 1999-08-27
/ NUMBER OF SEQ ID NOS: 1242
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 773
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-773

Query Match      27.8%; Score 5; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLTTLT 5
Db 11 SLTTLT 15

RESULT 73
US-10-084-813-774
/ Sequence 774, Application US/10084813
/ Publication No. US20030068615A1
/ GENERAL INFORMATION:
/ APPLICANT: SAXINGER, CARL
/ TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
/ FILE REFERENCE: 215875
/ CURRENT APPLICATION NUMBER: US/10/084,813
/ PRIOR FILING DATE: 2002-02-27
/ PRIOR APPLICATION NUMBER: PCT/US00/23505
/ PRIOR FILING DATE: 2000-08-25
/ PRIOR APPLICATION NUMBER: US 60/151,270
/ PRIOR FILING DATE: 1999-08-27
/ NUMBER OF SEQ ID NOS: 1242
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 774
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: binding peptide
```

US-10-084-813-774

```
Query Match      27.8%; Score 5; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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QY 1 SLTTLT 5
Db 10 SLTTLT 14
```

RESULT 74

```
US-09-829-855-225
/ Sequence 225, Application US/09829855
/ Patent No. US20020065609A1
/ GENERAL INFORMATION:
/ APPLICANT: Matthew, Ashby N.
/ TITLE OF INVENTION: Methods for the Survey and Genetic Analysis of Populations
/ FILE REFERENCE: ASHEY-1
/ CURRENT APPLICATION NUMBER: US/09/829,855
/ CURRENT FILING DATE: 2001-04-10
/ PRIOR APPLICATION NUMBER: US 60/196063
/ PRIOR FILING DATE: 2000-04-10
/ PRIOR APPLICATION NUMBER: US 60/196258
/ PRIOR FILING DATE: 2000-04-11
/ NUMBER OF SEQ ID NOS: 244
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 225
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: Desulfobulbus sp. BG25
US-09-829-855-225
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Query Match      27.8%; Score 5; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 13 PLPLV 17
Db 4 PLPLV 8
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RESULT 75

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US-09-983-802-664
/ Sequence 664, Application US/09983802
/ Publication No. US20030022185A1
/ GENERAL INFORMATION:
/ APPLICANT: Fischer et al.
/ TITLE OF INVENTION: 123 Human Secreted Proteins
/ FILE REFERENCE: PZ010P1
/ CURRENT APPLICATION NUMBER: US/09/983,802
/ CURRENT FILING DATE: 2001-10-25
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/227,357
/ PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-08
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US98/13684
/ PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-07
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,926
/ PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,793
/ PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,925
/ PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,929
/ PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,803
/ PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,732
/ PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,931
/ PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,932
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; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,916
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,930
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,918
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,920
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,733
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,795
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,919
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,928
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,722
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,723
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,948
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,949
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,953
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,950
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,947
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,964
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/056,360
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,684
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,984
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,954
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,785
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,664
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,660
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,661
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 664
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-983-802-664

Query Match      27.8%; Score 5; DB 11; Length 20;
Best Local Similarity 100.0%; Pred.No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      12 LPLPL 16
Db      1 LPLPL 5

Search completed: November 25, 2003, 20:37:00
Job time : 28.8837 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:16:22 ; Search time 14.5465 Seconds  
(without alignments)  
52.356 Million cell updates/sec

Title: US-09-641-801-23  
Perfect score: 18  
Sequence: 1 SLRLTDEKHLPLPLVQ 18

Scoring table: OUIGO  
Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3  
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5A COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	4	US-09-641-803-23
2	5	27.8	15	3	US-08-602-999A-385
3	5	27.8	15	3	US-08-602-999A-407
4	5	27.8	15	4	US-09-500-124-385
5	5	27.8	15	4	US-09-500-124-407
6	5	27.8	17	4	US-09-140-749-14
7	5	27.8	20	4	US-09-227-357-664
8	4	22.2	5	3	US-09-202-832-6
9	4	22.2	6	1	US-08-212-433A-32
10	4	22.2	6	3	US-08-716-256-32
11	4	22.2	6	4	US-09-211-877-1
12	4	22.2	6	5	PCT-US95-03239-32
13	4	22.2	7	1	US-08-081-539-113
14	4	22.2	7	1	US-08-466-647-113
15	4	22.2	7	4	US-09-904-615-132
16	4	22.2	8	1	US-08-320-373-78
17	4	22.2	9	1	US-08-454-207A-44
18	4	22.2	9	1	US-08-787-547-91
19	4	22.2	9	2	US-08-630-645-9
20	4	22.2	9	3	US-09-510-738A-84
21	4	22.2	9	3	US-09-510-738A-126
22	4	22.2	9	3	US-09-510-738A-170
23	4	22.2	9	4	US-08-197-484-38
24	4	22.2	9	4	US-08-766-596A-9
25	4	22.2	9	4	US-09-861-966-84
26	4	22.2	9	4	US-09-861-966-126
27	4	22.2	9	4	US-09-861-966-170



## ALIGNMENTS

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RESULT 1
US-09-641-803-23
; Sequence 23, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-641-803-23
Query Match 100.0%; Score 18; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.6e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTLTDVEKHLPLPLVQ 18
Db 1 SLTLTDVEKHLPLPLVQ 18

RESULT 2
US-08-602-999A-385
; Sequence 385, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; ADDRESS: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
```

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; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 385:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-385
Query Match 27.8%; Score 5; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LPLPL 16
Db 10 LPLPL 14

RESULT 3
US-08-602-999A-407
; Sequence 407, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 407:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-407
Query Match 27.8%; Score 5; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 12 LPLPL 16  
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Db 3 LPLPL 7

RESULT 4  
US-09-500-124-385  
; Sequence 385, Application US/09500124  
; Patent No. 6432920  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; APPLICATION DATA:  
; APPLICATION NUMBER: US/09/500,124  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 385:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-09-500-124-385

Query Match 27.8%; Score 5; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 64;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLPL 16  
| | | | |  
Db 10 LPLPL 14

RESULT 5  
US-09-500-124-407  
; Sequence 407, Application US/09500124  
; Patent No. 6432920  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.

; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; APPLICATION DATA:  
; APPLICATION NUMBER: US/09/500,124  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 407:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-09-500-124-407

Query Match 27.8%; Score 5; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 64;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LPLPL 16  
| | | | |  
Db 3 LPLPL 7

RESULT 6  
US-09-140-749-14  
; Sequence 14, Application US/09140749  
; Patent No. 6482795  
; GENERAL INFORMATION:  
; APPLICANT: Steck, Peter  
; APPLICANT: Pershouse, Mark A.  
; APPLICANT: Jasser, Samar  
; APPLICANT: Yung, Alfred W.K.  
; APPLICANT: Tavtighian, Sean V.  
; TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3  
; FILE REFERENCE: 2318-205  
; CURRENT APPLICATION NUMBER: US/09/140,749  
; CURRENT FILING DATE: 1998-08-26  
; EARLIER APPLICATION NUMBER: U.S. 08/791,115  
; EARLIER FILING DATE: 1997-01-30  
; EARLIER APPLICATION NUMBER: U.S. 60/057,750  
; EARLIER FILING DATE: 1997-08-26  
; EARLIER APPLICATION NUMBER: U.S. 60/083,563  
; EARLIER FILING DATE: 1998-04-30  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: Patentin Ver. 2.0



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RESULT 9
US-08-212-433A-32
; Sequence 32, Application US/08212433A
; Patent No. 5538897
; GENERAL INFORMATION:
; APPLICANT: Yates, III, John R.
; APPLICANT: Eng, James K.
; TITLE OF INVENTION: USE OF MASS SPECTROMETRY FRAGMENTATION
; TITLE OF INVENTION: PATTERNS OF PEPTIDES TO IDENTIFY AMINO ACID SEQUENCES IN
; TITLE OF INVENTION: DATABASES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart St. Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/212,433A
; FILING DATE: 14-MAR-1994
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Hughes, Richard L.
; REGISTRATION NUMBER: 31,264
; REFERENCE/DOCKET NUMBER: 16336-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-212-433A-32

Query Match 22.2%; Score 4; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PLPL 16
Db 3 PLPL 6

RESULT 10
US-08-716-256-32
; Sequence 32, Application US/08716256
; Patent No. 6017693
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: USE OF MASS SPECTROMETRY FRAGMENTATION
; TITLE OF INVENTION: PATTERNS TO IDENTIFY NUCLEOTIDE, AMINO ACID OR
; TITLE OF INVENTION: CARBOHYDRATE SEQUENCES IN DATABASES OR TO IDENTIFY
; TITLE OF INVENTION: ORGANISMS
; NUMBER OF SEQUENCES: 46
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/716,256
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: PCT/US95/03239
; FILING DATE: 14-MAR-1995
; APPLICATION NUMBER: US 08/212,433
; FILING DATE: 14-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 16336-2PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-716-256-32

Query Match 22.2%; Score 4; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PLPL 16
Db 3 PLPL 6

RESULT 11
US-09-211-877-1
; Sequence 1, Application US/09211877
; Patent No. 8458766
; GENERAL INFORMATION:
; APPLICANT: Fenical, William
; APPLICANT: Jensen, Paul R.
; APPLICANT: Rowley, David C.
; TITLE OF INVENTION: Halovir, An Antiviral Marine Natural Product, and
; FILE REFERENCE: P-UD 3148
; CURRENT APPLICATION NUMBER: US/09/211,877
; CURRENT FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Scytalidium CNL240
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Aib;
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: leucinol
US-09-211-877-1

Query Match 22.2%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 PLVQ 18
Db 2 PLVQ 5

RESULT 12
PCT-US95-03239-32
; Sequence 32, Application PC/TUS9503239
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: USE OF MASS SPECTROMETRY FRAGMENTATION
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;
; TITLE OF INVENTION: PATTERNS TO IDENTIFY NUCLEOTIDE, AMINO ACID OR
; TITLE OF INVENTION: CARBOHYDRATE SEQUENCES IN DATABASES OR TO IDENTIFY
; TITLE OF INVENTION: ORGANISMS
; NUMBER OF SEQUENCES: 46
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03239
; FILING DATE: 14-MAR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,433
; FILING DATE: 14-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 16336-2PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US95-03239-32

Query Match 22.2%; Score 4; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLPL 16
Db 3 PLPL 6

RESULT 13
US-08-081-539-113
; Sequence 113, Application US/08081539
; Patent No. 5501962
; GENERAL INFORMATION:
; APPLICANT: Braford-Goldberg, Sarah R.
; APPLICANT: Easton, Alan M.
; APPLICANT: Klein, Barbara K.
; APPLICANT: McKearn, John P.
; APPLICANT: Olins, Peter O.
; TITLE OF INVENTION: Interleukin-3 (IL-3) Human/Murine
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mary Jo Kanady, G. D. Searle & Co., Corporate
; ADDRESSEE: Patent Dept.
; STREET: P. O. Box 5110
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/081,539
; FILING DATE: 19930621
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kanady, Mary J.
```

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;
; REGISTRATION NUMBER: 28623
; REFERENCE/DOCKET NUMBER: 2724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (708)470-6501
; TELEFAX: (708)470-6881
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-081-539-113

Query Match 22.2%; Score 4; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLPL 16
Db 3 PLPL 6

RESULT 14
US-08-466-647-113
; Sequence 113, Application US/08466647
; Patent No. 5543141
; GENERAL INFORMATION:
; APPLICANT: Braford-Goldberg, Sarah R.
; APPLICANT: Easton, Alan M.
; APPLICANT: Klein, Barbara K.
; APPLICANT: McKearn, John P.
; APPLICANT: Olins, Peter O.
; TITLE OF INVENTION: Interleukin-3 (IL-3) Human/Murine
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mary Jo Kanady, G. D. Searle & Co., Corporate
; ADDRESSEE: Patent Dept.
; STREET: P. O. Box 5110
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,647
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/081,539
; FILING DATE: 21-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kanady, Mary J.
; REGISTRATION NUMBER: 28623
; REFERENCE/DOCKET NUMBER: 2724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (708)470-6501
; TELEFAX: (708)470-6881
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-466-647-113

Query Match 22.2%; Score 4; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 13 PLPL 16  
||||  
Db 3 PLPL 6

RESULT 15

US-09-904-615-132  
; Sequence 132: Application US/09904615  
; Patent No. 6566325  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 49 Human Secreted Proteins  
; FILE REFERENCE: P2032P1  
; CURRENT APPLICATION NUMBER: US/09/904,615  
; CURRENT FILING DATE: 2001-07-16  
; PRIOR APPLICATION NUMBER: 09/511,554  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 60/097,917  
; PRIOR FILING DATE: 1998-08-25  
; PRIOR APPLICATION NUMBER: 60/098,634  
; PRIOR FILING DATE: 1998-08-31  
; NUMBER OF SEQ ID NOS: 170  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 132  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-904-615-132

Query Match 22.2%; Score 4; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LTLT 5  
||||  
Db 3 LTLT 6

RESULT 16

US-08-320-373-78  
; Sequence 78, Application US/08320373  
; Patent No. 5559025  
; GENERAL INFORMATION:  
; APPLICANT: Ahorn, Horst  
; APPLICANT: Maurer-Poggy, Ingrid  
; APPLICANT: Sommergruber, Wolfgang  
; APPLICANT: Zophel, Andreas  
; APPLICANT: Blaas, Dieter  
; APPLICANT: Kuchler, Ernst  
; APPLICANT: Liebig, Hans-Dieter  
; APPLICANT: Skern, Timothy  
; TITLE OF INVENTION: Expression of Mature Proteinase 2A, the  
; TITLE OF INVENTION: Partial Purification Thereof and Preparation of Substrates  
; TITLE OF INVENTION: Having an Inhibitory Effect  
; NUMBER OF SEQUENCES: 91  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1225 Connecticut Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/320,373  
; FILING DATE: 11-OCT-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/971,619  
; FILING DATE: 06-NOV-1992  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 466-0800  
; TELEFAX: (202) 833-8716  
; TELEX: 248636 SSK  
; INFORMATION FOR SEQ ID NO: 78:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-320-373-78

Query Match 22.2%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 LPLV 17  
||||  
Db 4 LPLV 7

RESULT 17

US-08-454-207A-44  
; Sequence 44, Application US/08454207A  
; Patent No. 5710123  
; GENERAL INFORMATION:  
; APPLICANT: Heavner, George A.  
; APPLICANT: Kruszynski, Marian  
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF SELECTIN BINDING  
; NUMBER OF SEQUENCES: 70  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5710123ris LLP  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: U.S.A.  
; ZIP: 19103

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPerfect 6.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/454,207A  
; FILING DATE: 09-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/12110  
; FILING DATE: 13-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/997,771  
; FILING DATE: 18-DEC-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dianne B. Elderkin  
; REGISTRATION NUMBER: 28,598  
; REFERENCE/DOCKET NUMBER: CCOR-0183  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-568-3100  
; TELEFAX: 215-568-3439  
; INFORMATION FOR SEQ ID NO: 44:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-454-207A-44

Query Match 22.2%; Score 4; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 KLHL 12  
||||

Db 4 KLHL 7

RESULT 18

US-08-787-547-91

Sequence 91, Application US/08787547

Patent No. 5783567

GENERAL INFORMATION:

APPLICANT: Hedley, Mary Lynne

APPLICANT: Curley, Joanne M.

APPLICANT: Langer, Robert S.

TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY

TITLE OF INVENTION: OF NUCLEIC ACID

NUMBER OF SEQUENCES: 107

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: US

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows95

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/787,547

FILING DATE: 22-JAN-1997

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Fraser, Janis K.

REGISTRATION NUMBER: 34,819

REFERENCE/DOCKET NUMBER: 08191/003001

TELEPHONE: 617-542-5070

TELEPHONE: 617-542-5070

TELEFAX: 617-542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 91:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-787-547-91

Query Match 22.2%; Score 4; DB 1; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KLHL 12

Db 1 KLHL 4

RESULT 19

US-08-630-645-9

Sequence 9, Application US/08630645

Patent No. 5948763

GENERAL INFORMATION:

APPLICANT: SOTO-JARA, Claudio

APPLICANT: BAUMANN, Marc

APPLICANT: FRANGIONE, Blas

TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS

TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED

TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 400

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/630,645

FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/478,326

FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: YUN, Allen C.

REGISTRATION NUMBER: 37,971

REFERENCE/DOCKET NUMBER: SOTO-JARA=1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-630-645-9

Query Match 22.2%; Score 4; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLPL 16

Db 5 PLPL 8

RESULT 20

US-09-510-738A-84

Sequence 84, Application US/09510738A

Patent No. 6268165

GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of

TITLE OF INVENTION: Ovarian Cancer

FILE REFERENCE: D6223CIP-A

CURRENT APPLICATION NUMBER: US/09/510,738A

CURRENT FILING DATE: 2000-02-22

PRIOR APPLICATION NUMBER: 09/039,211

PRIOR FILING DATE: 03-14-1998

NUMBER OF SEQ ID NOS: 188

SEQ ID NO 84

LENGTH: 9

TYPE: PPT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: Residues 264-272 of the hepsin protein

US-09-510-738A-84

Query Match 22.2%; Score 4; DB 3; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Mismatches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLPL 16

Db 3 PLPL 6

RESULT 21

US-09-510-738A-126  
; Sequence 126, Application US/09510738A  
; Patent No. 6268165  
; GENERAL INFORMATION:

; APPLICANT: O'Brien, Timothy J.  
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of  
; TITLE OF INVENTION: Ovarian Cancer  
; FILE REFERENCE: D6223CIP-A

; CURRENT APPLICATION NUMBER: US/09/510,738A

; CURRENT FILING DATE: 2000-02-22

; PRIOR APPLICATION NUMBER: 09/039,211

; PRIOR FILING DATE: 03-14-1998

; NUMBER OF SEQ ID NOS: 188

; SEQ ID NO 126

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: Residues 265-273 of the hepsin protein

US-09-510-738A-126

Query Match 22.2%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLPL 16

Db ||||

2 PLPL 5

RESULT 22

US-09-510-738A-170  
; Sequence 170, Application US/09510738A  
; Patent No. 6268165  
; GENERAL INFORMATION:

; APPLICANT: O'Brien, Timothy J.

; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of

; TITLE OF INVENTION: Ovarian Cancer

; FILE REFERENCE: D6223CIP-A

; CURRENT APPLICATION NUMBER: US/09/510,738A

; CURRENT FILING DATE: 2000-02-22

; PRIOR APPLICATION NUMBER: 09/039,211

; PRIOR FILING DATE: 03-14-1998

; NUMBER OF SEQ ID NOS: 188

; SEQ ID NO 170

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: Residues 264-272 of the hepsin protein

US-09-510-738A-170

Query Match 22.2%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLPL 16

Db ||||

3 PLPL 6

RESULT 23

US-08-197-484-38  
; Sequence 38, Application US/08197484  
; Patent No. 641931  
; GENERAL INFORMATION:

; APPLICANT: VITIELLO, Maria A.

; APPLICANT: CHESTNUT, Robert W.

; APPLICANT: SETTE, Alessandro D.

; APPLICANT: CELIS, Esteban

; APPLICANT: GRAY, Howard

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING

; TITLE OF INVENTION: CTL IMMUNITY

; NUMBER OF SEQUENCES: 153  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Khourie and Crew

; STREET: Steuart Street Tower, One Market Plaza

; CITY: San Francisco

; STATE: California

; COUNTRY: US

; ZIP: 94105-1493

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/197,484

; FILING DATE: 16-FEB-1994

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/935,811

; FILING DATE: 26-AUG-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/874,491

; FILING DATE: 27-APR-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/827,682

; FILING DATE: 29-JAN-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/749,568

; FILING DATE: 26-AUG-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Parmelee, Steven W.

; REGISTRATION NUMBER: 31,990

; REFERENCE/DOCKET NUMBER: 14137-26-4

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 467-9600

; TELEFAX: (206) 623-6793

; INFORMATION FOR SEQ ID NO: 38:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids

; TYPE: amino acid

; STRANDEDNESS: unknown

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

US-08-197-484-38

Query Match 22.2%; Score 4; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KLHL 12

Db ||||

1 KLHL 4

Query Match 22.2%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLPL 16

Db ||||

3 PLPL 6

RESULT 24

US-08-766-596A-9

; Sequence 9, Application US/08766596A

; Patent No. 6462171

; GENERAL INFORMATION:

; APPLICANT: SOTO-JARA, Claudio

; APPLICANT: BAUMANN, Marc

; APPLICANT: FRANGIONE, Bias

; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL

; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES

; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIK

; TITLE OF INVENTION: DEPOSITS

; NUMBER OF SEQUENCES: 69

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NEIMARK

; STREET: 419 Seventh Street, N.W., Suite 400

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA



ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/766,596A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/630,645  
FILING DATE: 10-APR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/478,326  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: YUN, Allen C.  
REGISTRATION NUMBER: 37,971  
REFERENCE/DOCKET NUMBER: SOTO-JARA=1A  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-766-596A-9

Query Match 22.2%; Score 4; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLPL 16  
|||  
Db 5 PLPL 8

RESULT 25  
US-09-861-966-84  
; Sequence 84, Application US/09861966  
; Patent No. 6518028  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, Timothy J.  
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of  
; FILE REFERENCE: D6223CIP-A/Div  
; CURRENT APPLICATION NUMBER: US/09/861,966  
; CURRENT FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 09/510,738  
; PRIOR FILING DATE: 2000-02-22  
; NUMBER OF SEQ ID NOS: 188  
; SEQ ID NO 84  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Residues 264-272 of the hepsin protein  
US-09-861-966-84

Query Match 22.2%; Score 4; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLPL 16  
|||  
Db 3 PLPL 6

RESULT 26

US-09-861-966-126  
; Sequence 126, Application US/09861966  
; Patent No. 6518028  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, Timothy J.  
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of  
; FILE REFERENCE: D6223CIP-A/Div  
; CURRENT APPLICATION NUMBER: US/09/861,966  
; CURRENT FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 09/510,738  
; PRIOR FILING DATE: 2000-02-22  
; NUMBER OF SEQ ID NOS: 188  
; SEQ ID NO 126  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Residues 265-273 of the hepsin protein  
US-09-861-966-126

Query Match 22.2%; Score 4; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLPL 16  
|||  
Db 2 PLPL 5

RESULT 27  
US-09-861-966-170  
; Sequence 170, Application US/09861966  
; Patent No. 6518028  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, Timothy J.  
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of  
; FILE REFERENCE: D6223CIP-A/Div  
; CURRENT APPLICATION NUMBER: US/09/861,966  
; CURRENT FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 09/510,738  
; PRIOR FILING DATE: 2000-02-22  
; NUMBER OF SEQ ID NOS: 188  
; SEQ ID NO 170  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Residues 264-272 of the hepsin protein  
US-09-861-966-170

Query Match 22.2%; Score 4; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLPL 16  
|||  
Db 3 PLPL 6

RESULT 28  
US-09-311-784A-174  
; Sequence 174, Application US/09311784A  
; Patent No. 6534482  
; GENERAL INFORMATION:  
; APPLICANT: Fikes, John D.  
; APPLICANT: Hermanson, Gary G.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Ishioka, Glenn Y.  
; APPLICANT: Livingston, Brian  
; APPLICANT: Chesnut, Robert W.  
; APPLICANT: Epimmune Inc.

```

; TITLE OF INVENTION: Expression Vectors for Stimulating an
; TITLE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022-01
; CURRENT APPLICATION NUMBER: US/09/311,784A
; CURRENT FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 174
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HBV pol 489 (peptide 927.46)
US-09-311-784A-174

Query Match      22.2%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 KLHL 12
      ||||
Db      1 KLHL 4

RESULT 29
US-09-369-247-157
; Sequence 157, Application US/09369247
; Patent No. 6569992
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 44 Human Secreted Proteins
; FILE REFERENCE: P2024p1
; CURRENT APPLICATION NUMBER: US/09/369,247
; CURRENT FILING DATE: 1999-08-05
; EARLIER APPLICATION NUMBER: 60/074,118
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,157
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,137
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,341
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,141
; EARLIER FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 157
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-369-247-157

Query Match      22.2%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 EKLH 11
      ||||
Db      3 EKLH 6

RESULT 30
PCT-US95-02121-38
; Sequence 38, Application PC/TUS9502121
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02121
; FILING DATE: 16-FEB-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/197,484
; FILING DATE: 16-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
PCT-US95-02121-38

Query Match      22.2%; Score 4; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 KLHL 12
      ||||
Db      1 KLHL 4

RESULT 31
PCT-US96-10220-9
; Sequence 9, Application PC/TUS9610220
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
; TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10220
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326

```

; FILING DATE: 06-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/630,645  
; FILING DATE: 10-APR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: SOTO-JARA-1 PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; PCT-US96-10220-9

Query Match 22.2%; Score 4; DB 5; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PLPL 16  
Db 5 PLPL 8

RESULT 32  
5223606-10  
; Patent No. 5223606  
; APPLICANT: BLAUDIN DE THE, HUGHES, MARCHIO, AGNES, TIOLLAIS,  
; PIERRE, DEJEAN, ANNE  
; TITLE OF INVENTION: STEROID/THYROID HORMONE RECEPTOR-RELATED  
; PROTEIN INAPPROPRIATELY EXPRESSED IN HUMAN HEPATOCELLULAR CARCINOMA  
; NUMBER OF SEQUENCES: 11  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/134,130  
; FILING DATE: 17-DEC-1987  
; PRIOR APPLICATION DATA:  
; SEQ ID NO: 10:  
; LENGTH: 9

Query Match 22.2%; Score 4; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PLVQ 18  
Db 6 PLVQ 9

RESULT 33  
US-08-159-339A-351  
; Sequence 351, Application US/08159339A  
; Patent No. 6037135  
; GENERAL INFORMATION:  
; APPLICANT: Kubo, Ralph T.  
; APPLICANT: Grey, Howard M.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Celis, Esben  
; TITLE OF INVENTION: HLA Binding peptides and Their  
; NUMBER OF SEQUENCES: 1254  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111-3834

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/159,339A  
; FILING DATE: 29-NOV-1993  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/926,666  
; FILING DATE: 07-AUG-1992  
; APPLICATION NUMBER: US 08/027,746  
; FILING DATE: 05-MAR-1993  
; APPLICATION NUMBER: US 08/103,396  
; FILING DATE: 06-AUG-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Ellen Lauver  
; REGISTRATION NUMBER: 32,762  
; REFERENCE/DOCKET NUMBER: 018623-005030US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 351:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-159-339A-351

Query Match 22.2%; Score 4; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KLHL 12  
Db 6 KLHL 9

RESULT 34  
US-08-159-339A-352  
; Sequence 352, Application US/08159339A  
; Patent No. 6037135  
; GENERAL INFORMATION:  
; APPLICANT: Kubo, Ralph T.  
; APPLICANT: Grey, Howard M.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Celis, Esben  
; TITLE OF INVENTION: HLA Binding peptides and Their  
; NUMBER OF SEQUENCES: 1254  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/159,339A  
; FILING DATE: 29-NOV-1993  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/926,666  
; FILING DATE: 07-AUG-1992

APPLICATION NUMBER: US 08/027,746  
FILING DATE: 05-MAR-1993  
APPLICATION NUMBER: US 08/103,396  
FILING DATE: 06-AUG-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen Lauver  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 018623-005030US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
TELEX:

INFORMATION FOR SEQ ID NO: 352:

SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

US-08-159-339A-352

Query Match 22.2%; Score 4; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 KLHL 12  
Db 6 KLHL 9

RESULT 35

US-08-159-339A-353  
Sequence 353, Application US/08159339A  
Patent No. 6037135

GENERAL INFORMATION:  
APPLICANT: Kubo, Ralph T.

APPLICANT: Grey, Howard M.

APPLICANT: Sette, Alessandro

APPLICANT: Celis, Esben

TITLE OF INVENTION: HLA Binding peptides and Their

USes

NUMBER OF SEQUENCES: 1254

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/159,339A

FILING DATE: 29-NOV-1993

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/926,666

FILING DATE: 07-AUG-1992

APPLICATION NUMBER: US 08/027,746

FILING DATE: 05-MAR-1993

APPLICATION NUMBER: US 08/103,396

FILING DATE: 06-AUG-1993

ATTORNEY/AGENT INFORMATION:

NAME: Weber, Ellen Lauver

REGISTRATION NUMBER: 32,762

REFERENCE/DOCKET NUMBER: 018623-005030US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

TELEX:

INFORMATION FOR SEQ ID NO: 353:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-159-339A-353

Query Match 22.2%; Score 4; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 KLHL 12  
Db 6 KLHL 9

RESULT 36

US-08-908-643C-17

Sequence 17, Application US/08908643C

Patent No. 6120995

GENERAL INFORMATION:

APPLICANT: Waldman, Scott A.

APPLICANT: Pearlman, Joshua M.

APPLICANT: Barber, Michael T.

APPLICANT: Schultz, Stephanie

APPLICANT: Parkinson, Scott J.

TITLE OF INVENTION: COMPOSITIONS THAT SPECIFICALLY BIND TO  
COLORECTAL CANCER CELLS AND METHODS OF  
USING THE SAME

NUMBER OF SEQUENCES: 85

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6120995rls LLP

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: U.S.A.

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch disk, 1.44 Mb

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/908,643C

FILING DATE: 07-Aug-1997

CLASSIFICATION: N/A

PRIOR APPLICATION DATA:

APPLICATION NUMBER: <Unknown>

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Mark Deluca

REGISTRATION NUMBER: 33,229

REFERENCE/DOCKET NUMBER: TUU-2209

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-568-3100

TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 17:

US-08-908-643C-17

Query Match 22.2%; Score 4; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LHLP 13  
Db 6 KLHL 9

```
Db          4 HLPL 7

RESULT 37
US-08-637-759B-220
; Sequence 220, Application US/08637759B
; Patent No. 5876931
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/637,759B
; FILING DATE: 03-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/02875
; FILING DATE: 11-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RPMS 101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8795
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 220:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-637-759B-220

Query Match          22.2%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          11 HLPL 14
Db          5 HLPL 8

RESULT 38
US-08-637-759B-220
; Sequence 220, Application US/08637759B
; Patent No. 6015669
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/201,945
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/637,759
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RPMS 101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8795
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 220:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-637-759B-220

Query Match          22.2%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          11 HLPL 14
Db          5 HLPL 8

RESULT 39
US-09-201-945-220
; Sequence 220, Application US/09201945
; Patent No. 6342215
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/201,945
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/637,759
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RPMS 101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8795
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 220:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-871-355A-220

Query Match          22.2%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          11 HLPL 14
Db          5 HLPL 8
```

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404) 873-8794  
TELEFAX: (404) 873-8795  
INFORMATION FOR SEQ ID NO: 220:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
US-09-201-945-220

Query Match 22.2%; Score 4; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 11 HLPL 14  
Db 5 HLPL 8

RESULT 40  
US-07-756-250-3  
Sequence 3, Application US/07756250  
Patent No. 5268275  
GENERAL INFORMATION:  
APPLICANT: Wu, Sheue-Mei  
APPLICANT: Stafford, Darrel W.  
TITLE OF INVENTION: Vitamin K-Dependent Carboxylase  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kenneth D. Sibley; Bell, Seltzer, Park and  
ADDRESSEE: Gibson  
STREET: Post Office Drawer 34009  
CITY: Charlotte  
STATE: No. 5268275th Carolina  
COUNTRY: U.S.A.  
ZIP: 28234

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/756.250  
FILING DATE: 19910909  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/697,427  
FILING DATE: 08-MAY-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Sibley, Kenneth D.  
REGISTRATION NUMBER: 31,665  
REFERENCE/DOCKET NUMBER: 5470-34  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-881-3140  
TELEFAX: 919-881-3175  
TELEX: 575102

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-756-250-3

Query Match 22.2%; Score 4; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 15 PLVQ 18

Db 7 PLVQ 10

RESULT 41  
US-08-178-554-1  
Sequence 1, Application US/08178554  
Patent No. 5446019  
GENERAL INFORMATION:  
APPLICANT: ELY, SUSAN  
APPLICANT: TIPPETT, JANET MARY  
TITLE OF INVENTION: BACTERIAL STRAIN  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN  
STREET: 1100 New York Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-3918

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/178,554  
FILING DATE: 06-JAN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9300124.6  
FILING DATE: 06-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 206082/SEE 37367/US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 861-3000  
TELEFAX: (202) 822-0944  
TELEX: 6714627 CUSH

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-178-554-1

Query Match 22.2%; Score 4; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLTL 4  
Db 3 SLTL 6

RESULT 42  
US-08-036-555B-164  
Sequence 164, Application US/08036555B  
Patent No. 5530109  
GENERAL INFORMATION:  
APPLICANT: Goodearl, Andrew; Stroobant, Paul;  
APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;  
APPLICANT: Chen, Maio Su; Hiles, Ian  
TITLE OF INVENTION: Glial Mitogenic Factors, Their  
TITLE OF INVENTION: Preparation and Use  
NUMBER OF SEQUENCES: 184  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York City  
STATE: New York

```

; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/036,555B
; FILING DATE: 24-MAR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APRIL-1992
; APPLICATION NUMBER: U.K. 91 07566.3
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsai, Christine H.
; REGISTRATION NUMBER: 34,266
; REFERENCE/DOCKET NUMBER: LUD 5250.4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: Xaa in position 1 is unknown.
US-08-036-555B-164

Query Match 22.2%; Score 4; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DVEK 9
Db 9 DVEK 12

RESULT 43
US-08-469-569-164
; Sequence 164, Application US/08469569
; Patent No. 5606032
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew; Stroobant, Paul;
; APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
; APPLICANT: Chen, Maio Su; Hiles, Ian
; TITLE OF INVENTION: Glial Mitogenic Factors, Their
; PREPARATION AND USE
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM

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; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,569
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APRIL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.K. 91 07566.3
; FILING DATE: 10-APRIL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsai, Christine H.
; REGISTRATION NUMBER: 34,266
; REFERENCE/DOCKET NUMBER: LUD 5250.4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: Xaa in position 1 is unknown.
US-08-469-569-164

Query Match 22.2%; Score 4; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DVEK 9
Db 9 DVEK 12

RESULT 44
US-08-249-322A-164
; Sequence 164, Application US/08249322A
; Patent No. 5716930
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew; Stroobant, Paul;
; APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
; APPLICANT: Chen, Maio Su; Hiles, Ian
; TITLE OF INVENTION: Glial Mitogenic Factors, Their
; PREPARATION AND USE
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:

```

```

; APPLICATION NUMBER: US/08/249,322A
; FILING DATE: 26-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APRIL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.K. 91 07566.3
; FILING DATE: 10-APRIL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teal, Christine H.
; REGISTRATION NUMBER: 34,266
; REFERENCE/DOCKET NUMBER: LUD 250.4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: Xaa in position 1 is unknown.
US-08-249-322A-164

```

```

Query Match          22.2%; Score 4; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      6 DVEK 9
Db      9 DVEK 12

```

```

RESULT 45
US-08-469-526A-164
; Sequence 164, Application US/08/469526A
; Patent No. 5792849
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew
; APPLICANT: Stroobant, Paul
; APPLICANT: Minghetti, Luisa
; APPLICANT: Waterfield, Michael
; APPLICANT: Marchionni, Mark
; APPLICANT: Chen, Maio Su
; APPLICANT: Hiles, Ian
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; TITLE OF INVENTION: PREPARATION AND USE
; NUMBER OF SEQUENCES: 187
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; SOFTWARE: WordPerfect
; OPERATING SYSTEM: DOS

```

```

; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,526A
; FILING DATE: 06 June 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 03-JUN-1992
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APRIL-1992
; APPLICATION NUMBER: U.K. 91 07566.3
; FILING DATE: 10-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Bieker-Brady, Kristina
; REGISTRATION NUMBER: 39,109
; REFERENCE/DOCKET NUMBER: 04585/00200A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: Xaa in position 1 is unknown.
US-08-469-526A-164

```

```

Query Match          22.2%; Score 4; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      6 DVEK 9
Db      9 DVEK 12

```

```

RESULT 46
US-08-734-591A-164
; Sequence 164, Application US/08734591A
; Patent No. 5854220
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew
; APPLICANT: Stroobant, Paul
; APPLICANT: Minghetti, Luisa
; APPLICANT: Waterfield, Michael
; APPLICANT: Hiles, Ian
; APPLICANT: Marchionni, Mark
; APPLICANT: Chen, Mario
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; TITLE OF INVENTION: PREPARATION AND USE
; NUMBER OF SEQUENCES: 187
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible Pentium
; OPERATING SYSTEM: Windows95
; SOFTWARE: WordPerfect (Version 7.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/734,591A

```



```

; FILING DATE: 22-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/470,335
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 03-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 91 07566.3
; FILING DATE: 10-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Bieker-Brady, Kristina
; REGISTRATION NUMBER: 39,109
; REFERENCE/DOCKET NUMBER: 04585/00200P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 428-0200
; TELEFAX: (617) 428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: Xaa in position 1 is unknown.
US-08-734-591A-164

```

```

Query Match 22.2%; Score 4; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 6 DVEK 9
Db 9 DVEK 12

```

```

RESULT 47
US-08-469-660-164
; Sequence 164, Application US/08469660
; Patent No. 5876973
; GENERAL INFORMATION:
; APPLICANT: Gwynne, David I.; Marchionni, Mark;
; APPLICANT: McBurney, Robert N.
; TITLE OF INVENTION: INHIBITORS OF CELL PROLIFERATION,
; TITLE OF INVENTION: THEIR PREPARATION AND USE
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; ZIP: 02111-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,660

```

```

; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/011,396
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/984,085
; FILING DATE: 01-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/951,747
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/927,337
; FILING DATE: 10-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 04585/017004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: 200154
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: Xaa in position 1 is unknown.
US-08-469-660-164

```

```

Query Match 22.2%; Score 4; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 6 DVEK 9
Db 9 DVEK 12

```

```

RESULT 48
US-09-371-710-41
; Sequence 41, Application US/09371710A
; Patent No. 6146868
; GENERAL INFORMATION:
; APPLICANT: Kozel, Thomas R.
; APPLICANT: Bloomer, Sherri L.
; APPLICANT: Savoy, Anne C.
; TITLE OF INVENTION: Glucuronoxylomannan (GXM)-O-Acetylhydrolase of
; TITLE OF INVENTION: Cryptococcus neoformans and Uses Thereof
; FILE REFERENCE: D6245
; CURRENT APPLICATION NUMBER: US/09/371,710A
; CURRENT FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 50
; SEQ ID NO 41
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: associated amino acid sequence of PCR primer 45-mer
US-09-371-710-41

```

```

Query Match 22.2%; Score 4; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 9 KLHL 12
Db 3 KLHL 6

```

```

RESULT 49
US-08-470-335-164

```

; Sequence 164, Application US/08470335F  
; Patent No. 6147190  
; GENERAL INFORMATION:  
; APPLICANT: GOODEARL, ANDREW  
; APPLICANT: STROOBART, PAUL  
; APPLICANT: MINGHETTI, LUISA  
; APPLICANT: WATERFIELD, MICHAEL  
; APPLICANT: MARCHIONNI, MARK  
; APPLICANT: CHEN, MARIO S.  
; APPLICANT: HILES, IAN  
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR  
; TITLE OF INVENTION: PREPARATION AND USE  
; FILE REFERENCE: 04585/00200B  
; CURRENT APPLICATION NUMBER: US/08/470.335F  
; CURRENT FILING DATE: 1995-06-06  
; EARLIER APPLICATION NUMBER: 08/036.555  
; EARLIER FILING DATE: 1993-03-24  
; NUMBER OF SEQ ID NOS: 252  
; SOFTWARE: Fast-SEQ for Windows Version 4.0  
; SEQ ID NO 164  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Bos taurus  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (1)...(1)  
; OTHER INFORMATION: Xaa in position 1 is Lys or Arg.  
US-08-470-335-164  
  
Query Match 22.2%; Score 4; DB 3; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;  
  
Qy 6 DVEK 9  
Db 9 DVEK 12  
  
RESULT 50  
US-08-602-999A-253  
; Sequence 253, Application US/08602999A  
; Patent No. 6184205  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602.999A  
; FILING DATE: 16-FEB-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 253:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-602-999A-253  
  
Query Match 22.2%; Score 4; DB 3; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;  
  
Qy 12 LPLP 15  
Db 6 LPLP 9  
  
RESULT 51  
US-08-735-021-164  
; Sequence 164, Application US/08735021B  
; Patent No. 6194377  
; GENERAL INFORMATION:  
; APPLICANT: GOODEARL, ANDREW  
; APPLICANT: STROOBART, PAUL  
; APPLICANT: MINGHETTI, LUISA  
; APPLICANT: WATERFIELD, MICHAEL  
; APPLICANT: MARCHIONNI, MARK  
; APPLICANT: CHEN, MARIO S.  
; APPLICANT: HILES, IAN  
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR  
; TITLE OF INVENTION: PREPARATION AND USE  
; FILE REFERENCE: 04585/00200L  
; CURRENT APPLICATION NUMBER: US/08/735.021B  
; CURRENT FILING DATE: 1996-10-22  
; EARLIER APPLICATION NUMBER: 08/472.065  
; EARLIER FILING DATE: 1995-06-06  
; EARLIER APPLICATION NUMBER: 08/036.555  
; EARLIER FILING DATE: 1993-03-24  
; EARLIER APPLICATION NUMBER: 07/965.173  
; EARLIER FILING DATE: 1992-10-23  
; EARLIER APPLICATION NUMBER: 07/940.389  
; EARLIER FILING DATE: 1992-09-03  
; EARLIER APPLICATION NUMBER: 07/907.138  
; EARLIER FILING DATE: 1992-06-30  
; EARLIER APPLICATION NUMBER: 07/863.703  
; EARLIER FILING DATE: 1992-04-03  
; NUMBER OF SEQ ID NOS: 192  
; SOFTWARE: Fast-SEQ for Windows Version 3.0  
; SEQ ID NO 164  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (1)...(1)  
; OTHER INFORMATION: Xaa in 1 is unknown.  
US-08-735-021-164  
  
Query Match 22.2%; Score 4; DB 3; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;  
  
Qy 6 DVEK 9  
Db 9 DVEK 12  
  
RESULT 52  
US-08-734-664A-164

; Sequence 164, Application US/08734664A  
; Patent No. 6204241  
; GENERAL INFORMATION:  
; APPLICANT: Goodearl, Andrew  
; APPLICANT: Stroobant, Paul  
; APPLICANT: Minghetti, Luisa  
; APPLICANT: Waterfield, Michael  
; APPLICANT: Marchionni, Mark  
; APPLICANT: Chen, Mario  
; APPLICANT: Hiles, Ian  
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR  
; TITLE OF INVENTION: PREPARATION AND USE  
; NUMBER OF SEQUENCES: 187  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Clark & Elbing LLP  
; STREET: 176 Federal Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM Compatible Pentium  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/734,664A  
; FILING DATE: 22-OCT-1996  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/249,322  
; FILING DATE: 26-MAY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/036,555  
; FILING DATE: 24-MAR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/965,173  
; FILING DATE: 23-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/940,389  
; FILING DATE: 03-SEP-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/907,138  
; FILING DATE: 30-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/863,703  
; FILING DATE: 03-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: UK 91 07566.3  
; FILING DATE: 10-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bieker-Brady, Kristina  
; REGISTRATION NUMBER: 39,109  
; REFERENCE/DOCKET NUMBER: 04585/00200J  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 428-0200  
; TELEFAX: (617) 428-7045  
; TELE: \_\_\_\_\_  
; INFORMATION FOR SEQ ID NO: 164:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; FEATURE: \_\_\_\_\_  
; OTHER INFORMATION: Xaa in position 1 is unknown.  
US-08-734-664A-164  
Query Match 22.2%; Score 4; DB 3; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;  
QY 6 DVEK 9

Db 9 DVEK 12  
RESULT 53  
US-08-470-339-164  
; Sequence 164, Application US/08470339C  
; Patent No. 6232286  
; GENERAL INFORMATION:  
; APPLICANT: GOODEARL, ANDREW  
; APPLICANT: STROOBANT, PAUL  
; APPLICANT: MINGHETTI, LUISA  
; APPLICANT: WATERFIELD, MICHAEL  
; APPLICANT: MARCHIONNI, MARK  
; APPLICANT: CHEN, MARIO S.  
; APPLICANT: HILES, IAN  
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR  
; TITLE OF INVENTION: PREPARATION AND USE  
; FILE REFERENCE: 04585/002008  
; CURRENT APPLICATION NUMBER: US/08/470,339C  
; CURRENT FILING DATE: 1995-06-06  
; EARLIER APPLICATION NUMBER: 08/036,555  
; EARLIER FILING DATE: 1993-03-24  
; EARLIER APPLICATION NUMBER: 07/940,389  
; EARLIER FILING DATE: 1992-09-03  
; EARLIER APPLICATION NUMBER: 07/907,138  
; EARLIER FILING DATE: 1992-06-30  
; EARLIER APPLICATION NUMBER: 07/863,703  
; EARLIER FILING DATE: 1992-04-03  
; EARLIER APPLICATION NUMBER: 91 07566.3 GB  
; EARLIER FILING DATE: 1999-04-10  
; NUMBER OF SEQ ID NOS: 226  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 164  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Bos taurus  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (1)...(1)  
; OTHER INFORMATION: Xaa in position 1 is Lys or Arg.  
US-08-470-339-164  
Query Match 22.2%; Score 4; DB 3; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;  
QY 6 DVEK 9  
Db 9 DVEK 12  
RESULT 54  
US-09-648-386-41  
; Sequence 41, Application US/09648386  
; Patent No. 6284508  
; GENERAL INFORMATION:  
; APPLICANT: Kozel, Thomas R.  
; APPLICANT: Bloomer, Sherri L.  
; APPLICANT: SAVOY, Anne C.  
; TITLE OF INVENTION: Glucuronoxylomannan (GXM)-O-Acetylhydrolase of  
; TITLE OF INVENTION: Cryptococcus neoformans and Uses Thereof  
; FILE REFERENCE: D6245D  
; CURRENT APPLICATION NUMBER: US/09/648,386  
; CURRENT FILING DATE: 2000-08-25  
; PRIOR APPLICATION NUMBER: US 09/371,710  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 50  
; SEQ ID NO 41  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE: \_\_\_\_\_

OTHER INFORMATION: associated amino acid sequence of PCR primer 45-mer  
US-09-648-386-41

Query Match 22.2%; Score 4; DB 3; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 KLHL 12  
Db 3 KLHL 6

## RESULT 55

US-09-500-124-253  
Sequence 253, Application US/09500124  
Patent No. 6432920  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
TITLE OF INVENTION: ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/500.124  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/602,999

FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Mirock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 253:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-09-500-124-253

Query Match 22.2%; Score 4; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LPLP 15  
Db 6 LPLP 9

## RESULT 56

US-08-467-602-164

Sequence 164, Application US/08467602C  
Patent No. 644642  
GENERAL INFORMATION:  
APPLICANT: Sklar, Robert  
APPLICANT: Marchionni, Mark  
APPLICANT: Gwynne, David I.  
TITLE OF INVENTION: METHODS FOR TREATING MUSCLE DISEASES AND  
TITLE OF INVENTION: DISORDERS  
FILE REFERENCE: 04585/028003  
CURRENT APPLICATION NUMBER: US/08/467,602C  
CURRENT FILING DATE: 1995-06-06  
EARLIER APPLICATION NUMBER: 08/209,204  
EARLIER FILING DATE: 1994-03-08  
EARLIER APPLICATION NUMBER: 08/059,022  
EARLIER FILING DATE: 1993-05-06  
NUMBER OF SEQ ID NOS: 420  
SOFTWARE: Fast-SEQ for Windows Version 4.0  
SEQ ID NO 164  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Bos taurus  
FEATURE:  
NAME/KEY: VARIANT  
LOCATION: (1)...(1)  
OTHER INFORMATION: Xaa in position 1 is Lys or Arg.  
US-08-467-602-164

Query Match 22.2%; Score 4; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DVEK 9  
Db 9 DVEK 12

## RESULT 57

PCT-US94-05083C-160  
Sequence 160, Application PC/TUS9405083C  
GENERAL INFORMATION:  
APPLICANT: Robert Sklar, Mark Marchionni,  
APPLICANT: David I. Gwynne  
TITLE OF INVENTION: METHODS FOR ALTERING  
TITLE OF INVENTION: MUSCLE CONDITION  
NUMBER OF SEQUENCES: 185  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360  
MEDIUM TYPE: kb storage  
COMPUTER: IBM  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/05083C  
FILING DATE: 06-MAY-94  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/209,204  
FILING DATE: 08-MAR-94  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/059,022  
FILING DATE: 06-May-93  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 04585/028W01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070

; TELEFAX: (617) 542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 160:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; FEATURE:  
; OTHER INFORMATION: Xaa in position 1 is  
; OTHER INFORMATION: unknown.  
PCT-US94-05083C-160

Query Match 22.2%; Score 4; DB 5; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DVEK 9  
|||  
Db 9 DVEK 12

RESULT 58  
PCT-US95-06846A-164

; Sequence 164, Application PC/TUS9506846A  
; GENERAL INFORMATION:  
; APPLICANT: Goodearl, Andrew David; Stroobant, Paul;  
; APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;  
; APPLICANT: Chen, Mao Su; Hiles, Ian  
; TITLE OF INVENTION: Glial Mitogenic Factors, Their  
; TITLE OF INVENTION: Preparation and Use  
; NUMBER OF SEQUENCES: 178  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: Felife & Lynch  
; STREET: 805 Third Avenue  
; CITY: New York City  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10022

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

COMPUTER: IBM  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/06846A  
FILING DATE: 25-MAY-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/249,322  
FILING DATE: 26-MAY-1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/036,555  
FILING DATE: 24-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/965,173  
FILING DATE: 23-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/940,389  
FILING DATE: 03-SEP-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/907,138  
FILING DATE: 30-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/863,703  
FILING DATE: 03-APRIL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.K. 91 07566.3  
FILING DATE: 10-APRIL-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, Norman D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LUD 5250.5

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 688-9200  
; TELEFAX: (212) 838-3884  
; INFORMATION FOR SEQ ID NO: 164:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; FEATURE:  
; OTHER INFORMATION: Xaa in position 1 is unknown.  
PCT-US95-06846A-164

Query Match 22.2%; Score 4; DB 5; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DVEK 9  
|||  
Db 9 DVEK 12

RESULT 59

US-08-291-601-3  
; Sequence 3, Application US/08291601  
; Patent No. 5679527  
; GENERAL INFORMATION:  
; APPLICANT: Humphreys, Robert E.  
; TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE STRUCTURE  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: Kevin M. Farrell, P.C.  
; STREET: P.O. Box 999  
; CITY: York Harbor  
; STATE: Maine  
; COUNTRY: US  
; ZIP: 03911  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/291,601  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Farrell, Kevin M.  
REGISTRATION NUMBER: 35,505  
REFERENCE/DOCKET NUMBER: REH-9401M  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (207) 363-0558  
TELEFAX: (207) 363-0528  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-291-601-3

Query Match 22.2%; Score 4; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LTLT 5  
|||  
Db 8 LTLT 11

RESULT 60

US-08-602-999A-92  
; Sequence 92, Application US/08602999A

Patent No. 6184205  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
TITLE OF INVENTION: ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,999A  
FILING DATE: 16-FEB-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 92:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-602-999A-92

Query Match 22.2%; Score 4; DB 3; Length 13;  
Best Local Similarity 100.0%; Pred. No. 5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PLPL 16  
Db 5 PLPL 8

RESULT 61  
US-09-177-249-248  
Sequence 248, Application US/09177249  
Patent No. 6229064  
GENERAL INFORMATION:  
APPLICANT: Fischer, Robert L.  
APPLICANT: Ohad, Nir  
APPLICANT: Kiyosue, Tomohiro  
APPLICANT: Yadegari, Ramin  
APPLICANT: Margossian, Linda  
APPLICANT: Harada, John  
APPLICANT: Goldberg, Robert B.  
APPLICANT: The Regents of the University of California  
TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit  
TITLE OF INVENTION: Development in Plants  
FILE REFERENCE: 023070-086120US  
CURRENT APPLICATION NUMBER: US/09/177,249  
CURRENT FILING DATE: 1998-10-22  
EARLIER APPLICATION NUMBER: US 09/071,838  
EARLIER FILING DATE: 1998-05-01

NUMBER OF SEQ ID NOS: 324  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 248  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Arabidopsis sp.  
US-09-177-249-248  
Query Match 22.2%; Score 4; DB 3; Length 13;  
Best Local Similarity 100.0%; Pred. No. 5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SLTL 4  
Db 9 SLTL 12  
RESULT 62  
US-08-278-865-92  
Sequence 92, Application US/08278865  
Patent No. 6303574  
GENERAL INFORMATION:  
APPLICANT: KAY, BRIAN K.  
APPLICANT: SPARKS, ANDREW B.  
APPLICANT: THORN, JUDITH M.  
APPLICANT: QUILLIAM, LAWRENCE A.  
APPLICANT: DER, CHANNING J.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
TITLE OF INVENTION: ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBION, SPIVAK, MCJELLELAND, MAIER & NEUSTADT,  
ADDRESSEE: P.C.  
STREET: 1755 S. Jefferson Davis Highway, Suite #00  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/278,865  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Villacorta, Gilberto M.  
REGISTRATION NUMBER: 34,038  
REFERENCE/DOCKET NUMBER: 4980-007-0  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 413 3000  
TELEFAX: (703) 413-2220  
TELEX: 248855 OPAT UR  
INFORMATION FOR SEQ ID NO: 92:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-278-865-92

Query Match 22.2%; Score 4; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PLPL 16  
Db 5 PLPL 8

RESULT 63

US-09-500-124-92  
; Sequence 92, Application US/09500124  
; Patent No. 6432920  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/09/500,124  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 92:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-09-500-124-92  
  
Query Match 22.2%; Score 4; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 13 PLPL 16  
Db 5 PLPL 8  
  
RESULT 64  
US-07-956-700B-82  
; Sequence 82, Application US/07956700B  
; Patent No. 5539092  
; GENERAL INFORMATION:  
; APPLICANT: Robert Haselkorn and Piotr Gornicki  
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA  
; TITLE OF INVENTION: Carboxylase  
; NUMBER OF SEQUENCES: 116  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: 321 No. 5539092th Clark Street  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA

ZIP: 60610  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy Disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII-DOS  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/956,700B  
; FILING DATE: 19921002  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Thomas E. No. 5539092thrup  
; REGISTRATION NUMBER: 33,268  
; REFERENCE/DOCKET NUMBER: ARCD:058  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 1-312-744-0090  
; TELEFAX: 1-312-755-4489  
; INFORMATION FOR SEQ ID NO: 82:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: Amino acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; MOLECULE TYPE: Peptide  
US-07-956-700B-82  
  
Query Match 22.2%; Score 4; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 10 LHLPL 13  
Db 5 LHLPL 8  
  
RESULT 65  
US-08-258-851-6  
; Sequence 6, Application US/08258851  
; Patent No. 5585244  
; GENERAL INFORMATION:  
; APPLICANT: Elizabeth A. Allegretto  
; APPLICANT: J. Wesley Pike  
; TITLE OF INVENTION: DETECTION OF RETINOID  
; TITLE OF INVENTION: RECEPTOR SUBTYPE  
; TITLE OF INVENTION: PROTEINS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 611 West Sixth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90017  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/258,851  
; FILING DATE: 10 June 1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA: including application  
; PRIOR APPLICATION DATA: described below:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 207/199  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600

```
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 AMINO ACIDS
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PEPTIDE
; FEATURE:
; OTHER INFORMATION:
US-08-258-851-6

Query Match 22.2%; Score 4; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PLVQ 18
Db 10 PLVQ 13

RESULT 66
US-08-440-391-11
; Sequence 11, Application US/08440391
; Patent No. 5656725
; GENERAL INFORMATION:
; APPLICANT: CHITTENDEN, Thomas D.; and
; APPLICANT: LUTZ, Robert J.
; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
; MODULATE APOPTOSIS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hale and Dorr
; STREET: 1455 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,391
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: WIXON, HENRY N.
; REGISTRATION NUMBER: 32,073
; REFERENCE/DOCKET NUMBER: 104322.147
; TELEPHONE: 202-942-8400
; TELEFAX: 202-942-8484
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-440-391-11

Query Match 22.2%; Score 4; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 LPLV 17
Db 11 LPLV 14

RESULT 67
US-08-476-537-82
; Sequence 82, Application US/08476537
```

```
; Patent No. 5756290
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; CARBOXYLASE
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5792627th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,537
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/956,700
; FILING DATE: 10/21/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5756290thrup
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD:058
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
US-08-476-537-82

Query Match 22.2%; Score 4; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LHLP 13
Db 5 LHLP 8

RESULT 68
US-08-485-607-82
; Sequence 82, Application US/08485607
; Patent No. 5792627
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; CARBOXYLASE
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5792627th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,607
```



;; FILING DATE: 07-JUN-1995  
;; CLASSIFICATION: B00  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 07/956,700  
;; FILING DATE: 10/21/92  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Thomas E. No. 5792627thrup  
;; REGISTRATION NUMBER: 33,268  
;; REFERENCE/DOCKET NUMBER: ARCD:058  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 1-312-744-0090  
;; TELEFAX: 1-312-755-4489  
;; INFORMATION FOR SEQ ID NO: 82:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 14 amino acids  
;; TYPE: Amino acid  
;; STRANDEDNESS: Single  
;; TOPOLOGY: Linear  
;; MOLECULE TYPE: Peptide  
US-08-485-607-82

Query Match 22.2%; Score 4; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 10 LHLP 13  
|||  
Db 5 LHLP 8

RESULT 69  
US-08-908-597A-11  
;; Sequence 11, Application US/08908597A  
;; Patent No. 5863795  
;; GENERAL INFORMATION:  
;; APPLICANT: CHITTENDEN, Thomas D.; and  
;; APPLICANT: LUTZ, Robert J.  
;; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH  
;; TITLE OF INVENTION: MODULATE APOPTOSIS  
;; NUMBER OF SEQUENCES: 34  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Hale and Dorr  
;; STREET: 1455 Pennsylvania Avenue, N.W.  
;; CITY: Washington  
;; STATE: D.C.  
;; ZIP: 20004  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/908,597A  
;; FILING DATE:  
;; CLASSIFICATION: 530  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/440,391  
;; FILING DATE: 12-MAY-1995  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: WIXON, HENRY N.  
;; REGISTRATION NUMBER: 32,073  
;; REFERENCE/DOCKET NUMBER: 104322.147  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-942-8400  
;; TELEFAX: 202-942-8484  
;; INFORMATION FOR SEQ ID NO: 11:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 14 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-908-597A-11

Query Match 22.2%; Score 4; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 14 LPLV 17  
|||  
Db 11 LPLV 14

RESULT 70  
US-08-764-640-34  
;; Sequence 34, Application US/08764640  
;; Patent No. 5869451  
;; Patent No. 5869451 5837683  
;; GENERAL INFORMATION:  
;; APPLICANT: Dower, William J.  
;; APPLICANT: Barrett, Ronald W.  
;; APPLICANT: Cwirlla, Steven E.  
;; APPLICANT: Gates, Christian  
;; APPLICANT: Schatz, Peter J.  
;; APPLICANT: Balasubramanian, Palaniappan  
;; APPLICANT: Wagstrom, Christopher R.  
;; APPLICANT: Hendren, Richard W.  
;; APPLICANT: Deprence, Randolph B.  
;; APPLICANT: Podduturi, Surekha  
;; APPLICANT: Yin, Qun  
;; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A  
;; TITLE OF INVENTION: RECEPTOR  
;; NUMBER OF SEQUENCES: 244  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Glaxo Wellcome  
;; STREET: Five Moore Drive, P.O. Box 13398  
;; CITY: Research Triangle Park  
;; STATE: NC  
;; COUNTRY: USA  
;; ZIP: 27709  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/764,640  
;; FILING DATE: 11-DEC-1996  
;; CLASSIFICATION: 514  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Hrubiec, Robert T.  
;; REGISTRATION NUMBER: 36,392  
;; REFERENCE/DOCKET NUMBER: PK3281  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 919-248-1000  
;; INFORMATION FOR SEQ ID NO: 34:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 14 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-764-640-34

Query Match 22.2%; Score 4; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 LTLT 5  
|||  
Db 5 LTLT 8

RESULT 71  
US-08-475-879-82  
;; Sequence 82, Application US/08475879  
;; Patent No. 5972644

Patent No. 5972644 5786170  
; GENERAL INFORMATION:  
; APPLICANT: Robert Haselkorn and Piotr Gornicki  
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA  
; OPERATING SYSTEM: Carboxylase  
; NUMBER OF SEQUENCES: 116  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: 321 No. 5972644 5786170th Clark Street  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60610  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy Disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII-DOS  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/475,879  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/956,700  
; FILING DATE: 10/21/92  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Thomas E. No. 5972644 5786170thrup  
; REGISTRATION NUMBER: 33,268  
; REFERENCE/DOCKET NUMBER: ARCD:058  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 1-312-744-0090  
; TELEFAX: 1-312-755-4489  
; INFORMATION FOR SEQ ID NO: 82:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: Amino acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; MOLECULE TYPE: Peptide  
; US-08-475-879-82  
  
Query Match 22.2%; Score 4; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;  
Caps 0;  
  
QY 10 LHLP 13  
Db 5 LHLP 8  
|||||  
  
RESULT 72  
US-08-973-225-34  
; Sequence 34, Application US/08973225A  
; Patent No. 6083913  
; GENERAL INFORMATION:  
; APPLICANT: Dower, William J.  
; Barrett, Ronald W.  
; Cwirla, Steven E.  
; Duffin, David J.  
; Gates, Christian  
; Haselden, Sherril S.  
; Mattheakis, Larry C.  
; Schatz, Peter J.  
; Wagstrom, Christopher R.  
; Wrighton, Nicholas C.  
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A  
; NUMBER OF SEQUENCES: 232  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Glaxo Wellcome  
; STREET: Five Moore Drive, P.O. Box 13398  
; CITY: Research Triangle Park  
; STATE: NC

COUNTRY: USA  
; ZIP: 27709  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/973,225A  
; FILING DATE: 04-Dec-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hrubic, Robert T.  
; REGISTRATION NUMBER: 36,392  
; REFERENCE/DOCKET NUMBER: PK3065USW  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-248-1000  
; INFORMATION FOR SEQ ID NO: 34:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 34:  
US-08-973-225-34  
  
Query Match 22.2%; Score 4; DB 3; Length 14;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;  
Caps 0;  
  
QY 2 LTLT 5  
Db 5 LTLT 8  
|||||  
  
RESULT 73  
US-09-244-298A-34  
; Sequence 34, Application US/09244298A  
; Patent No. 6121238  
; GENERAL INFORMATION:  
; APPLICANT: Dower, William J.  
; Barrett, Ronald W.  
; APPLICANT: Cwirla, Steven E.  
; APPLICANT: Gates, Christian  
; APPLICANT: Schatz, Peter J.  
; APPLICANT: Balasubramanian, Palaniappan  
; APPLICANT: Wagstrom, Christopher R.  
; APPLICANT: Hendren, Richard W.  
; APPLICANT: Deprince, Randolph B.  
; APPLICANT: Podduturi, Surekha  
; APPLICANT: Yin, Qun  
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A  
; NUMBER OF SEQUENCES: 244  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Glaxo Wellcome  
; STREET: Five Moore Drive, P.O. Box 13398  
; CITY: Research Triangle Park  
; STATE: NC  
; COUNTRY: USA  
; ZIP: 27709  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/244,298A  
; FILING DATE: 11-Dec-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hrubic, Robert T.  
; REGISTRATION NUMBER: 36,392

REFERENCE/DOCKET NUMBER: PK3281  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-248-1000  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-244-298A-34

Query Match 22.2%; Score 4; DB 3; Length 14;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LTLT 5  
Db 5 LTLT 8

RESULT 74  
US-09-236-385A-11  
Sequence 11, Application US/09236385A  
Patent No. 6221615  
GENERAL INFORMATION:  
APPLICANT: CHITTENDEN, Thomas D.; and  
LUTZ, Robert J.  
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH  
MODULATE APOPTOSIS  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr  
STREET: 1455 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/236,385A  
FILING DATE: 25-Jan-1999  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: WIXON, HENRY N.  
REGISTRATION NUMBER: 32,073  
(C) ATTORNEY DOCKET NO. 104322.147CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-942-8400  
TELEFAX: 202-942-8484  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-09-236-385A-11

Query Match 22.2%; Score 4; DB 3; Length 14;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 LPLV 17  
Db 11 LPLV 14

RESULT 75  
US-09-516-704-34

Sequence 34, Application US/09516704  
Patent No. 6251864  
GENERAL INFORMATION:  
APPLICANT: Dower, William J.  
Barrett, Ronald W.  
Cwirla, Steven E.  
Gates, Christian  
Schatz, Peter J.  
Balasubramanian, Palaniappan  
Wagstrom, Christopher R.  
Hendren, Richard W.  
Deprince, Randolph B.  
Poddaturi, Surekha  
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A  
RECEPTOR  
NUMBER OF SEQUENCES: 244  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Glaxo Wellcome  
STREET: Five Moore Drive, P.O. Box 13398  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/516,704  
FILING DATE: 01-Mar-2000  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Hrubiec, Robert T.  
REGISTRATION NUMBER: 36,392  
REFERENCE/DOCKET NUMBER: PK3281  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-248-1000  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 34:  
US-09-516-704-34  
Query Match 22.2%; Score 4; DB 3; Length 14;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 LTLT 5  
Db 5 LTLT 8  
Search completed: November 25, 2003, 20:30:00  
Job time : 15.5465 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:28:30 ; Search time 4.80233 Seconds  
(without alignments)  
140.178 Million cell updates/sec

Title: US-09-641-801-24

Perfect score: 7

Sequence: 1 SMWQPP 7

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

PIR.76.\*

1: pirl.\*

2: pirl.\*

3: pirl.\*

4: pirl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	42.9	7	2	PT1299
2	3	42.9	7	2	IG heavy chain CRD
3	3	42.9	10	2	PT0322
4	3	42.9	11	2	YHRT
5	3	42.9	11	2	YHHU
6	3	42.9	11	2	YHBO
7	3	42.9	11	2	YHXAE
8	3	42.9	11	2	YHJPHY
9	3	42.9	12	2	PN0046
10	3	42.9	13	2	Ge1458
11	3	42.9	15	2	B39109
12	3	42.9	15	2	A60221
13	3	42.9	17	2	S10786
14	3	42.9	19	2	PC1323
15	3	42.9	19	2	S59486
16	3	42.9	19	2	A37968
17	3	42.9	20	2	S28779
18	2	28.6	4	2	PT0661
19	2	28.6	5	2	A32516
20	2	28.6	5	2	B37988
21	2	28.6	5	2	PT0580
22	2	28.6	6	2	A31263
23	2	28.6	6	2	A61068
24	2	28.6	6	2	S71349
25	2	28.6	7	2	A61081
26	2	28.6	7	2	PC1316
27	2	28.6	7	2	I46868
28	2	28.6	7	2	A39690
29	2	28.6	7	2	A58718

30	2	28.6	7	2	PN0649	pullulanase (EC 3.
31	2	28.6	8	2	S10596	adipokinetic hormo
32	2	28.6	8	2	PQ0012	cholecystokinin -
33	2	28.6	8	2	A43001	cholecystokinin -
34	2	28.6	8	2	B24749	neuropeptide B - b
35	2	28.6	8	2	S43971	tumor-associated a
36	2	28.6	8	2	B39745	endoglycosylcerami
37	2	28.6	8	2	S16324	hypothetical prote
38	2	28.6	8	2	S21288	lectin - potato (f
39	2	28.6	8	2	PT0030	inulinase (EC 3.2.
40	2	28.6	8	2	JS0315	leucokinin V - Mad
41	2	28.6	8	2	JS0316	leucokinin VI - Ma
42	2	28.6	8	2	JS0317	leucokinin VII - M
43	2	28.6	8	2	JS0318	leucokinin VIII -
44	2	28.6	8	2	E47193	neuropeptide calla
45	2	28.6	8	2	A14683	aspartate transami
46	2	28.6	8	2	PT0368	ig gamma chain C r
47	2	28.6	8	2	S10783	enamelin f - bovin
48	2	28.6	8	2	PT0559	T-cell receptor be
49	2	28.6	8	2	A38887	T-cell receptor ga
50	2	28.6	8	2	C39690	neural cell adhesi
51	2	28.6	9	2	A61102	parathyroid hormon
52	2	28.6	9	2	A24244	adipokinetic hormo
53	2	28.6	9	2	A61357	phyllocaerulein -
54	2	28.6	9	2	A61358	bradykinin-like pe
55	2	28.6	9	2	A61057	Thr-6 bradykinin -
56	2	28.6	9	2	A26744	bradykinin-like pe
57	2	28.6	9	2	A61363	bradykinin - commo
58	2	28.6	9	2	A60579	bradykinin-like pe
59	2	28.6	9	2	B60246	ornitho-kinin - ch
60	2	28.6	9	2	B41983	orf downstream to b
61	2	28.6	9	2	S55696	phosphoenolpyruvat
62	2	28.6	9	2	D57444	neuropeptide Grb-A
63	2	28.6	9	2	A61620	locustamyotropin I
64	2	28.6	9	2	S65433	bradykinin - horn
65	2	28.6	9	2	S77984	cytochrome-c oxida
66	2	28.6	9	2	PT0299	ig heavy chain CRD
67	2	28.6	9	2	S26508	collagen alpha 2(V
68	2	28.6	9	2	I58350	gene c-mpl protein
69	2	28.6	9	2	B30572	T-cell receptor be
70	2	28.6	9	2	A43065	hydroxyproline-3-b
71	2	28.6	10	1	XAV16B	angiotensin-conver
72	2	28.6	10	1	XASNPC	angiotensin-conver
73	2	28.6	10	1	RHAQ1	gonadoliberin I -
74	2	28.6	10	1	SPPGNK	thyromedin K - pig
75	2	28.6	10	2	JC1367	thryoliberin poten
76	2	28.6	10	2	A61337	caerulein - frog (
77	2	28.6	10	2	A13687	caerulein-like pep
78	2	28.6	10	2	PC2171	triacylglycerol li
79	2	28.6	10	2	S39030	lysyl-bradykinin -
80	2	28.6	10	2	S18396	probable glucose-6
81	2	28.6	10	2	C35389	urease (EC 3.5.1.5
82	2	28.6	10	2	A59272	peptide-N4-(N-acet
83	2	28.6	10	2	B59272	peptide-N4-(N-acet
84	2	28.6	10	2	H28027	protein P11 - curl
85	2	28.6	10	2	A36454	trypsin-modulating
86	2	28.6	10	2	B37196	bradykinin-potenti
87	2	28.6	10	2	H7196	bradykinin-potenti
88	2	28.6	10	2	S26506	collagen alpha 1(V
89	2	28.6	10	2	S10785	enamelin, 22K - bo
90	2	28.6	10	2	B38887	T-cell receptor ga
91	2	28.6	10	2	S65387	cytochrome-c oxida
92	2	28.6	10	2	C30572	T-cell receptor be
93	2	28.6	10	2	PH0923	T-cell receptor be
94	2	28.6	10	2	B61218	alpha-gliadin 6Ha
95	2	28.6	10	2	S53789	neuropeptide Pec-H
96	2	28.6	11	1	XAV1BH	bradykinin-potenti
97	2	28.6	11	1	XASNEA	bradykinin-potenti
98	2	28.6	11	1	EOOCC	eledoisin - curled
99	2	28.6	11	1	EOOCC	eledoisin - musky
100	2	28.6	11	2	D60409	kassinin-like pept

## ALIGNMENTS

## RESULT 1

S71299  
ICL2 protein - Paramesidium tetraurelia (fragment)

C:Species: Paramesidium tetraurelia  
C>Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 07-Dec-1999  
C:Accession: S71299  
R:Madeddu, L.; Klotz, C.; le Caer, J.P.; Beisson, J.  
Eur. J. Biochem. 238, 121-128, 1996  
A>Title: Characterization of centrin genes in Paramesidium.  
A:Reference number: S71298; MUID:96248429; PMID:8665928  
A:Accession: S71299  
A:Molecule type: protein  
A:Residues: 1-7 <MAD>  
A:Experimental source: strain d4-2  
C:Genetics:  
A:Genetic code: SGC5

Query Match 42.9%; Score 3; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7  
Db 2 QPP 4

## RESULT 2

PT0283  
Ig heavy chain CRD3 region (clone 4-94B) - human (fragment)

C:Species: Homo sapiens (man)  
C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C:Accession: PT0283  
R:Yanada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A>Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J  
A:Reference number: PT0222; MUID:91108337; PMID:1899102  
A:Accession: PT0283  
A:Molecule type: DNA  
A:Residues: 1-7 <YAM>  
A:Experimental source: B lymphocyte  
C:Keywords: heterotetramer; immunoglobulin

Query Match 42.9%; Score 3; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7  
Db 5 QPP 7

## RESULT 3

PT0322  
Ig heavy chain CRD3 region (clone J2-106A) - human (fragment)

C:Species: Homo sapiens (man)  
C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C:Accession: PT0322  
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A>Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J  
A:Reference number: PT0222; MUID:91108337; PMID:1899102  
A:Accession: PT0322  
A:Molecule type: DNA  
A:Residues: 1-10 <YAM>  
A:Experimental source: B lymphocyte  
C:Keywords: heterotetramer; immunoglobulin

Query Match 42.9%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SWM 3  
Db 6 SWM 8

## RESULT 4

YHRT

morphogenetic neuropeptide - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000  
C:Accession: A01427  
R:Bodenmuller, H.; Schaller, H.C.  
Nature 293, 579-580, 1981  
A>Title: Conserved amino acid sequence of a neuropeptide, the head activator, from C  
A:Reference number: A93266; MUID:82035850; PMID:7290191  
A:Accession: A01427  
A:Molecule type: protein  
A:Residues: 1-11 <BOD>  
R:Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.  
FEBS Lett. 131, 317-321, 1981  
A>Title: Synthesis of a new neuropeptide, the head activator from hydra.  
A:Reference number: A91296; MUID:82050803; PMID:7297679  
A:Contents: annotation; synthesis  
A:Note: the synthetic peptide was identical with the natural peptide in chemical str  
C:Comment: This peptide was first isolated from nerve cells of hydra and was called  
C:Superfamily: unassigned animal peptides  
C:Keywords: growth factor; hormone; hypothalamus; intestine; neuropeptide; pyroglutar  
P:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 42.9%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7  
Db 1 QPP 3

## RESULT 5

YHHU

morphogenetic neuropeptide - human  
C:Species: Homo sapiens (man)  
C>Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000  
C:Accession: B01427; A01427  
R:Bodenmuller, H.; Schaller, H.C.  
Nature 293, 579-580, 1981  
A>Title: Conserved amino acid sequence of a neuropeptide, the head activator, from C  
A:Reference number: A93266; MUID:82035850; PMID:7290191  
A:Accession: B01427  
A:Molecule type: protein  
A:Residues: 1-11 <BOD>  
R:Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.  
FEBS Lett. 131, 317-321, 1981  
A>Title: Synthesis of a new neuropeptide, the head activator from hydra.  
A:Reference number: A91296; MUID:82050803; PMID:7297679  
A:Contents: annotation; synthesis  
A:Note: the synthetic peptide was identical with the natural peptide in chemical str  
C:Comment: This peptide was first isolated from nerve cells of hydra and was called  
C:Superfamily: unassigned animal peptides  
C:Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neur  
P:1/Modified site: blocked amino end (Gln) (probably Pyrrolidone carboxylic acid) #s

Query Match 42.9%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7  
Db 1 QPP 3

## RESULT 6

YHBO  
morphogenetic neuropeptide - bovine  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000  
C;Accession: C01427; A01427  
R;Bodenmuller, H.; Schaller, H.C.  
Nature 293, 579-580, 1991  
A;Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelenterate Hydra attenuata  
A;Reference number: A93266; MUID:82035850; PMID:7290191  
A;Accession: C01427  
A;Molecule type: protein  
A;Residues: 1-11 <SCH>  
R;Birrr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.  
FEBS Lett. 131, 317-321, 1981  
A;Title: Synthesis of a new neuropeptide, the head activator from hydra.  
A;Reference number: A91296; MUID:82050803; PMID:7297679  
A;Contents: annotation; synthesis  
A;Note: the synthetic peptide was identical with the natural peptide in chemical structure  
C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator  
C;Superfamily: unassigned animal peptides  
C;Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuropeptide  
F;/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status experimental

Query Match 42.9%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7

Db 1 QPP 3

## RESULT 7

YHXA  
morphogenetic neuropeptide - sea anemone (Anthopleura elegantissima)  
N;Alternate names: head activator  
C;Species: Anthopleura elegantissima  
C;Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000  
C;Accession: A93900; A01427  
R;Schaller, H.C.; Bodenmuller, H.  
Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981  
A;Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.  
A;Reference number: A93900  
A;Accession: A93900  
A;Molecule type: protein  
A;Residues: 1-11 <SCH>  
R;Birrr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.  
FEBS Lett. 131, 317-321, 1981  
A;Title: Synthesis of a new neuropeptide, the head activator from hydra.  
A;Reference number: A91296; MUID:82050803; PMID:7297679  
A;Contents: annotation; synthesis  
A;Note: the synthetic peptide was identical with the natural peptide in chemical structure  
C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator  
C;Superfamily: unassigned animal peptides  
C;Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid  
F;/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 42.9%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7

Db 1 QPP 3

## RESULT 8

YHJFHY  
morphogenetic neuropeptide - Hydra attenuata

N;Alternate names: head activator  
C;Species: Hydra attenuata  
C;Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000  
C;Accession: B93900; A01427  
R;Schaller, H.C.; Bodenmuller, H.  
Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981  
A;Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.  
A;Reference number: A93900  
A;Accession: B93900  
A;Molecule type: protein  
A;Residues: 1-11 <SCH>  
R;Birrr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.  
FEBS Lett. 131, 317-321, 1981  
A;Title: Synthesis of a new neuropeptide, the head activator from hydra.  
A;Reference number: A91296; MUID:82050803; PMID:7297679  
A;Contents: annotation; synthesis  
A;Note: the synthetic peptide was identical with the natural peptide in chemical structure  
C;Comment: This peptide was first isolated from nerve cells of hydra and was called head activator  
C;Superfamily: unassigned animal peptides  
C;Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid  
F;/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 42.9%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7

Db 1 QPP 3

## RESULT 9

PN0046  
ATP synthase D chain, mitochondrial - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 29-Oct-1997 #sequence\_revision 29-Oct-1997 #text\_change 23-Jan-1998  
C;Accession: PN0046  
R;Kato, H.  
Kawasaki Igakkaishi 22, 245-259, 1996  
A;Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse neuroblastoma cells  
A;Reference number: PN0041  
A;Accession: PN0046  
A;Molecule type: protein  
A;Residues: 1-12 <KAR>  
A;Experimental source: neuroblastoma cell  
C;Comment: The molecular mass is 24,400 and the pI is 5.37. The amino-terminus is blocked  
C;Keywords: brain; mitochondrion

Query Match 42.9%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QPP 6

Db 6 QPP 8

## RESULT 10

G61458  
Ig lambda chain V-II region (AZI) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 15-Oct-1994 #sequence\_revision 15-Oct-1994 #text\_change 16-Aug-1996  
C;Accession: G61458; PLO159  
R;Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.  
J. Exp. Med. 170, 1551-1558, 1989  
A;Title: Expression of a public idiotype by human monoclonal IGM directed to myelin basic protein  
A;Reference number: A61458; MUID:90039128; PMID:2478651  
A;Accession: G61458  
A;Molecule type: protein  
A;Residues: 1-13 <BRO>  
C;Comment: This protein is one of monoclonal IGM reactive with myelin-associated glycoprotein  
C;Keywords: heterotetramer; immunoglobulin

Query Match 42.9%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7  
 |||  
 Db 6 QPP 8

RESULT 11  
 B39109  
 hypothetical 1.5K protein - hepatitis C virus  
 N:Alternate names: hypothetical protein 2  
 C:Species: hepatitis C virus  
 C>Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 07-May-1999  
 C:Accession: B39109; JQ1585  
 R:Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Tekamp-  
 Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991  
 A:Title: Characterization of the terminal regions of hepatitis C viral RNA: identification  
 A:Reference number: A39109; MUID:91156678; PMID:1705704  
 A:Accession: B39109  
 A>Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-15 <HAN>  
 A:Cross-references: GB:MS8406  
 R:Kumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.  
 J. Gen. Virol. 73, 1521-1525, 1992  
 A:Title: Cloning and sequencing of the structural region and expression of putative core  
 A:Reference number: JQ1584; MUID:92300349; PMID:1318944  
 A:Accession: JQ1585  
 A:Molecule type: genomic RNA  
 A:Residues: 1-15 <KUM>  
 A:Experimental source: strain U.K.

Query Match 42.9%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7  
 |||  
 Db 5 QPP 7

RESULT 12  
 A60221  
 apolipoprotein A-I - common carp (fragment)  
 C:Species: Cyprinus carpio (common carp)  
 C>Date: 10-Nov-1992 #sequence\_revision 10-Nov-1992 #text\_change 31-Dec-1993  
 C:Accession: A60221  
 R:Harel, A.; Fainaru, M.; Rubinstein, M.; Tal, N.; Schwartz, M.  
 J. Neurochem. 55, 1237-1243, 1990  
 A:Title: Fish apolipoprotein-A-I has heparin binding activity: implication for nerve reg  
 A:Reference number: A60221; MUID:90376100; PMID:2118944  
 A:Accession: A60221  
 A:Molecule type: protein  
 A:Residues: 1-15 <HAR>  
 A>Note: protein from plasma and from optic nerve yielded the same sequence  
 C:Keywords: lipid binding; lipoprotein

Query Match 42.9%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7  
 |||  
 Db 2 QPP 4

RESULT 13  
 S10786  
 enamel, 26K - bovine (fragment)  
 C:Species: Bos primigenius taurus (cattle)

C>Date: 19-Mar-1997 #sequence\_revision 21-Nov-1998 #text\_change 21-Nov-1998  
 C:Accession: S10786  
 R:Strawich, E.; Glimcher, M.J.  
 Eur. J. Biochem. 191, 47-56, 1990  
 A:Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is  
 A:Reference number: S10780; MUID:90336641; PMID:2379503  
 A:Accession: S10786  
 A:Molecule type: protein  
 A:Residues: 1-17 <STR>  
 C:Keywords: enamel; phosphoprotein

Query Match 42.9%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7  
 |||  
 Db 3 QPP 5

RESULT 14  
 PC1323  
 endopeptidase Clp (EC 3.4.21.92) chain P [similarity] - curled-leaved tobacco chloroi  
 C:Species: chloroplast Nicotiana glauca (curled-leaved tobacco)  
 C>Date: 03-May-1994 #sequence\_revision 07-Oct-1994 #text\_change 08-Dec-2000  
 C:Accession: PC1323  
 R:Fejes, E.; Engler, D.; Maliga, P.  
 Theor. Appl. Genet. 79, 28-32, 1990  
 A:Title: Extensive homologous chloroplast DNA recombination in the pt14 Nicotiana so  
 A:Reference number: PC1321  
 A:Accession: PC1323  
 A:Molecule type: DNA  
 A:Residues: 1-19 <FEJ>  
 C:Genetics:  
 A:Genome: chloroplast  
 C:Function:  
 A>Description: ATP-driven cleavage of proteins to small peptides  
 A>Note: magnesium required  
 C:Superfamily: endopeptidase Clp chain P  
 C:Keywords: ATP; chloroplast; hydrolase; serine proteinase  
 F3/Active site: His #status predicted

Query Match 42.9%; Score 3; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QPP 6  
 |||  
 Db 3 QPP 5

RESULT 15  
 S59486  
 cell wall protein, 22K - kidney bean (fragment)  
 C:Species: Phaseolus vulgaris (kidney bean)  
 C>Date: 27-Apr-1996 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997  
 C:Accession: S59486  
 R:Wojtaszek, P.; Trethowan, J.; Bolwell, G.P.  
 Plant Mol. Biol. 28, 1075-1087, 1995  
 A:Title: Specificity in the immobilisation of cell wall proteins in response to diff.  
 A:Reference number: S59481; MUID:96011753; PMID:7548825  
 A:Accession: S59486  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-19 <WOJ>

Query Match 42.9%; Score 3; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7  
 |||  
 Db 3 QPP 5

RESULT 16  
A37968  
neural surface protein Bravo - chicken (fragment)  
C;Species: Gallus gallus (chicken)  
C;Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 15-Aug-1997  
C;Accession: A37968; A36345  
R;de la Rosa, E.J.; Kayyem, J.F.; Roman, J.M.; Stierhof, Y.D.; Dreyer, W.J.; Schwarz, U.  
J. Cell Biol. 112, 1049, 1991  
A;Reference number: A37968; MUID:91154309; PMID:1999455  
A;Contents: erratum  
A;Accession: A37968  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-19 <DEL>  
R;de la Rosa, E.J.; Kayyem, J.F.; Roman, J.M.; Stierhof, Y.D.; Dreyer, W.J.; Schwarz, U.  
J. Cell Biol. 111, 3087-3096, 1990  
A;Title: Topologically restricted appearance in the developing chick retinotectal system  
A;Reference number: A36345; MUID:91100421; PMID:2269667  
A;Accession: A36345  
A;Molecule type: protein  
A;Residues: 1-7, 9-19 <DE2>

Query Match 42.9%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 6.8e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7  
|||  
Db 15 QPP 17

RESULT 17  
S28779  
octopamine receptor - common eastern firefly (fragment)  
C;Species: Photinus pyralis (common eastern firefly)  
C;Date: 28-May-1993 #sequence\_revision 28-May-1993 #text\_change 23-Feb-1997  
C;Accession: S28779  
R;Nathanson, J.A.; Kantham, L.; Hunnicutt, E.J.  
FEBS Lett. 259, 117-120, 1989  
A;Title: Isolation and N-terminal amino acid sequence of an octopamine ligand binding pr  
A;Reference number: S28779; MUID:90092510; PMID:2513233  
A;Accession: S28779  
A;Molecule type: protein  
A;Residues: 1-20 <NAN>  
C;Keywords: G protein-coupled receptor; membrane protein; neurotransmitter receptor

Query Match 42.9%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MHQ 5  
|||  
Db 18 MHQ 20

RESULT 18  
PT0661  
T-cell receptor beta chain V-D-J region (121-1BV) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0661  
R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0661  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-4 <FEE>  
A;Experimental source: day 4 postnatal thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 28.6%; Score 2; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SW 2  
||  
Db 2 SW 3

RESULT 19  
A32516  
cholecystokinin-5 - dog  
N;Alternate names: CCK-5  
C;Species: Canis lupus familiaris (dog)  
C;Date: 18-Oct-1989 #sequence\_revision 18-Oct-1989 #text\_change 18-Aug-2000  
C;Accession: A32516  
R;Shively, J.; Reeve Jr., J.R.; Eysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J.  
Am. J. Physiol. 252, G272-G275, 1987  
A;Title: CCK-5: sequence analysis of a small cholecystokinin from canine brain and in  
A;Reference number: A32516; MUID:87153871; PMID:3826354  
A;Accession: A32516  
A;Molecule type: protein  
A;Residues: 1-5 <SHI>  
A;Comment: This peptide corresponds to the five carboxyl-terminal residues of cholecy  
C;Superfamily: gastrin  
C;Keywords: amidated carboxyl end; neuropeptide  
F;5/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 WM 3  
||  
Db 2 WM 3

RESULT 20  
B37988  
acid proteinase light chain - slime mold (Physarum polycephalum) (fragment)  
C;Species: Physarum polycephalum  
C;Date: 28-Jun-1991 #sequence\_revision 28-Jun-1991 #text\_change 30-Sep-1993  
C;Accession: B37988  
R;Murakami-Murofushi, K.; Takahashi, T.; Minowa, Y.; Iino, S.; Takeuchi, T.; Kitagaki  
J. Biol. Chem. 265, 19898-19903, 1990  
A;Title: Purification and characterization of a novel intracellular acid proteinase f  
A;Reference number: A37988; MUID:91060608; PMID:2246266  
A;Accession: B37988  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-5 <MUR>

Query Match 28.6%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7  
||  
Db 3 PP 4

RESULT 21  
PT0580  
T-cell receptor beta chain V-D-J region (159-2B) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0580  
R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0580



A;Status: translation not shown  
 A;Molecule type: mRNA  
 A;Residues: 1-5 <FEE>  
 A;Experimental source: day 19 fetal thymus, strain BALB/c  
 C;Keywords: T-cell receptor

Query Match 28.6%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2  
 ||  
 DB 3 SW 4

## RESULT 22

A31263  
 A;Title: dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Plasmodium falciparum  
 C;Species: Plasmodium falciparum  
 C;Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 20-Mar-1996  
 C;Accession: A31263

R;Peterson, D.S.; Walliker, D.; Welles, T.E.

Proc. Natl. Acad. Sci. U.S.A. 85, 9114-9118, 1988

A;Title: Evidence that a point mutation in dihydrofolate reductase-thymidylate synthase  
 A;Reference number: A34217; PMID:89057886; PMID:2904149

A;Accession: A31263

A;Status: not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-6 <PPT>

C;Keywords: methyltransferase; NADP; oxidoreductase

Query Match 28.6%; Score 2; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2  
 ||  
 DB 2 SW 3

## RESULT 23

A61068  
 A;Title: locustakinin - migratory locust  
 C;Species: Locusta migratoria (migratory locust)  
 C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 08-Dec-1995  
 C;Accession: A61068  
 R;Schoofs, L.; Holman, G.M.; Proost, P.; Van Damme, J.; Hayes, T.K.; De Loof, A.  
 Regul. Pept. 37, 49-57, 1992

A;Title: Locustakinin, a novel myotropic peptide from Locusta migratoria, isolation, pri

A;Reference number: A61068; PMID:92262851; PMID:1585017

A;Accession: A61068

A;Molecule type: protein

A;Residues: 1-6 <SCH>

C;Keywords: amidated carboxyl end; cephalomotropic peptide; neuropeptide

F;6/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2  
 ||  
 DB 4 SW 5

## RESULT 24

S71349  
 A;Title: beta-crystallin B2 - rat (fragment)  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 29-Jan-1998 #sequence\_revision 06-Feb-1998 #text\_change 07-May-1999  
 C;Accession: S71349  
 R;Dirks, R.P.H.; Kraft, H.J.; van Genesen, S.T.; Klok, E.J.; Pfundt, R.; Schoenmakers, J.  
 Eur. J. Biochem. 239, 23-32, 1996

A;Title: The cooperation between two silencers creates an enhancer element that cont;

A;Reference number: S71349; PMID:96305362; PMID:8706714

A;Accession: S71349

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-6 <DIR>

A;Cross-references: EMBL:X83671

A;Experimental source: strain Wistar; lens epithelial cells

C;Genetics:

A;Gene: CRYBB2

Query Match 28.6%; Score 2; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQ 5  
 ||  
 DB 5 HQ 6

## RESULT 25

A61081  
 A;Title: tryptophyllin, basic - Rohde's leaf frog  
 C;Species: Phyllomedusa rohdei (Rohde's leaf frog)  
 C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 18-Aug-2000  
 C;Accession: A61081  
 R;Montecucchi, P.C.; Vincenti, M.; Lazarini, A.M.; Rusconi, L.; Erspamer, V.  
 Int. J. Pept. Protein Res. 33, 391-395, 1989

A;Title: Isolation, structure determination and synthesis of a novel tryptophan-cont.

A;Reference number: A61081

A;Accession: A61081

A;Molecule type: protein

A;Residues: 1-7 <MON>

C;Comment: The biological activity of this peptide was not determined.

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; hydroxyproline; skin

F;3/Modified site: 4-hydroxyproline (Pro) #status experimental

F;7/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2  
 ||  
 DB 4 SW 5

## RESULT 26

PC1316  
 A;Title: large granule L3 chain - horseshoe crab (Tachypileus tridentatus) (fragment)  
 C;Species: Tachypileus tridentatus  
 C;Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 07-May-1999  
 C;Accession: PC1316  
 R;Shigenaga, T.; Takavenoki, Y.; Kawasaki, S.; Seki, N.; Muta, T.; Toh, Y.; Ito, A.;  
 J. Biochem. 114, 307-316, 1993

A;Title: Separation of large and small granules from horseshoe crab (Tachypileus trid

A;Reference number: PC1309; PMID:94110249; PMID:8282718

A;Accession: PC1316

A;Molecule type: protein

A;Residues: 1-7 <SHI>

C;Comment: This protein participates in immobilization of invading microbes.

Query Match 28.6%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6  
 ||  
 DB 3 QP 4

## RESULT 27

I46868  
 alpha-myosin heavy chain - rabbit (fragment)  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C>Date: 14-Feb-1997 #sequence\_revision 14-Feb-1997 #text\_change 05-Nov-1999  
 C:Accession: I46868  
 R:Friedman, D.J.; Umeda, P.K.; Sinha, A.M.; Hsu, H.  
 Proc. Natl. Acad. Sci. U.S.A. 81, 3044-3048, 1984  
 A>Title: Characterization of genomic clones specifying rabbit alpha- and beta-ventricular  
 A:Reference number: I46868; MUID:84221901; PMID:6328491  
 A:Accession: I46868  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-7 <FRT>  
 A:Cross-references: GB:X01698; NID:G165538; PIDN:AAA1415.1; PID:G165539

Query Match 28.6%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MH 4  
 ||  
 Db 3 MH 4

RESULT 28  
 A39690  
 neural cell adhesion molecule, cardiac splice form -, -, - - rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 16-Jul-1999  
 C:Accession: A39690  
 R:Reyes, A.A.; Small, S.J.; Akesson, R.  
 Mol. Cell. Biol. 11, 1654-1661, 1991  
 A>Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule mRNA  
 A:Reference number: A39690; MUID:91141516; PMID:1996115  
 A:Accession: A39690  
 A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
 A:Molecule type: mRNA  
 A:Residues: 1-7 <REY>  
 A:Cross-references: GB:M63970  
 C:Keywords: cardiac muscle; cell adhesion; heart

Query Match 28.6%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6  
 ||  
 Db 1 QP 2

RESULT 29  
 A58718  
 carnocin UI49 - Carnobacterium sp. (fragment)  
 C:Species: Carnobacterium sp.  
 C>Date: 23-Jan-1998 #sequence\_revision 30-Jan-1998 #text\_change 30-Jan-1998  
 C:Accession: A58718  
 R:Stoffels, G.; Nissen-Meyer, J.; Gudmundsdottir, A.; Sletten, K.; Holo, H.; Nes, I.F.  
 Appl. Environ. Microbiol. 58, 1417-1422, 1992  
 A>Title: Purification and characterization of a new bacteriocin isolated from a Carnobac  
 A:Reference number: A58718; MUID:92321768; PMID:1622206  
 A:Accession: A58718  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-7 <STO>  
 C:Keywords: antibiotic; lanthionine

Query Match 28.6%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6  
 ||  
 Db 5 QP 6

RESULT 30  
 PN0649  
 pullulanase (EC 3.2.1.41) - Bacillus sp. (strain S-1) (fragment)  
 C:Species: Bacillus sp.  
 C>Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 03-Jun-2002  
 C:Accession: PN0649  
 R:Kim, C.H.; Choi, H.I.; Lee, D.S.  
 Biosci. Biotechnol. Biochem. 57, 1632-1637, 1993  
 A>Title: Purification and biochemical properties of an alkaline pullulanase from alka  
 A:Reference number: PN0649; MUID:94080025; PMID:7764261  
 A:Accession: PN0649  
 A:Molecule type: protein  
 A:Residues: 1-7 <KIM>  
 C:Comment: This enzyme is used together with glucoamylase to improve the efficiency of  
 nent in high maltose syrups.  
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 28.6%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2  
 ||  
 Db 5 SW 6

RESULT 31  
 S10596  
 adipokinetic hormone - pond skimmer  
 C:Species: Libellula auripennis  
 C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 14-Nov-1997  
 C:Accession: S10596  
 R:Gaede, G.  
 Biol. Chem. Hoppe-Seyler 371, 475-483, 1990  
 A>Title: The putative ancestral peptide of the adipokinetic/red-pigment-concentrating  
 A:Reference number: S10596; MUID:90359055; PMID:2390213  
 A:Accession: S10596  
 A:Molecule type: protein  
 A:Residues: 1-8 <BIO>  
 C:Comment: This peptide has both adipokinetic and hypertrehalosemic activities.  
 C:Superfamily: adipokinetic hormone  
 C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyrogluta  
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2  
 ||  
 Db 7 SW 8

RESULT 32  
 PQ0012  
 cholecystokinin - southeastern quoll  
 N:Alternate names: CCK  
 C:Species: Dasyurus viverrinus (southeastern quoll)  
 C>Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 13-Sep-1996  
 C:Accession: PQ0012  
 R:Fan, Z.W.; Eng, J.; Shaw, G.; Yalow, R.S.  
 Peptides 9, 429-431, 1988  
 A>Title: Cholecystokinin octapeptide purified from brains of Australian marsupials.  
 A:Reference number: PQ0012; MUID:88234141; PMID:3375140  
 A:Accession: PQ0012  
 A:Molecule type: protein  
 A:Residues: 1-8 <FAN>  
 C:Superfamily: Gastrin  
 C:Keywords: amidated carboxyl end; hormone; neuropeptide; sulfoprotein  
 F;2/Binding site: sulfate (Tyr) (covalent) #status predicted

F;/s/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 28.6%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0;  
Matches 2; Conservative 0; Mismatches 0; Gaps 0;

Qy 2 WM 3  
||  
Db 5 WM 6

#### RESULT 33

A43001  
cholecystokinin - tamar wallaby  
N;Alternate names: CCK  
C;Species: Macropus eugenii (tamar wallaby)  
C;Date: 30-Oct-1992 #sequence\_revision 30-Oct-1992 #text\_change 13-Sep-1996  
C;Accession: A43001; PQ0012  
Peptides 9, 429-431, 1988  
R;Fan, Z.W.; Eng, J.; Shaw, G.; Yalow, R.S.  
A;Title: Cholecystokinin octapeptide purified from brains of Australian marsupials.  
A;Reference number: PQ0012; PMID:88234141; PMID:3375140  
A;Accession: A43001  
A;Molecule type: protein  
A;Residues: 1-8 <FAN>  
C;Superfamily: Gastrin  
C;Keywords: amidated carboxyl end; hormone; neuropeptide; sulfoprotein  
F;/Binding site: sulfate (Tyr) (covalent) #status predicted  
F;/s/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 28.6%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0;  
Matches 2; Conservative 0; Mismatches 0; Gaps 0;

Qy 2 WM 3  
||  
Db 5 WM 6

#### RESULT 34

B24749  
neuropeptide B - bovine  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 28-Jul-1987 #sequence\_revision 28-Jul-1987 #text\_change 18-Aug-2000  
C;Accession: B24749  
R;Xang, H.Y.T.; Fratta, W.; Majane, E.A.; Costa, E.  
Proc. Natl. Acad. Sci. U.S.A. 82, 7757-7761, 1985  
A;Title: Isolation, sequencing, synthesis, and pharmacological characterization of two h  
A;Reference number: A94074; PMID:86067985; PMID:3865193  
A;Accession: B24749  
A;Molecule type: protein  
A;Residues: 1-8 <FAN>  
C;Superfamily: unassigned animal peptides  
C;Keywords: neuropeptide

Query Match 28.6%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0;  
Matches 2; Conservative 0; Mismatches 0; Gaps 0;

Qy 5 QP 6  
||  
Db 4 QP 5

#### RESULT 35

S43971  
tumour-associated antigen MUT1 - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 20-Oct-1994 #sequence\_revision 17-Nov-1995 #text\_change 18-Aug-2000  
C;Accession: S43971  
R;Hendelboim, O.; Berke, G.; Fridkin, M.; Feldman, M.; Eisenbach, L.  
Nature 369, 67-71, 1994  
A;Title: CTL induction by a tumour-associated antigen octapeptide derived from a murine

A;Reference number: S43971; PMID:94217811; PMID:8164742  
A;Accession: S43971  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-8 <MAN>  
C;Superfamily: unassigned animal peptides

Query Match 28.6%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0;  
Matches 2; Conservative 0; Mismatches 0; Gaps 0;

Qy 5 QP 6  
||  
Db 7 QP 8

#### RESULT 36

B39745  
endoglycosylceramidase (EC 3.2.1.123) I - Rhodococcus sp. (fragment)  
C;Species: Rhodococcus sp.  
C;Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 31-Dec-1993  
C;Accession: B39745  
R;Ito, M.; Ikegami, Y.; Yanagata, T.  
J. Biol. Chem. 266, 7919-7926, 1991.  
A;Title: Activator proteins for glycosphingolipid hydrolysis by endoglycosylceramidases.  
Die using these activator proteins.

A;Reference number: A39745; PMID:91210321; PMID:1850427  
A;Accession: B39745  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-8 <ITO>  
C;Keywords: glycosidase; hydrolase

Query Match 28.6%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0;  
Matches 2; Conservative 0; Mismatches 0; Gaps 0;

Qy 6 PP 7  
||  
Db 2 PP 3

#### RESULT 37

S16324  
hypothetical protein 2 - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 21-Nov-1993 #sequence\_revision 12-May-1995 #text\_change 21-Jul-2000  
C;Accession: S16324  
R;Ruberti, I.; Sessa, G.; Lucchetti, S.; Morelli, G.  
EMBO J. 10, 1787-1791, 1991.  
A;Title: A novel class of plant proteins containing a homeodomain with a closely lin  
A;Reference number: S16323; PMID:91266907; PMID:1675603  
A;Accession: S16324  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-8 <RUB>  
A;Cross-references: EMBL:X58821; NID:G16327; PIDN:CAA41624.1; PID:G579259

Query Match 28.6%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0;  
Matches 2; Conservative 0; Mismatches 0; Gaps 0;

Qy 6 PP 7  
||  
Db 7 PP 8

#### RESULT 38

S21288  
lectin - potato (fragment)  
C;Species: Solanum tuberosum (potato)  
C;Date: 19-Mar-1997 #sequence\_revision 05-Dec-1998 #text\_change 05-Dec-1998  
C;Accession: S21288

R;Millar, D.J.; Allen, A.K.; Smith, C.G.; Sidebottom, C.; Slabas, A.R.; Bolwell, G.P.  
 Biochem. J. 283, 813-821, 1992  
 A;Title: Chitin-binding proteins in potato (*Solanum tuberosum* L.) tuber. Characterization  
 A;Reference number: S21288; PMID:92272683; PMID:1590771  
 A;Accession: S21288  
 A;Molecule type: protein  
 A;Residues: 1-8 <HOL>  
 A;Experimental source: var. Ulster Sceptre  
 C;Function:  
 A;Description: may be involved in defence mechanism of the plant  
 C;Keywords: hydroxyproline, lectin

Query Match 28.6%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7  
 ||  
 7 PP 8

Db

RESULT 39

PT0030  
 inulinase (EC 3.2.1.7) - *Aspergillus ficuum* (fragment)  
 N;Alternate names: inulase  
 C;Species: *Aspergillus ficuum*  
 C;Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 07-May-1999  
 C;Accession: PT0030  
 R;Etalib, M.; Baratti, J.C.  
 Agric. Biol. Chem. 54, 61-68, 1990  
 A;Title: Molecular and kinetic properties of *Aspergillus ficuum* inulinases.  
 A;Reference number: PT0030; PMID:90344234; PMID:1368526  
 A;Accession: PT0030  
 A;Molecule type: protein  
 A;Residues: 1-8 <ETT>  
 C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 28.6%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QP 6  
 ||  
 5 QP 6

Db

RESULT 40

JS0315  
 leucokinin V - *Madeira cockroach*  
 C;Species: *Leucophaea maderae* (*Madeira cockroach*)  
 C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Jun-2000  
 C;Accession: JS0315  
 R;Holman, G.M.; Cook, B.J.; Nachman, R.J.  
 Comp. Biochem. Physiol. C 88, 27-30, 1987  
 A;Title: Isolation, primary structure, and synthesis of leucokinins V and VI: myotrop  
 A;Reference number: JS0315  
 A;Accession: JS0315  
 A;Molecule type: protein  
 A;Residues: 1-8 <HOL>  
 C;Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile  
 C;Keywords: amidated carboxyl end; cephalomyotropic peptide  
 F;8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SW 2  
 ||  
 6 SW 7

Db

RESULT 41

JS0317  
 leucokinin VII - *Madeira cockroach*  
 C;Species: *Leucophaea maderae* (*Madeira cockroach*)  
 C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Jun-2000  
 C;Accession: JS0317  
 R;Holman, G.M.; Cook, B.J.; Nachman, R.J.  
 Comp. Biochem. Physiol. C 88, 31-34, 1987  
 A;Title: Isolation, primary structure and synthesis of leucokinins VII and VIII: the  
 A;Reference number: JS0317  
 A;Accession: JS0317  
 A;Molecule type: protein  
 A;Residues: 1-8 <HOL>  
 C;Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile  
 C;Keywords: amidated carboxyl end; cephalomyotropic peptide  
 F;8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SW 2  
 ||  
 6 SW 7

Db

RESULT 43

JS0318  
 leucokinin VIII - *Madeira cockroach*  
 C;Species: *Leucophaea maderae* (*Madeira cockroach*)  
 C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Jun-2000  
 C;Accession: JS0318  
 R;Holman, G.M.; Cook, B.J.; Nachman, R.J.  
 Comp. Biochem. Physiol. C 88, 31-34, 1987  
 A;Title: Isolation, primary structure and synthesis of leucokinins VII and VIII: the  
 A;Reference number: JS0317  
 A;Accession: JS0318  
 A;Molecule type: protein  
 A;Residues: 1-8 <HOL>  
 C;Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile  
 C;Keywords: amidated carboxyl end; cephalomyotropic peptide  
 F;8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SW 2  
 ||  
 6 SW 7

Db

JS0316  
 leucokinin VI - *Madeira cockroach*  
 C;Species: *Leucophaea maderae* (*Madeira cockroach*)  
 C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Jun-2000  
 C;Accession: JS0316  
 R;Holman, G.M.; Cook, B.J.; Nachman, R.J.  
 Comp. Biochem. Physiol. C 88, 27-30, 1987  
 A;Title: Isolation, primary structure, and synthesis of leucokinins V and VI: myotrop  
 A;Reference number: JS0315  
 A;Accession: JS0316  
 A;Molecule type: protein  
 A;Residues: 1-8 <HOL>  
 C;Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile  
 C;Keywords: amidated carboxyl end; cephalomyotropic peptide; pyroglutamic acid  
 F;7/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F;8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SW 2  
 ||  
 6 SW 7

Db

RESULT 42

JS0317  
 leucokinin VII - *Madeira cockroach*  
 C;Species: *Leucophaea maderae* (*Madeira cockroach*)  
 C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Jun-2000  
 C;Accession: JS0317  
 R;Holman, G.M.; Cook, B.J.; Nachman, R.J.  
 Comp. Biochem. Physiol. C 88, 31-34, 1987  
 A;Title: Isolation, primary structure and synthesis of leucokinins VII and VIII: the  
 A;Reference number: JS0317  
 A;Accession: JS0317  
 A;Molecule type: protein  
 A;Residues: 1-8 <HOL>  
 C;Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile  
 C;Keywords: amidated carboxyl end; cephalomyotropic peptide  
 F;8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SW 2  
 ||  
 6 SW 7

Db

Qy 1 SW 2  
||  
6 SW 7

Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQ 5  
||  
Db 2 HQ 3

## RESULT 44

E47393  
C:Species: Calliphora vomitoria  
C:Date: 16-Feb-1994 #sequence\_revision 18-Nov-1994 #text\_change 03-Mar-1995  
C:Accession: E47393  
R:Duve, H.; Johnsen, A.H.; Scott, A.G.; Yu, C.G.; Yagi, K.J.; Tobe, S.S.; Thorpe, A.  
Proc. Natl. Acad. Sci. U.S.A. 90, 2456-2460, 1993  
A:Title: Callatostatin: neuroptides from the blowfly Calliphora vomitoria with sequen  
A:Reference number: A47393; MUID:93211980; PMID:8460157  
A:Accession: E47393  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-8 <DUV>  
A:Experimental source: whole flies  
A>Note: sequence extracted from NCBI backbone (NCBIP:128482)

Query Match 28.6%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7  
||  
Db 2 PP 3

## RESULT 45

A14683  
C:Species: Gallus gallus (chicken)  
C:Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 31-Mar-2000  
C:Accession: A14683  
R:Wilson, K.J.; Hunziker, P.; Hughes, G.J.  
FEBS Lett. 108, 98-102, 1979  
A:Title: Microsequence analysis: IV. Automatic liquid-phase sequencing using DABITC.  
A:Reference number: A14683; MUID:80092116; PMID:520566  
A:Accession: A14683  
A:Molecule type: protein  
A:Residues: 1-8 <WIL>  
C:Keywords: aminotransferase; mitochondrion

Query Match 28.6%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QP 6  
||  
Db 6 QP 7

## RESULT 46

PT0368  
IG gamma chain C region (gamma-1) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 16-Aug-1996  
C:Accession: PT0368  
R:Milili, M.; Fougereau, M.; Guglielmi, P.; Schiff, C.  
Mol. Immunol. 28, 753-761, 1991  
A:Title: Early occurrence of immunoglobulin isotype switching in human fetal liver.  
A:Reference number: PT0368; MUID:91312348; PMID:1906981  
A:Accession: PT0368  
A:Molecule type: mRNA  
A:Residues: 1-8 <MIL>  
A:Experimental source: fetal liver  
C:Keywords: immunoglobulin

Query Match 28.6%; Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQ 5  
||  
Db 2 HQ 3

## RESULT 47

S10783  
enamelin f - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 19-Mar-1997 #sequence\_revision 21-Nov-1998 #text\_change 21-Nov-1998  
C:Accession: S10783  
R:Strawich, E.; Glimcher, M.J.  
Eur. J. Biochem. 191, 47-56, 1990  
A:Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is a  
A:Reference number: S10780; MUID:90336641; PMID:2379503  
A:Accession: S10783  
A:Molecule type: protein  
A:Residues: 1-8 <STR>  
C:Keywords: enamel; phosphoprotein

Query Match 28.6%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7  
||  
Db 4 PP 5

## RESULT 48

PT0559  
T-cell receptor beta chain V-D-J region (126-1BH) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0559  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions  
A:Reference number: PT0509; MUID:91277601; PMID:1711558  
A:Accession: PT0559  
A:Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-8 <FEE>  
A:Experimental source: day 18 fetal thymus, strain BALB/c  
C:Keywords: T-cell receptor

Query Match 28.6%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7  
||  
Db 4 PP 5

## RESULT 49

A38887  
T-cell receptor gamma chain (5t.2) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 07-May-1999  
C:Accession: A38887  
R:Whetzel, M.; Mosley, R.L.; Whetzel, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.  
Mol. Cell. Biol. 11, 5902-5909, 1991  
A:Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma  
A:Reference number: A41946; MUID:92049316; PMID:1658619  
A:Accession: A38887  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-8 <WHE>  
C:Keywords: T-cell receptor

Query Match 28.6%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2  
 ||  
 2 SW 3

Db

RESULT 50

C39690

neural cell adhesion molecule, cardiac splice form -, -, + - rat (fragment)  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 16-Jul-1999  
 C;Accession: C39690  
 R;Reyes, A.A.; Small, S.J.; Akeson, R.  
 Mol. Cell. Biol. 11, 1654-1661, 1991  
 A;Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule mR  
 A;Reference number: A39690; MUID:91141516; PMID:11996115  
 A;Accession: C39690  
 A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
 A;Molecule type: mRNA  
 A;Residues: 1-8 <REV>  
 A;Cross-references: GB:M63970  
 C;Keywords: cardiac muscle; cell adhesion; heart

Query Match 28.6%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6  
 ||  
 1 QP 2

Db

# RESULT 51

A61102

parathyroid hormone-like protein, humoral hypercalcemia of malignancy - dog (fragment)  
 C;Species: Canis lupus familiaris (dog)  
 C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 17-Mar-1999  
 C;Accession: A61102  
 R;Weir, E.C.; Burtis, W.J.; Morris, C.A.; Brady, T.G.; Insogna, K.L.  
 Endocrinology 123, 2744-2751, 1988  
 A;Title: Isolation of 16,000-Dalton parathyroid hormone-like proteins from two animal tu  
 A;Reference number: A61102; MUID:89064600; PMID:3197642  
 A;Accession: A61102  
 A;Molecule type: protein  
 A;Residues: 1-9 <WEI>  
 A;Experimental source: apocrine cell adenocarcinoma  
 C;Superfamily: parathyroid hormone-related protein; parathyroid hormone homology  
 C;Keywords: hormone; humoral hypercalcemia

Query Match 28.6%; Score 2; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQ 5  
 ||  
 6 HQ 7

Db

# RESULT 52

A24244

adipokinetic hormone - bollworm  
 N;Alternate names: Hez-AKH  
 C;Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)  
 C;Date: 31-Mar-1988 #sequence\_revision 23-Mar-1995 #text\_change 31-Oct-1997  
 C;Accession: A24244  
 R;Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Holman, G.M.; Wagner, R.M.; Ridgway  
 Biochem. Biophys. Res. Commun. 135, 622-628, 1986  
 A;Title: Isolation and primary structure of a peptide from the corpora cardiaca of Helic  
 A;Reference number: A24244; MUID:86186794; PMID:3964263

A;Accession: A24244  
 A;Molecule type: protein  
 A;Residues: 1-9 <JAF>  
 C;Superfamily: adipokinetic hormone  
 C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglute  
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F;9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2  
 ||  
 7 SW 8

Db

# RESULT 53

A61357

Phyllocaerulein - Sauvage's leaf frog  
 C;Species: Phyllomedusa sauvagei (Sauvage's leaf frog)  
 C;Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 02-Sep-2000  
 C;Accession: A61357  
 R;Anastasi, A.; Bertaccini, G.; Cei, J.M.; De Caro, G.; Erspamer, V.; Impicciatore, V.  
 Br. J. Pharmacol. 37, 198-206, 1969  
 A;Title: Structure and pharmacological actions of phyllocaerulein, a caerulein-like p  
 A;Reference number: A61357; MUID:70005484; PMID:5824931  
 A;Accession: A61357  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-9 <ANA>  
 C;Superfamily: gastrin

C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid; skin; sulfoprotei  
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F;3/Binding site: sulfat (Tyr) (covalent) #status experimental  
 F;9/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WM 3  
 ||  
 6 WM 7

Db

# RESULT 54

A61358

bradykinin-like peptide I - Japanese pond frog  
 C;Species: Rana nigromaculata (Japanese pond frog)  
 C;Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 02-Sep-2000  
 C;Accession: A61358  
 R;Nakajima, T.  
 Chem. Pharm. Bull. 16, 769-770, 1968  
 A;Title: Occurrence of a new active peptide on smooth muscle and bradykinin in the sk  
 A;Reference number: A61358; MUID:68412013; PMID:5677638  
 A;Accession: A61358  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-9 <NAK>  
 C;Superfamily: unassigned animal peptides  
 C;Keywords: skin

Query Match 28.6%; Score 2; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7  
 ||  
 2 PP 3

Db

# RESULT 55

A61057  
Thr-6 bradykinin - scoliid wasp (Colpa interrupta)  
C:Species: Colpa interrupta  
C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 18-Aug-2000  
C:Accession: A61057  
R:Piek, T.; Hue, B.; Mantel, P.; Nakajima, T.; Pelhate, M.; Yasuhara, T.  
Comp. Biochem. Physiol. C 96, 157-162, 1990  
A:Title: Threonine(6)-bradykinin in the venom of the wasp Colpa interrupta (F.) presynap  
A:Reference number: A61057; MUID:91130217; PMID:1980872  
A:Accession: A61057  
A:Molecule type: protein  
A:Residues: 1-9 <PIE>  
C:Superfamily: unassigned animal peptides  
C:Keywords: bradykinin; presynaptic neurotoxin; venom

Query Match 28.6%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7  
DB 2 PP 3

RESULT 56  
A26744  
bradykinin-like peptide - garden dagger wasp  
N:Alternate names: Thr-6-bradykinin  
C:Species: Megascollia flavifrons (garden dagger wasp)  
C:Date: 08-Mar-1989 #sequence\_revision 08-Mar-1989 #text\_change 18-Aug-2000  
C:Accession: A26744  
R:Yasuhara, T.; Mantel, P.; Nakajima, T.; Piek, T.  
Toxicol 25, 527-535, 1987  
A:Title: Two kinins isolated from an extract of the venom reservoirs of the solitary wasp  
A:Reference number: A94322; MUID:87293024; PMID:3617088  
A:Accession: A26744  
A:Molecule type: protein  
A:Residues: 1-9 <YAS>  
C:Superfamily: unassigned animal peptides

Query Match 28.6%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7  
DB 2 PP 3

RESULT 57  
A61363  
bradykinin - common frog  
C:Species: Rana temporaria (common frog)  
C:Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 18-Aug-2000  
C:Accession: A61363  
R:Anastasi, A.; Brspamer, V.; Bertaccini, G.  
Comp. Biochem. Physiol. A 14, 43-52, 1965  
A:Title: Occurrence of bradykinin in the skin of Rana temporaria.  
A:Reference number: A61363  
A:Accession: A61363  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-9 <ANA>  
C:Superfamily: unassigned animal peptides  
C:Keywords: skin

Query Match 28.6%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7  
DB 2 PP 3

RESULT 58  
A60579  
bradykinin-like peptide - slider turtle  
C:Species: Pseudemys scripta (slider)  
C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 18-Aug-2000  
C:Accession: A60579  
R:Conlon, J.M.; Hicks, J.W.; Smith, D.D.  
Endocrinology 126, 985-991, 1990  
A:Title: Isolation and biological activity of a novel kinin ([Thr(6)]bradykinin) from  
A:Reference number: A60579; MUID:90126625; PMID:2298179  
A:Accession: A60579  
A:Molecule type: protein  
A:Residues: 1-9 <CON>  
C:Comment: This peptide increases aortic blood flow but, unlike bradykinin in mammal  
C:Superfamily: unassigned animal peptides  
C:Keywords: plasma

Query Match 28.6%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7  
DB 2 PP 3

RESULT 59  
B60246  
ornitho-kinin - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 11-Dec-1992 #sequence\_revision 11-Dec-1992 #text\_change 18-Aug-2000  
A:Accession: B60246  
R:Kimura, M.; Sueyoshi, T.; Morita, T.; Tanaka, K.; Iwanaga, S.  
Adv. Exp. Med. Biol. 247A, 359-367, 1989  
A:Title: Ornitho-kininogen and ornitho-kinin: isolation, characterization and chemi  
A:Reference number: A60246; MUID:90102072; PMID:2603803  
A:Accession: B60246  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-9 <KIM>  
C:Superfamily: unassigned animal peptides

Query Match 28.6%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7  
DB 2 PP 3

RESULT 60  
B41983  
orf downstream to bacterioferritin - Azotobacter vinelandii (fragment)  
C:Species: Azotobacter vinelandii  
C:Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 08-Oct-1999  
C:Accession: B41983  
R:Grossman, M.J.; Hinton, S.M.; Minak-Bernero, V.; Slaughter, C.; Stiefel, E.I.  
Proc. Natl. Acad. Sci. U.S.A. 89, 2419-2423, 1992  
A:Title: Unification of the ferritin family of proteins.  
A:Reference number: A41983; MUID:92196129; PMID:1549605  
A:Accession: B41983  
A>Status: preliminary; not compared with conceptual translation  
A:Molecule type: nucleic acid; protein  
A:Residues: 1-9 <GRO>  
A:Cross-references: GB:M83692; NID:9142297; PIDN:AAA22122.1; PID:9142299  
A:Note: sequence extracted from NCBI backbone (NCBIF:88442)

Query Match 28.6%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7  
||  
Db 3 PP 4

RESULT 61  
S55696  
Phosphoenolpyruvate carboxykinase - Trypanosoma brucei  
C;Species: Trypanosoma brucei  
C;Date: 28-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 07-May-1999  
C;Accession: S55696  
R;Hunt, M.; Koehler, P.  
Biochim. Biophys. Acta 1249, 15-22, 1995  
A;Title: Purification and characterization of phosphoenolpyruvate carboxykinase from Trypanosoma brucei  
A;Reference number: S55696; MUID:95284106; PMID:7766679  
A;Accession: S55696  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-9 <HUN>

Query Match 28.6%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6  
||  
Db 1 QP 2

RESULT 62  
D57444  
neuropeptide Grb-AST B4 - two-spotted cricket  
C;Species: Gryllus bimaculatus (two-spotted cricket)  
C;Date: 26-Jan-1996 #sequence\_revision 26-Jan-1996 #text\_change 26-Jan-1996  
C;Accession: D57444  
R;Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.  
J. Biol. Chem. 270, 21103-21108, 1995  
A;Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the cricket Gryllus bimaculatus  
A;Reference number: A57444; MUID:95403341; PMID:7673141  
A;Accession: D57444  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-9 <LOR>

Query Match 28.6%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2  
||  
Db 8 SW 9

RESULT 63  
A61620  
locustamytotropin III - migratory locust  
C;Species: Locusta migratoria (migratory locust)  
C;Date: 21-Jul-1995 #sequence\_revision 28-Jul-1995 #text\_change 11-Jul-1997  
C;Accession: A61620  
R;Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; Kochansky, J.P.; De Loof, A.  
Insect Biochem. Mol. Biol. 22, 447-452, 1992  
A;Title: Isolation, identification and synthesis of locustamytotropin III and IV, two additional members of the locustamytotropin family  
A;Reference number: A61620  
A;Accession: A61620  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-9 <SCH>  
C;Keywords: amidated carboxyl end; neuropeptide  
F;9/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6  
||  
Db 3 QP 4

RESULT 64  
S65433  
bradykinin - horn fly (fragment)  
C;Species: Haematobia irritans (horn fly)  
C;Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997  
C;Accession: S65433  
R;Wijffels, G.; Fitzgerald, C.; Gough, J.; Riding, G.; Elvin, C.; Kemp, D.; Willadsen, Eur. J. Biochem. 237, 414-423, 1996  
A;Title: Cloning and characterisation of angiotensin-converting enzyme from the diptere Haematobia irritans  
A;Reference number: S65431; MUID:96215437; PMID:8647080  
A;Accession: S65433  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-9 <WID>  
A;Note: the source is designated as Haematobia irritans exigua

Query Match 28.6%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7  
||  
Db 2 PP 3

RESULT 65  
S77984  
cytochrome-c oxidase (EC 1.9.3.1) chain Via - bigeye tuna (fragment)  
C;Species: Thunnus obesus (bigeye tuna)  
C;Date: 17-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 30-Jan-1998  
C;Accession: S77984  
R;Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lottspeich, F.; Kadenbach, B.  
Submitted to the Protein Sequence Database, June 1997  
A;Reference number: S77980  
A;Accession: S77984  
A;Molecule type: protein  
A;Residues: 1-9 <ARN>  
A;Experimental source: heart  
A;Genome: nuclear  
C;Function:  
A;Pathway: oxidative phosphorylation; respiratory chain  
C;Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane

Query Match 28.6%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6  
||  
Db 3 QP 4

RESULT 66  
PT0299  
Ig heavy chain CDR3 region (clone 5-103B) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C;Accession: PT0299  
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and A;Reference number: PT0222; MUID:91108337; PMID:1899102  
A;Accession: PT0299  
A;Molecule type: DNA  
A;Residues: 1-9 <YAM>



A;Experimental source: B lymphocyte  
C;Keywords: heterotetramer; immunoglobulin

Query Match 28.6%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2  
||  
Db 3 SW 4

## RESULT 67

S26508  
collagen alpha 2(VI) chain - bovine (fragment)  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 05-Dec-1998  
C;Accession: S26508  
R;Jander, R.; Rautenberg, J.; Glanville, R.W.  
Eur. J. Biochem. 133, 39-46, 1983  
A;Title: Further characterization of the three polypeptide chains of bovine and human sh  
A;Reference number: S26506; MUID:83209648; PMID:6852033  
C;Accession: S26508  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-9 <JAN>  
C;Keywords: hydroxyproline  
F;7/Modified site: hydroxyproline (Pro) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7  
||  
Db 6 PP 7

## RESULT 68

I58350  
gene c-mpl protein - mouse (fragment)  
C;Species: Mus sp. (mouse)  
C;Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 28-Feb-1997  
C;Accession: I58350  
R;Alexander, W.S.; Dunn, A.R.  
Oncogene 10, 795-803, 1995  
A;Title: Structure and transcription of the genomic locus encoding murine c-Mpl, a recep  
A;Reference number: I58350; MUID:95166571; PMID:7862460  
C;Accession: I58350  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-9 <RES>  
A;Cross-references: GB:S76841; NID:G912992  
C;Genetics:  
A;Gene: c-mpl

Query Match 28.6%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2  
||  
Db 3 SW 4

## RESULT 69

B30572  
T-cell receptor beta chain C region (CRTE29) - rat (fragment)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 03-Apr-1989 #sequence\_revision 03-Apr-1989 #text\_change 30-May-1997  
C;Accession: B30572  
R;Williams, C.B.; Gutman, G.A.  
J. Immunol. 142, 1027-1035, 1989

A;Title: T cell receptor beta-chain genes in the rat. Availability and pattern of ut  
A;Reference number: A30563; MUID:89110038; PMID:2563271  
A;Accession: B30572

A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-9 <WIL>  
C;Keywords: T-cell receptor

Query Match 28.6%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7  
||  
Db 8 PP 9

## RESULT 70

A43065  
hydroxyproline-3-bradykinin - frog (Heleophryne purcelli)  
C;Species: Heleophryne purcelli  
C;Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 07-May-1999  
C;Accession: A43065  
R;Nakajima, T.; Yasuhara, T.; Erspamer, G.F.; Visser, J.  
Experientia 35, 1133, 1979  
A;Title: Occurrence of Hyp(3)-bradykinin in methanol extracts of the skin of the Sou  
A;Reference number: A43065; MUID:80024576; PMID:486255  
C;Accession: A43065  
A;Molecule type: protein  
A;Residues: 1-9 <NAK>  
C;Keywords: bradykinin; hydroxyproline; skin  
F;3/Modified site: hydroxyproline (Pro) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7  
||  
Db 2 PP 3

## RESULT 71

XA1168  
angiotensin-converting enzyme inhibitor V-6-II - jararaca  
C;Species: Bothrops jararaca (jararaca)  
C;Date: 13-Jul-1981 #sequence\_revision 13-Jul-1981 #text\_change 08-Dec-1995  
C;Accession: A01255  
R;Ondetti, M.A.; Williams, N.J.; Sabo, E.F.; Pluscec, J.; Weaver, E.R.; Kocyl, O.  
Biochemistry 10, 4033-4039, 1971  
A;Title: Angiotensin-converting enzyme inhibitors from the venom of Bothrops jararac  
A;Reference number: A90356; MUID:72118526; PMID:4334402  
C;Accession: A01255  
A;Molecule type: protein  
A;Residues: 1-10 <OND>  
A;Note: the structure of the peptide was confirmed by synthesis  
C;Comment: this peptide also potentiates bradykinin by inhibiting the kinases that i  
C;Superfamily: bradykinin-potentiating peptide  
C;Keywords: angiotensin-converting enzyme inhibitor; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 28.6%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.5e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7  
||  
Db 9 PP 10

## RESULT 72

XASNPC  
angiotensin-converting enzyme inhibitor - aspic viper

C;Species: Vipera aspis (aspic viper)  
 C;Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 08-Dec-1995  
 C;Accession: A60377  
 R;Komori, Y.; Sugihara, H.  
 Int. J. Biochem. 22, 767-771, 1990  
 A;Title: Characterization of a new inhibitor for angiotensin converting enzyme from the  
 A;Reference number: A60377; MUID:90382616; PMID:2169439  
 A;Accession: A60377  
 A;Molecule type: protein  
 A;Residues: 1-10 <KOW>  
 C;Superfamily: bradykinin-potentiating peptide  
 C;Keywords: angiotensin-converting enzyme inhibitor; pyroglutamic acid  
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 28.6%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7  
 ||  
 Db 9 PP 10

## RESULT 73

RHAQ1  
 gonadoliberin I - American alligator  
 N;Alternate names: gonadotropin-releasing hormone I  
 C;Species: Alligator mississippiensis (American alligator)  
 C;Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 18-Mar-1997  
 C;Accession: A60066  
 R;Lovejoy, D.A.; Fischer, W.H.; Parker, D.B.; McRory, J.E.; Park, M.; Lance, V.; Swanson  
 Regul. Pept. 33, 105-116, 1991  
 A;Title: Primary structure of two forms of gonadotropin-releasing hormone from brains of  
 A;Reference number: A60066; MUID:91352338; PMID:1882082  
 A;Accession: A60066  
 A;Molecule type: protein  
 A;Residues: 1-10 <LOV>  
 C;Superfamily: gonadoliberin  
 C;Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid  
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F;10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 28.6%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6  
 ||  
 Db 8 QP 9

## RESULT 74

SPPGNK  
 neuromedin K - pig  
 C;Species: Sus scrofa domestica (domestic pig)  
 C;Date: 19-Feb-1984 #sequence\_revision 19-Feb-1984 #text\_change 23-Aug-1996  
 C;Accession: A01560  
 R;Kangawa, K.; Minamino, N.; Fukuda, A.; Matsuo, H.  
 Biochem. Biophys. Res. Commun. 114, 533-540, 1983  
 A;Title: Neuromedin K: a novel mammalian tachykinin identified in porcine spinal cord.  
 A;Reference number: A01560; MUID:83282812; PMID:6576785  
 A;Accession: A01560  
 A;Molecule type: protein  
 A;Residues: 1-10 <KAN>  
 A;Note: the structure of the peptide was confirmed by synthesis  
 C;Comment: The biological source of this peptide is spinal cord. It stimulates smooth mu  
 C;Superfamily: neurokinin B precursor  
 C;Keywords: amidated carboxyl end; hormone; spinal cord  
 F;10/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 28.6%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MH 4  
 ||  
 Db 2 MH 3

## RESULT 75

JC1367  
 thyroliberin potentiating neuropeptide - bovine  
 N;Alternate names: thyrotropin-releasing hormone potentiating peptide; TRH-potentiati  
 C;Species: Bos primigenius taurus (cattle)  
 C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 13-Mar-1997  
 C;Accession: JC1367  
 R;Bulant, M.; Ladram, A.; Montagne, J.J.; Delfour, A.; Nicolas, P.  
 Biochem. Biophys. Res. Commun. 189, 1110-1118, 1992  
 A;Title: Isolation and amino acid sequence of the TRH-potentiating peptide from bovin  
 A;Reference number: JC1367; MUID:93111999; PMID:1472021  
 A;Accession: JC1367  
 A;Molecule type: protein  
 A;Residues: 1-10 <BUL>  
 A;Experimental source: hypothalamus  
 C;Comment: This neuropeptide corresponds to a region of the rat thyroliberin precurs  
 C;Function:  
 A;Description: potentiates thyroliberin-induced thyrotropin secretion  
 C;Superfamily: thyroliberin precursor  
 C;Keywords: hypothalamus; neuropeptide

Query Match 28.6%; Score 2; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WM 3  
 ||  
 Db 4 WM 5

Search completed: November 25, 2003, 19:36:09  
 Job time : 4.80233 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:17:40 ; Search time 2.48256 Seconds  
(without alignments)  
132.600 Million cell updates/sec

Title: US-09-641-801-24

Perfect score: 7

Sequence: 1 SWHQPP 7

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	42.9	11	1	MORN HUMAN
2	3	42.9	20	1	OAR PHOPV
3	2	28.6	4	1	OCF3 OCTMI
4	2	28.6	6	1	EIO1_LITRU
5	2	28.6	6	1	LCK1_LOCMI
6	2	28.6	7	1	LANC_CARUI
7	2	28.6	7	1	TPFY_PACDA
8	2	28.6	7	1	UF04_MOUSE
9	2	28.6	8	1	AKH_LIBAU
10	2	28.6	8	1	ALL5_CALVO
11	2	28.6	8	1	CKKN_WACEU
12	2	28.6	8	1	LCK1_LEUMA
13	2	28.6	8	1	LCK2_LEUMA
14	2	28.6	8	1	LCK3_LEUMA
15	2	28.6	8	1	LCK4_LEUMA
16	2	28.6	8	1	LCK5_LEUMA
17	2	28.6	8	1	LCK6_LEUMA
18	2	28.6	8	1	LCK7_LEUMA
19	2	28.6	8	1	LCK8_LEUMA
20	2	28.6	8	1	NPB_BOVIN
21	2	28.6	8	1	PPK2_PERAM
22	2	28.6	9	1	ALI0_CARMA
23	2	28.6	9	1	COXE_THUOB
24	2	28.6	9	1	FAR3_PENMO
25	2	28.6	9	1	FAR4_PENMO
26	2	28.6	9	1	FRF1_SARBU
27	2	28.6	9	1	KNL3_BOMVA
28	2	28.6	9	1	LMT3_LOCOMI
29	2	28.6	9	1	RT33_BOVIN
30	2	28.6	9	1	YBFR_AZOVI
31	2	28.6	10	1	AH3_PRUSE
32	2	28.6	10	1	BPP2_BOTIN
33	2	28.6	10	1	BPP2_BOTJA
34	2	28.6	10	1	BPP8_BOTIN
35	2	28.6	10	1	BPP_VIPAS
36	2	28.6	10	1	BRK_ONCMY
37	2	28.6	10	1	CAER_LITXA
38	2	28.6	10	1	COXM_RAT
39	2	28.6	10	1	FAR6_PANRE
40	2	28.6	10	1	GON1_ALLMI
41	2	28.6	10	1	TKNK_PIG
42	2	28.6	10	1	TMOF_AEDAE
43	2	28.6	10	1	UPA2_HUMAN
44	2	28.6	10	1	UPA5_HUMAN
45	2	28.6	10	1	URE3_MORMO
46	2	28.6	11	1	ASL1_BACSE
47	2	28.6	11	1	BPP3_BOTIN
48	2	28.6	11	1	BPP4_BOTIN
49	2	28.6	11	1	BPPB_AGRHA
50	2	28.6	11	1	BPP_AGRHP
51	2	28.6	11	1	BRK_MEGFL
52	2	28.6	11	1	CA31_LITCI
53	2	28.6	11	1	CEP1_ACHFU
54	2	28.6	11	1	LADD_ONCMY
55	2	28.6	11	1	TKN1_PSEGU
56	2	28.6	11	1	TKN1_UPERU
57	2	28.6	11	1	TKN2_PSEGU
58	2	28.6	11	1	TKN3_PSEGU
59	2	28.6	11	1	TKN4_PSEGU
60	2	28.6	11	1	TKN5_PSEGU
61	2	28.6	11	1	TKNA_ONCMY
62	2	28.6	11	1	TKN_ELENO
63	2	28.6	12	1	FAR7_PENMO
64	2	28.6	12	1	FAR1_CALVO
65	2	28.6	12	1	FIF1_SARBU
66	2	28.6	12	1	HS9A_RAT
67	2	28.6	12	1	TKN2_KASMA
68	2	28.6	13	1	ACT7_SOYEN
69	2	28.6	13	1	AH4_PRUSE
70	2	28.6	13	1	BPP1_BOTJA
71	2	28.6	13	1	BRK_FARID
72	2	28.6	13	1	EI22_LITRU
73	2	28.6	13	1	EP65_HUMAN
74	2	28.6	13	1	LMT4_LOCOMI
75	2	28.6	13	1	ME1_MICOC
76	2	28.6	13	1	TV13_PHYRO
77	2	28.6	14	1	MARI_ALTRSP
78	2	28.6	14	1	MAST_VESBA
79	2	28.6	14	1	PH1_PRUSE
80	2	28.6	14	1	TAT_HV1W2
81	2	28.6	14	1	TAT_HV1W2
82	2	28.6	15	1	AF1L_MALPA
83	2	28.6	15	1	AH2_PRUSE
84	2	28.6	15	1	CH1L_PEA
85	2	28.6	15	1	CXA2_CONAL
86	2	28.6	15	1	FKB7_PINPS
87	2	28.6	15	1	IRBP_CRISP
88	2	28.6	15	1	MK1_PALPR
89	2	28.6	15	1	NUO8_SOLITU
90	2	28.6	15	1	PH3_PRUSE
91	2	28.6	15	1	PRP_MYCBO
92	2	28.6	15	1	RES_PHYPA
93	2	28.6	15	1	SODM_STRGR
94	2	28.6	15	1	UC06_MAIZE
95	2	28.6	15	1	UC19_MAIZE
96	2	28.6	15	1	UE15_HORVU
97	2	28.6	15	1	UN01_PINPS
98	2	28.6	15	1	UP01_METAN
99	2	28.6	15	1	URE2_MORMO
100	2	28.6	16	1	AF1S_MALPA

## ALIGNMENTS

RESULT 1

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MORN HUMAN
ID MORN HUMAN STANDARD; PRT; 11 AA.
AC P01163;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Morphogenetic neuroepitide (Head activator) (HA).
OS Homo sapiens (Human),
OS Rattus norvegicus (Rat),
OS Bos taurus (Bovine),
OS Anthopleura elegantissima (Sea anemone), and
OS Hydra attenuata (Hydra) (Hydra vulgaris).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606, 10116, 9913, 6110, 6087;
RN [1]
RP SEQUENCE.
RC SPECIES=Human, Rat, and Bovine;
RX MEDLINE=82035850; PubMed=7230191;
RA Bodenmuller H., Schaller H.C.;
RT "Conserved amino acid sequence of a neuroepitide, the head activator,
RT from coelenterates to humans.";
RL Nature 293:579-580(1981).
RN [2]
RP SEQUENCE.
RC SPECIES=A.elegantissima, and H.attenuata;
RA Schaller H.C., Bodenmuller H.;
RT "Isolation and amino acid sequence of a morphogenetic peptide from
RT hydra.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7000-7004(1981).
RN [3]
RP SYNTHESIS.
RX MEDLINE=82050803; PubMed=7297679;
RA Birr C., Zachmann B., Bodenmuller H., Schaller H.C.;
RT "Synthesis of a new neuroepitide, the head activator from hydra.";
RL FEBS Lett. 131:317-321(1981).
RN [4]
RP FUNCTION.
RX MEDLINE=90059923; PubMed=2583101;
RA Schaller H.C., Druffel-Augustin S., Dubel S.;
RT "Head activator acts as an autocrine growth factor for NIH5-CA2 cells
RT in the G2/mitosis transition.";
RL EMBO J. 8:3311-3318(1989).
CC -!- FUNCTION: HA ACTS AS AN AUTOCRINE GROWTH FACTOR FOR NEURAL CELLS
CC IN THE G2/MITOSIS TRANSITION.
CC -!- CAUTION: THIS PEPTIDE WAS FIRST ISOLATED FROM NERVE CELLS OF HYDRA
CC AND WAS CALLED HEAD ACTIVATOR BY THE AUTHORS, BECAUSE IT INDUCED
CC HEAD-SPECIFIC GROWTH AND DIFFERENTIATION IN THIS ANIMAL. IT HAS
CC BEEN FOUND IN MAMMALIAN INTESTINE AND HYPOTHALAMUS.
DR PIR; A01427; YHRT.
DR PIR; A93900; YHXA.
DR PIR; B01427; YHHA.
DR PIR; B93900; YHJFY.
DR PIR; C01427; YHBO.
DR GK; P01163; -.
KW Growth factor; Cell cycle; Mitosis; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1142 MW; 37927417C3258878 CRC64;

Query Match 42.9%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
DB 1 QPP 3

RESULT 2
ID_OAR_PHOPY STANDARD; PRT; 20 AA.
AC P14803;
DT 01-APR-1990 (Rel. 14, Created)

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DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Octopamine receptor (Octopamine binding protein) (Fragment).
OC Photinus pyralis (North American firefly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Caenarthrozoa; Coleoptera; Polyphaga; Elateriformia;
OX NCBI_TaxID=7054;
RN [1]
RP SEQUENCE.
RC TISSUE=Light organ;
RX MEDLINE=90092510; PubMed=2513233;
RA Nathanson J.A., Kantham L., Hunnicutt E.J.;
RT "Isolation and N-terminal amino acid sequence of an octopamine ligand
RT binding protein.";
RL FEBS Lett. 259:117-120(1989).
CC -!- FUNCTION: PUTATIVE RECEPTOR FOR OCTOPAMINE. OCTOPAMINE (OA) IS A
CC NEUROTRANSMITTER, NEUROHORMONE, AND NEUROMODULATOR IN
CC INVERTEBRATES. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G
CC PROTEINS WHICH ACTIVATE ADENYL CYCLASE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR PIR; S28779; S28779.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; PARTIAL.
KW G-protein coupled receptor.
FT UNSURE 2 2
FT UNSURE 9 9
FT UNSURE 19 19
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2500 MW; ACBC81A11BB8D4AB CRC64;

Query Match 42.9%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHQ 5
DB 18 MHQ 20

RESULT 3
ID_OCP3_OCTMI STANDARD; PRT; 4 AA.
AC P58649;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cardioactive peptides Ocp-3/Ocp-4.
OS Octopus minor (Octopus).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
OX NCBI_TaxID=89766;
RN [1]
RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
RC TISSUE=Brain;
RX MEDLINE=20336815; PubMed=10876044;
RA Iwakoshi E., Hisada M., Minakata H.;
RT "Cardioactive peptides isolated from the brain of a Japanese octopus,
RT Octopus minor.";
RL Peptides 21:623-630(2000).
CC -!- FUNCTION: Cardioactive; has both positive chronotropic and
CC inotropic effects on the heart. Ocp-4 is a 1000 time less
CC active than Ocp-3.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: Ocp-4 has D-Ser instead of L-Ser.
CC -!- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.
KW Hormone; D-amino acid.
FT MOD RES 2 2 D-SERINE (IN OCP-4).
SQ SEQUENCE 4 AA; 463 MW; 6AB365B810000000 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;

```

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 28.6%; Score 2; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2  
||  
Db 4 SW 5

## RESULT 6

LANC\_CARUI STANDARD; PRT; 7 AA.  
ID LANC\_CARUI  
AC P36960;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Lantibiotic carnocin UI49 (Fragment).  
OS Carnobacterium sp. (strain UI49).  
OC Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;  
OC Carnobacterium.  
OX NCBI\_TaxID=35782;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92321768; PubMed=1622206;  
RA Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,  
RA Nes I.P.;  
RT "Purification and characterization of a new bacteriocin isolated from  
RT a Carnobacterium sp.";  
RL Appl. Environ. Microbiol. 58:1417-1422(1992).  
CC -!- FUNCTION: LANTHIONINE-CONTAINING PEPTIDE ANTIBIOTIC (LANTIBIOTIC).  
CC ACTIVE ON GRAM-POSITIVE BACTERIA.  
KW Antibiotic; Bacteriocin; Lantibiotic.  
FT NON TER 7  
SQ SEQUENCE 7 AA; 786 MW; 741776D05B05B810 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6  
||  
Db 5 QP 6

## RESULT 7

TPFY\_PACDA STANDARD; PRT; 7 AA.  
ID TPFY\_PACDA  
AC P83455;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE tryptophyllin-1 (pdt-1).  
OS Pachymedusa dactinolor (Giant mexican leaf frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
OC Phyllomedusinae; Pachymedusa.  
OX NCBI\_TaxID=75988;  
RN [1]  
RP SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF  
RP PRO-7.  
RC TISSUE=Skin secretion;  
RA Chen T.B., Orr D.F., Shaw C.;  
RT "Pachymedusa dactinolor tryptophyllin-1 (pdt-1): structural  
RT characterization, pharmacological activity and cloning of precursor  
RT cDNA.";  
RL Submitted (SEP-2002) to the SWISS-PROT data bank.  
CC -!- FUNCTION: Myoactive. Has selective relaxing activity on vascular  
CC smooth muscle.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
CC -!- MASS SPECTROMETRY: MW=809.2; METHOD=WALDI.  
DR GO; GO:0005576; C:extracellular; NAS.

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 28.6%; Score 2; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2  
||  
Db 4 SW 5

## RESULT 4

EIO1\_LITRU STANDARD; PRT; 6 AA.  
ID EIO1\_LITRU  
AC P82036;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Electrin 1.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
OC Pelodyadinae; Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
RT "Peptides from the skin glands of the Australian buzzing tree frog  
RT Litoria electrica. Comparison with the skin peptides from Litoria  
RT rubella.";  
RL Aust. J. Chem. 52:639-645(1999).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
KW Amphibian defense peptide; Amidation.  
FT MOD RES 6  
SQ SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WM 3  
||  
Db 5 WM 6

## RESULT 5

LOK1\_LOCM1 STANDARD; PRT; 6 AA.  
ID LOK1\_LOCM1  
AC P41431;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Locustakinin I.  
OS Locusta migratoria (Migratory locust).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;  
OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
OX NCBI\_TaxID=7004;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Corpora cardiaca;  
RX MEDLINE=92262851; PubMed=1585017;  
RA Schoofs L., Holman G.M., Proost P., van Damme J., Hayes T.K.,  
RA de Loof A.;  
RT "Locustakinin, a novel myotropic peptide from Locusta migratoria,  
RT isolation, primary structure and synthesis.";  
RL Regul. Pept. 37:149-157(1992).  
CC -!- FUNCTION: Myotropic peptide. May be important in the stimulation  
CC of ion transport and inhibition of diuretic activity in Malpighian  
CC tubules.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
DR PIR; A61068.  
KW Neuropeptide; Amidation.  
FT MOD RES 6  
SQ SEQUENCE 6 AA; 654 MW; 686365A5B9CDB000 CRC64;

DR GO; GO:0045986; P:negative regulation of smooth muscle contra. . .; NAS.  
 KW Amphibian defense peptide; Amidation; Hydroxylation.  
 FT MOD RES 3 3  
 FT MOD RES 7 7  
 FT MOD RES 7 7  
 SQ SEQUENCE 7 AA; 794 MW; 7772D37DC776350 CRC64;  
 Query Match 28.6%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred.No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 pp 7  
 ||  
 Db 2 pp 3

RESULT 8  
 UF04\_MOUSE  
 ID \_UF04\_MOUSE STANDARD; PRT; 7 AA.  
 AC P38642;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 01-FEB-1995 (Rel. 31, Last annotation update)  
 DE Unknown protein from 2D-page of fibroblasts (P46) (Fragment).  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Fibroblast; PubMed=7523108;  
 RX MEDLINE=95009907; Wichter L.L., He C., Selkirk J.K.;  
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;  
 RT "Separation and sequencing of familial and novel murine proteins  
 using preparative two-dimensional gel electrophoresis.";  
 RL Electrophoresis 15:735-745(1994).  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 5.0, ITS MW IS: 46 kDa.  
 CC NON TER 7  
 FT SEQUENCE 7 AA; 766 MW; 68640AB777632700 CRC64;  
 SQ SEQUENCE 7 AA; 766 MW; 68640AB777632700 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred.No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 pp 7  
 ||  
 Db 3 pp 4

RESULT 9  
 AKH\_LIBAU  
 ID \_AKH\_LIBAU STANDARD; PRT; 8 AA.  
 AC P25418;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Adipokinetic hormone (AKH).  
 OS Libellula auripennis (Skimmer dragonfly).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Palaeoptera; Odonata; Anisoptera; Libellulidae; Libellula.  
 OX NCBI\_TaxID=6966;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Corpora cardiaca;  
 RX MEDLINE=90359055; PubMed=2390213;  
 RA Gaede G.;  
 RT "The putative ancestral peptide of the adipokinetic/red-pigment-  
 concentrating hormone family isolated and sequenced from a  
 dragonfly.";  
 RT Biol. Chem. Hoppe-Seyler 371:475-483(1990).  
 CC -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA  
 CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF  
 CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT

CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.  
 CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.  
 DR PIR; S10596; S10596.  
 DR InterPro; IPR002047; AKH.  
 DR PROSITE; PS00256; AKH; 1.  
 KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.  
 FT MOD RES 1 1  
 FT MOD RES 8 8  
 FT MOD RES 8 8  
 SQ SEQUENCE 8 AA; 978 MW; 8665A771A9C452D6 CRC64;  
 Query Match 28.6%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred.No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SW 2  
 ||  
 Db 7 SW 8

RESULT 10  
 ALL5\_CALVO  
 ID \_ALL5\_CALVO STANDARD; PRT; 8 AA.  
 AC P41841;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Callatostatin 5 (Met-callatostatin 1) ([Hyp3]Met-callatostatin).  
 OS Calliphora vomitoria (Blue blowfly).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 CC Calliphoridae; Calliphora.  
 OX NCBI\_TaxID=27454;  
 RN [1]  
 RP SEQUENCE.  
 RC MEDLINE=93211980; PubMed=8460157;  
 RX Duve H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.,  
 RA Thorpe A.;  
 RT "Callatostatin: neuropeptides from the blowfly Calliphora vomitoria  
 with sequence homology to cockroach allatostatins.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).  
 RN [2]  
 RP CHARACTERIZATION, AND HYDROXYLATION.  
 RC TISSUE=Head;  
 RX MEDLINE=94342269; PubMed=8063725;  
 RA Duve H., Johnsen A.H., Scott A.G., East P., Thorpe A.;  
 RT "[Hyp3]Met-callatostatin. Identification and biological properties of  
 a novel neuropeptide from the blowfly Calliphora vomitoria.";  
 RL J. Biol. Chem. 269:21059-21066(1994).  
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR AND PLAY  
 CC A ROLE IN THE INTEGRATION OF INFORMATION WITHIN THE BRAIN. MAY BE  
 CC INVOLVED IN THE CONTROL OF VISCERAL MUSCLES DUE TO ITS ABILITY TO  
 CC BEHAVE AS POTENT INHIBITORS OF PERISTALTIC MOVEMENTS. MAY ALSO  
 CC FULFILL A NEUROHORMONAL ROLE ON MUSCLES OF THE GUT AND HEART.  
 CC -!- TISSUE SPECIFICITY: NEURONS WITHIN BRAIN AND ABDOMINAL GANGLION.  
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 DR PIR; E47393; E47393  
 KW Neuropeptide; Amidation; Hydroxylation.  
 FT MOD RES 3 3  
 FT MOD RES 8 8  
 FT MOD RES 8 8  
 SQ SEQUENCE 8 AA; 883 MW; 7D9879CAB8477768 CRC64;  
 Query Match 28.6%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred.No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 pp 7  
 ||  
 Db 2 pp 3

RESULT 11  
 CCKN\_MACEU  
 ID \_CCKN\_MACEU STANDARD; PRT; 8 AA.

AC P30369;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Cholecystokinin (CCK).  
 GN CCK.  
 OS Macropus eugenii (Tamar wallaby), and  
 OS Dasyurus viverrinus (Southeastern quoll).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.  
 OX NCBI\_TaxID=9315, 9279;  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES=M.eugenii, and D.viverrinus;  
 RC TISSUE=Brain;  
 RX MEDLINE=88234141; PubMed=3375140;  
 RA Fan Z.W., Eng J., Shaw G., Yalow R.S.;  
 RT "Cholecystokinin octapeptide purified from brains of Australian  
 marsupials."  
 RL Peptides 9:429-431(1988).  
 CC -!- FUNCTION: THIS PEPTIDE HORMONE INDUCES GALL BLADDER CONTRACTION  
 AND THE RELEASE OF PANCREATIC ENZYMES IN THE GUT. ITS FUNCTION  
 IN THE BRAIN IS NOT CLEAR.  
 CC -!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.  
 DR PIR; A43001; A43001.  
 DR PIR; PQ0012; PQ0012.  
 DR InterPro; IPR001651; Gastrin.  
 DR PROSITE; PS00259; GASTRIN; 1.  
 KW Amidation; Sulfation; Hormone.  
 FT MOD\_RES 2 2 SULFATION.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 1064 MW; DDCAA68378768B5A CRC64;  
 Query Match 28.6%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 WM 3  
 DB 5 WM 6

RESULT 12  
 LCK1\_LEUMA  
 ID LCK1\_LEUMA STANDARD; PRT; 8 AA.  
 AC P21140;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 01-MAY-1991 (Rel. 18, Last annotation update)  
 DE Leucokinin I (L-I).  
 OS Leucophaea maderae (Madeira cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;  
 OC Blaberidae; Leucophaea.  
 OX NCBI\_TaxID=6988;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Head;  
 RA Holman G.M., Cook B.J., Nachman R.J.;  
 RT "Isolation, primary structure and synthesis of two neuropeptides  
 from Leucophaea maderae: members of a new family of  
 Cephalomyotropins."  
 RL Comp. Biochem. Physiol. 84C:205-211(1986).  
 CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE  
 ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).  
 CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 893 MW; DC635B449CDC76A CRC64;  
 Query Match 28.6%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WM 3  
 DB 5 WM 6

RESULT 13  
 LCK2\_LEUMA  
 ID LCK2\_LEUMA STANDARD; PRT; 8 AA.  
 AC P21141;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 01-MAY-1991 (Rel. 18, Last annotation update)  
 DE Leucokinin II (L-II).  
 OS Leucophaea maderae (Madeira cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;  
 OC Blaberidae; Leucophaea.  
 OX NCBI\_TaxID=6988;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Head;  
 RA Holman G.M., Cook B.J., Nachman R.J.;  
 RT "Isolation, primary structure and synthesis of two neuropeptides  
 from Leucophaea maderae: members of a new family of  
 Cephalomyotropins."  
 RL Comp. Biochem. Physiol. 84C:205-211(1986).  
 CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE  
 ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).  
 CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 852 MW; DC6365A5B9C8676A CRC64;  
 Query Match 28.6%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2  
 DB 6 SW 7

RESULT 14  
 LCK3\_LEUMA  
 ID LCK3\_LEUMA STANDARD; PRT; 8 AA.  
 AC P21142;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 01-MAY-1991 (Rel. 18, Last annotation update)  
 DE Leucokinin III (L-III).  
 OS Leucophaea maderae (Madeira cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;  
 OC Blaberidae; Leucophaea.  
 OX NCBI\_TaxID=6988;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Head;  
 RA Holman G.M., Cook B.J., Nachman R.J.;  
 RT "Primary structure and synthesis of two additional neuropeptides  
 from Leucophaea maderae: members of a new family of  
 Cephalomyotropins."  
 RL Comp. Biochem. Physiol. 84C:271-276(1986).  
 CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE  
 ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).  
 CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 910 MW; DC6365B449C866DA CRC64;  
 Query Match 28.6%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SW 2  
 ||  
 6 SW 7

RESULT 15  
 LCK4 LEUMA  
 ID LCK4 LEUMA STANDARD; PRT; 8 AA.  
 AC P21143;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 01-MAY-1991 (Rel. 18, Last annotation update)  
 DE Leucokinin IV (L-IV).  
 OS Leucophaea maderae (Madeira cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;  
 OC Blaberoidea; Leucophaea.  
 OX NCBI\_TaxID=6988;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE-Head;  
 RA Holman G.M., Cook B.J., Nachman R.J.;  
 RT "Primary structure and synthesis of two additional neuropeptides  
 from Leucophaea maderae: members of a new family of  
 Cephalomyotropins.";  
 RL Comp. Biochem. Physiol. 84C:271-276(1986).  
 CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE  
 ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).  
 CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.  
 CC Neuropeptide; Amidation.  
 KW MOD RES 8 8  
 FT MOD RES 8 8  
 SQ SEQUENCE 8 AA; 906 MW; DC6365B1E9D5BDDA CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2  
 ||  
 6 SW 7

RESULT 16  
 LCK5 LEUMA  
 ID LCK5 LEUMA STANDARD; PRT; 8 AA.  
 AC P19987;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Leucokinin V (L-V).  
 OS Leucophaea maderae (Madeira cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;  
 OC Blaberoidea; Leucophaea.  
 OX NCBI\_TaxID=6988;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE-Head;  
 RX MEDLINE=87052651; PubMed-2877794;  
 RA Holman G.M., Cook B.J., Nachman R.J.;  
 RT "Isolation, primary structure, and synthesis of leucokinin V and VI:  
 myotropic peptides of Leucophaea maderae.";  
 RL Comp. Biochem. Physiol. 88C:27-30(1987).  
 CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE  
 ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).  
 CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.  
 CC Neuropeptide; Amidation.  
 DR PIR; JS0315; JS0315.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 8 8  
 SQ SEQUENCE 8 AA; 784 MW; 736365A5B9C865B8 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2  
 ||  
 6 SW 7

RESULT 17  
 LCK6 LEUMA  
 ID LCK6 LEUMA STANDARD; PRT; 8 AA.  
 AC P19988;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Leucokinin VI (L-VI).  
 OS Leucophaea maderae (Madeira cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;  
 OC Blaberoidea; Leucophaea.  
 OX NCBI\_TaxID=6988;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE-Head;  
 RX MEDLINE=87052651; PubMed-2877794;  
 RA Holman G.M., Cook B.J., Nachman R.J.;  
 RT "Isolation, primary structure, and synthesis of leucokinin V and VI:  
 myotropic peptides of Leucophaea maderae.";  
 RL Comp. Biochem. Physiol. 88C:27-30(1987).  
 CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE  
 ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).  
 CC -!- SIMILARITY: TO THE OTHER LEUCOKININS, AND TO MANDUCA SEXTA AND  
 HELIOTHIS ZEA ADIPOKINETIC HORMONE.  
 CC PIR; JS0316; JS0316.  
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.  
 FT MOD RES 1 1  
 FT MOD RES 8 8  
 SQ SEQUENCE 8 AA; 935 MW; 9D6365B1E9D5A5A6 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2  
 ||  
 6 SW 7

RESULT 18  
 LCK7 LEUMA  
 ID LCK7 LEUMA STANDARD; PRT; 8 AA.  
 AC P19989;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 01-FEB-1991 (Rel. 17, Last annotation update)  
 DE Leucokinin VII (L-VII).  
 OS Leucophaea maderae (Madeira cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;  
 OC Blaberoidea; Leucophaea.  
 OX NCBI\_TaxID=6988;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE-Head;  
 RA Holman G.M., Cook B.J., Nachman R.J.;  
 RT "Isolation, primary structure and synthesis of leucokinin VII and  
 VIII: the final members of this new family of cephalomyotropic  
 peptides isolated from head extracts of Leucophaea maderae.";  
 RL Comp. Biochem. Physiol. 88C:31-34(1987).  
 CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE  
 ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).  
 CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.



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DR PIR; JS0317; JS0317.
KW Neuropeptide; Amidation.
FT MOD RES 8
SQ SEQUENCE 8 AA; 866 MW; DC6365A5B9CDD76A CRC64;
    Query Match 28.6%; Score 2; DB 1; Length 8;
    Best Local Similarity 100.0%; Pred. No. 1.3e+05;
    Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SW 2
   ||
Db 6 SW 7

RESULT 19
LCK8 LEUMA STANDARD; PRT; 8 AA.
AC P1990;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Leucokinin VIII (L-VIII).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of leucokinin VII and
RT VIII: the final members of this new family of cephalomyotropic
RT peptides isolated from head extracts of Leucophaea maderae.";
RL Comp. Biochem. Physiol. 88C:31-34(1987).
CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.
DR PIR; JS0318; JS0318.
KW Neuropeptide; Amidation.
FT MOD RES 8
SQ SEQUENCE 8 AA; 902 MW; 736365AB59CAADD8 CRC64;
    Query Match 28.6%; Score 2; DB 1; Length 8;
    Best Local Similarity 100.0%; Pred. No. 1.3e+05;
    Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SW 2
   ||
Db 6 SW 7

RESULT 20
NPB BOVIN STANDARD; PRT; 8 AA.
AC P15507;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuropeptide B.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=86067985; PubMed=3865193;
RA Yang H.-Y.T., Fratta W., Majane E.A., Costa E.;
RT "Isolation, sequencing, synthesis, and pharmacological
RT characterization of two brain neuropeptides that modulate the action
RT of morphine.";
DR Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).
CC -1- FUNCTION: MODULATES THE ACTION OF MORPHINE.
DR PIR; B24749; B24749.
KW Neuropeptide; Amidation.
FT MOD RES 8
SQ SEQUENCE 8 AA; 1082 MW; 87D416C76D9C729 CRC64;
    Query Match 28.6%; Score 2; DB 1; Length 8;
    Best Local Similarity 100.0%; Pred. No. 1.3e+05;
    Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 QP 6
   ||
Db 4 QP 5

RESULT 21
PPK2 PERAM STANDARD; PRT; 8 AA.
AC P82692;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokiniin-2 (Pea-PK-2) (FXPRL-amide).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=97353923; PubMed=9210163;
RA Predel R., Kellner R., Kaufmann R., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of two pyrokiniins from the
RT retrocerebral complex of the American cockroach.";
RL Peptides 18:473-478(1997).
RN [2]
RP TISSUE SPECIFICITY.
RX MEDLINE=20189894; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Tagma-specific distribution of FXPRLamides in the nervous system of
RT the American cockroach.";
RL J. Comp. Neurol. 419:352-363(2000).
CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -1- TISSUE SPECIFICITY: CORPORA CARDIACA.
CC -1- MASS SPECTROMETRY: MW=883; METHOD=MALDI.
CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR InterPro; IPR001484; Pyrokiniin.
DR PROSITE; PS00539; PYROKININ; FALSE_NEG.
KW Neuropeptide; Amidation; Pyrokiniin.
FT MOD RES 8
SQ SEQUENCE 8 AA; 884 MW; C634176DD9D7775 CRC64;
    Query Match 28.6%; Score 2; DB 1; Length 8;
    Best Local Similarity 100.0%; Pred. No. 1.3e+05;
    Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 PP 7
   ||
Db 2 PP 3

RESULT 22
AL10 CARMA STANDARD; PRT; 9 AA.
AC P81813;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 10.
OS Carcinus maenas (Common shore crab) (Green crab).

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OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734 (1997).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 9 9
FT SEQUENCE 9 AA; 963 MW; 372D79DCB4776C7 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
DB 3 QP 4

RESULT 23
COXE THUOB
ID COXE THUOB STANDARD; PRT; 9 AA.
AC P80975;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Cytochrome c oxidase polypeptide Via (EC 1.9.3.1) (Fragment).
OS Thunnus obesus (Bigeye tuna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8241;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=97454291; PubMed=9310366;
RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
RA Kadenbach B.;
RT "The subunit structure of cytochrome-c oxidase from tuna heart and
RT liver.";
RL Eur. J. Biochem. 248:99-103 (1997).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE. THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIA FAMILY.
DR PIR; S77984; S77984.
DR InterPro; IPR001349; COX6A.
DR PROSITE; PS01329; COX6A; PARTIAL.
KW Oxidoreductase; Inner membrane; Mitochondrion.
FT NON_TER 1 1
FT NON_TER 9 9
FT SEQUENCE 9 AA; 1136 MW; 62E072C9CB0776DB CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
DB 3 QP 4

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RESULT 24
FAR3 PENMO STANDARD; PRT; 9 AA.
ID FAR3 PENMO STANDARD; PRT; 9 AA.
AC P83318;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLP3 (AQPSMRLRF-amide).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupuem J., Krungkasem C., Longyant S.,
RA Chaivuthangkura P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Penaeus monodon.";
RL Comp. Biochem. Physiol. 131B:325-337 (2002).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1121.2; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 9 9
FT SEQUENCE 9 AA; 1105 MW; CCD107340685A776 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
DB 2 QP 3

RESULT 25
FAR4 PENMO STANDARD; PRT; 9 AA.
ID FAR4 PENMO STANDARD; PRT; 9 AA.
AC P83319;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLP4 (SQPSMRLRF-amide).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupuem J., Krungkasem C., Longyant S.,
RA Chaivuthangkura P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Penaeus monodon.";
RL Comp. Biochem. Physiol. 131B:325-337 (2002).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1119.8; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 9 9
FT SEQUENCE 9 AA; 1121 MW; DA0E07340685A776 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;

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Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QP 6

Db 2 QP 3

# RESULT 26

FRF1\_SARBU STANDARD; PRT; 9 AA.  
AC P83350;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Neb-FMRamide 1.  
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Sarcophagidae; Sarcophaga.  
OX NCBI\_TaxID=7385;  
[1]

SEQUENCE, AMIDATION, AND FUNCTION.

TISSUE=CNS;  
MEDLINE=22342733; PubMed=12438685;  
RA Meusen T., Mertens I., Clynen E., Baggerman G., Nichols R.,  
RA Nachman R.J., Huybrechts R., De Loof A., Schoofs L.;  
RT "Identification in *Drosophila melanogaster* of the invertebrate G  
protein-coupled FMRamide receptor."  
Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).  
RL

CC -!- FUNCTION: Has modulatory actions at skeletal neuromuscular  
junctions.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)  
FAMILY.

KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.

FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD\_RES 9 9 AMIDATION.

SQ SEQUENCE 9 AA; 1155 MW; 2D81069CAB6C5A7 CRC64;

Query Match

Best Local Similarity 28.6%; Score 2; DB 1; Length 9;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QP 6

Db 1 QP 2

# RESULT 27

KNL3\_BOMVA STANDARD; PRT; 9 AA.  
AC P83058;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE [Thr6]bradykinin.  
OS Bombina variegata (Yellow-bellied toad).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.  
OX NCBI\_TaxID=8348;  
[1]

SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.

TISSUE=Skin secretion;

RA Chen T.B., Orr D.F., Bjourson A.J., McClean S., Rao P.F., Shaw C.;

RT "Cloning and post-translational processing of frog skin kininogens.;"

RL Submitted (JUL-2001) to the SWISS-PROT data bank.

CC -!- FUNCTION: [Thr6]bradykinin produces in vitro relaxation of rat

arterial smooth muscle and constriction of intestinal smooth

muscle.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Skin.

CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.

KW Amphibian defense peptide; Vasodilator; Bradykinin.

SQ SEQUENCE 9 AA; 1074 MW; 3393D771A9C86777 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;

Best Local Similarity 100.0%; Pred.No. 1.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7

Db 2 PP 3

# RESULT 28

LMT3\_LOCMI STANDARD; PRT; 9 AA.

ID LMT3\_LOCMI

AC P41489;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE Locustamyotropin 3 (LOM-MT-3).

OS Locusta migratoria (Migratory locust).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;

OC Acridoidea; Acrididae; Oedipodinae; Locusta.

OX NCBI\_TaxID=7004;

RN [1]

RP SEQUENCE, AND SYNTHESIS.

RC TISSUE=Brain;

RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kocharsky J.P.,

RA de Loof A.;

RT "Isolation, identification and synthesis of locustamyotropin III and

IV, two additional neuropeptides of *Locusta migratoria*: members of the

locustamyotropin peptide family."

RL Insect Biochem. Mol. Biol. 22:447-452(1992).

CC -!- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY

(MYOTROPIC ACTIVITY).

CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.

DR PIR; A61620; A61620.

DR InterPro; IPR001484; Pyrokinin.

DR PROSITE; PS00539; PYROKININ; 1.

KW Neuropeptide; Amidation; Pyrokinin.

FT MOD\_RES 9 9 AMIDATION.

SQ SEQUENCE 9 AA; 1140 MW; D5AE1772C9D776C6 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;

Best Local Similarity 100.0%; Pred.No. 1.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QP 6

Db 3 QP 4

# RESULT 29

RT33\_BOVIN

ID RT33\_BOVIN

AC P82926;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Mitochondrial 28S ribosomal protein S33 (S33mt) (MRP-S33) (Fragment).

GN MRPS33.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI\_TaxID=9913;

RN [1]

RP SEQUENCE.

RC TISSUE=Liver;

RX MEDLINE=21276436; PubMed=11279123;

RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;

RT "The small subunit of the mammalian mitochondrial ribosome:

identification of the full complement of ribosomal proteins present.;"

```

RL J. Biol. Chem. 276:19363-19374(2001).
CC -!- SUBUNIT: Component of the mitochondrial ribosome small subunit
CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.
CC -!- SUBCELLULAR LOCATION: Mitochondrial.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 1 9
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1032 MW; D341D73776DB05B9 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
Db 5 QP 6

RESULT 30
YBFR_AZOVI
ID YBFR_AZOVI STANDARD; PRT; 9 AA.
AC P25825;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in bfr 3' region (Fragment).
OS Azotobacter vinelandii.
CC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
CC Pseudomonadaceae; Azotobacter.
OX NCBI_TaxID=354;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=921196129; PubMed=1549605;
RA Grossman M.J., Hinton S.M., Minak-Bernero V., Slaughter C.,
RA Stiefel E.I.;
RT "Unification of the ferritin family of proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2419-2423(1992).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M83692; AAA22122.1; --
DR PIR; B41983; B41983.
KW Hypothetical protein.
FT NON_TER 9
FT NON_TER 9
SQ SEQUENCE 9 AA; 947 MW; DF98B5A1B41776D CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
Db 3 PP 4

RESULT 31
AH3_PRUSE
ID AH3_PRUSE STANDARD; PRT; 10 AA.
AC P29261;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Amygdalin beta-glucosidase II (EC 3.2.1.117) (Amygdalin hydrolase
DE isozyme II) (AH II) (Fragment).
OS Prunus serotina (Black cherry).
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

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OX eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=23207;
RN [1]
RP SEQUENCE.
RC TISSUE=Seed;
RA Li C.P., Swain E., Poulton J.E.;
RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase.";
RL Plant Physiol. 100:282-290(1992).
CC -!- CATALYTIC ACTIVITY: (R)-amygdalin + H(2)O = (R)-prunasin + D-
CC Glucose.
CC -!- SUBUNIT: Monomer.
CC -!- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS
CC UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COTYLEDON
CC DEVELOPMENT. THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR
CC EMBRYONAL TISSUES.
CC -!- PTM: GLYCOSYLATED.
KW Glycosidase; Hydrolase; Glycoprotein; Multigene family.
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1033 MW; 3331B8D051E04777 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
Db 3 PP 4

RESULT 32
BPP2_BOTIN
ID BPP2_BOTIN STANDARD; PRT; 10 AA.
AC P30422;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S4,3,1 (10C) (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Lepidosauria; Squamata; Scieroglossa; Serpentes; Colubroidae;
CC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; B37196; B37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1
FT MOD_RES 1
SQ SEQUENCE 10 AA; 1213 MW; 30C53546C761F773 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
Db 9 PP 10

RESULT 33
BPP2_BOTJA
ID BPP2_BOTJA STANDARD; PRT; 10 AA.
AC P01022;

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DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bradykinin-potentiating peptide 10B (Angiotensin-converting enzyme inhibitor V-6-II).  
 DE Bothrops jararaca (Jararaca).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Bothrops.  
 OC NCBI\_TaxID=8724;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom; PubMed=4334402;  
 RX Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R., Kocoy O.;  
 RA "Angiotensin-converting enzyme inhibitors from the venom of Bothrops jararaca. Isolation, elucidation of structure, and synthesis."; Biochemistry 10:4033-4039(1971).  
 RL  
 CC -1- FUNCTION: This peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin by inhibiting the kinases that inactivate it. It acts as an indirect hypotensive agent.  
 CC PIR; A01255; XAVI6B.  
 DR Hypotensive agent; Pyrrolidone carboxylic acid.  
 KW MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT SEQUENCE 10 AA; 1232 MW; 30C53546C77411773 CRC64;  
 SQ  
 Query Match 28.6%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 6 PP 7  
 Db 9 PP 10  
 RESULT 34  
 BPP8\_BOTIN  
 ID BPP8\_BOTIN STANDARD; PRT; 10 AA.  
 AC P30426;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bradykinin-potentiating peptide S5,1 (Angiotensin-converting enzyme inhibitor).  
 DE Bothrops insularis (Island jararaca) (Queimada jararaca).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Bothrops.  
 OC NCBI\_TaxID=8723;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom; PubMed=2386615;  
 RX MEDLINE=90351557; Cintra A.C.O., Vieira C.A., Gigglio J.R.;  
 RA "Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom."; J. Protein Chem. 9:221-227(1990).  
 RL  
 CC -1- FUNCTION: This peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin by inhibiting the kinases that inactivate it. It acts as an indirect hypotensive agent.  
 CC PIR; H37196; H37196.  
 DR Hypotensive agent; Pyrrolidone carboxylic acid.  
 KW MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT SEQUENCE 10 AA; 1173 MW; 2FF835545761FD8 CRC64;  
 SQ  
 Query Match 28.6%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 6 PP 7  
 Db 9 PP 10

Db 9 PP 10  
 RESULT 35  
 BPP\_VIPAS  
 ID BPP\_VIPAS STANDARD; PRT; 10 AA.  
 AC P31351;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bradykinin-potentiating peptide (Angiotensin-converting enzyme inhibitor).  
 DE Vipera aspis (Aspic viper).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Viperinae; Vipera.  
 OC NCBI\_TaxID=8706;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom; PubMed=2169439;  
 RX MEDLINE=90382616; Komori Y., Sugihara H.;  
 RA "Characterization of a new inhibitor for angiotensin converting enzyme from the venom of Vipera aspis aspis."; Int. J. Biochem. 22:767-771(1990).  
 RL  
 CC -1- FUNCTION: This peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin by inhibiting the kinases that inactivate it. It acts as an indirect hypotensive agent.  
 CC PIR; A60377; XASNPC.  
 DR Hypotensive agent; Pyrrolidone carboxylic acid.  
 KW MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT SEQUENCE 10 AA; 1062 MW; 3BA827C327686773 CRC64;  
 SQ  
 Query Match 28.6%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 6 PP 7  
 Db 9 PP 10  
 RESULT 36  
 BRK\_ONCMY  
 ID BRK\_ONCMY STANDARD; PRT; 10 AA.  
 AC Q9PRZ1;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Lysyl-bradykinin-like.  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 OC NCBI\_TaxID=8022;  
 RN [1]  
 RP SEQUENCE.  
 RC MEDLINE=94039817; PubMed=8224232;  
 RX Conlon J.M., Olson K.R.;  
 RA "Purification of a vasoactive peptide related to lysyl-bradykinin from trout plasma."; FEBS Lett. 334:75-78(1993).  
 RL  
 CC -1- FUNCTION: SMOOTH MUSCLE CONTRACTION. PROBABLY PLAYS A ROLE FOR THIS SYSTEM IN CARDIOVASCULAR REGULATION IN FISH.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Plasma.  
 CC -1- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.  
 DR PIR; S39030; S39030.  
 KW Bradykinin; Vasodilator.  
 SQ SEQUENCE 10 AA; 1193 MW; 33C59075A3786777 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7  
 DB 3 PP 4

RESULT 37  
 CAER\_LITXA  
 ID CAER\_LITXA STANDARD; PRT; 10 AA.  
 AC P56264;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Caerulein.  
 OS Litoria xanthomera (Orange-thighed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
 OC Pelodyadinae; Litoria.  
 OC NCBI\_TaxID=79697;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=97374000; PubMed=9230483;  
 RA Steinborner S.T., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.,  
 RA Ramsay S.L.;  
 RT "New caerin antibacterial peptides from the skin glands of the  
 RT Australian tree frog *Litoria xanthomera*.";  
 RL J. Pept. Sci. 3:191-185 (1997).  
 CC -!- FUNCTION: HYPOTENSIVE NEUROPEPTIDE.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.  
 CC -!- MASS SPECTROMETRY: MW=1354; METHOD=FAB.  
 CC -!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.  
 DR InterPro: IPR001651; Gastrin.  
 DR PROSITE: PS00259; GASTRIN; 1.  
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;  
 KW Pyroglutidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 4 4 SULFATION.  
 FT MOD\_RES 10 10 AMIDATION.  
 FT MOD\_RES 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1290 MW; 99DEF3837861BBSA CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WM 3  
 DB 7 WM 8

RESULT 38  
 COXM\_RAT  
 ID COXM\_RAT STANDARD; PRT; 10 AA.  
 AC P80431;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cytochrome c oxidase polypeptide VIIb, mitochondrial (EC 1.9.3.1)  
 DE (Fragment).  
 DE COX7B.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OC NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=Wistar; TISSUE=Liver;  
 RX MEDLINE=95324529; PubMed=7601105;  
 RA Schaeffer H., Noack H., Halangk W., Brandt U., von Jagow G.;

RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and  
 RT amino-terminal sequences suggest identity of the fetal heart and the  
 RT adult liver isoform."  
 RL Eur. J. Biochem. 230:235-241 (1995).  
 CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE  
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN  
 CC MITOCHONDRIAL ELECTRON TRANSPORT.  
 CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome  
 CC c + 2 H(2)O.  
 DR PIR; S65387; S65387.  
 KW Oxidoreductase; Mitochondrion.  
 FT NON\_TER 10  
 SQ SEQUENCE 10 AA; 1210 MW; CFC70EB771A33326 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQ 5  
 DB 2 HQ 3

RESULT 39  
 FAR6\_PANRE  
 ID FAR6\_PANRE STANDARD; PRT; 10 AA.  
 AC P82550;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE FMRFamide-like neuropeptide PF6 (NGAPQPFVRP-amide).  
 OS Panagrellus redivivus.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
 OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.  
 OC NCBI\_TaxID=6233;  
 RN [1]  
 RP SEQUENCE, FUNCTION, AND AMIDATION.  
 RA Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,  
 RA Maule A.G.;  
 RT "Isolation, characterization and pharmacology of FMRFamide-related  
 RT peptides (FaRPs) from free-living nematode, *Panagrellus redivivus*."  
 RL Submitted (JUL-2000) to the SWISS-PROT data bank.  
 CC -!- FUNCTION: MYOACTIVE.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 10 10 AMIDATION.  
 FT MOD\_RES 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1132 MW; CB13E4C9D776C76D CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6  
 DB 5 QP 6

RESULT 40  
 GON1\_ALLMI  
 ID GON1\_ALLMI STANDARD; PRT; 10 AA.  
 AC P37041; P20407;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Gonadoliberin I (Gonadotropin-releasing hormone I) (GnRH-I) (LH-RH I)  
 DE (Luliberin I).  
 OS Alligator mississippiensis (American alligator).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Crocodylidae; Alligatorinae; Alligator.  
 OC NCBI\_TaxID=8496;  
 RN [1]  
 RP SEQUENCE.

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RC TISSUE=Brain;
RX MEDLINE=91352338; PubMed=1892082;
RA Lovejoy D.A., Fischer W.H., Parker D.B., McRory J.E., Park M.,
RA Lance V., Swanson P., Rivier J.B., Sherwood N.M.;
RT "Primary structure of two forms of gonadotropin-releasing hormone
RT from brains of the American alligator (Alligator mississippiensis).";
RL Regul. Pept. 33:105-116(1991).
CC -!- FUNCTION: Stimulates the secretion of gonadotropins.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the GnRH family.
DR PIR; A60066; RHAQ1.
DR InterPro; IPR002012; GnRH.
DR Pfam; PF00446; GnRH; 1.
DR PROSITE; PS00473; GnRH; 1.
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1172 MW; 284B23D7286B45A3 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
DB 8 QP 9

RESULT 41
TKNK_PIG STANDARD; PRT; 10 AA.
AC P01292;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neurokinin B (NKB) (Neuromedin K).
GN TAC3 OR NKNB.
OS Sus scrofa (Pig), and
OS Rana ridibunda (Laughing frog) (Marsh frog).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823, 8406;
RN [1]
RP SEQUENCE.
RC SPECIES=Pig; TISSUE=Spinal cord;
RX MEDLINE=83282812; PubMed=6576785;
RA Kangawa K., Minamino N., Fukuda A., Matsuo H.;
RT "Neuromedin K: a novel mammalian tachykinin identified in porcine
RT spinal cord.";
RL Biochem. Biophys. Res. Commun. 114:533-540(1983).
RN [2]
RP SEQUENCE.
RC SPECIES=R. ridibunda; TISSUE=Brain;
RX MEDLINE=92044543; PubMed=1658233;
RA O'Harcie F., Burcher E., Lovas S., Smith D.D., Vaudry H., Conlon J.M.;
RT "Ranakinin: a novel NK1 tachykinin receptor agonist isolated with
RT neurokinin B from the brain of the frog Rana ridibunda.";
RL J. Neurochem. 57:2086-2091(1991).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; A01560; SPNGNK.
DR InterPro; IPR002040; Tachykinin.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1211 MW; E1FA7C62C9C9CAA1 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;

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Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MH 4
DB 2 MH 3

RESULT 42
TMOF_AEDAE STANDARD; PRT; 10 AA.
AC P19425;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Trypsin-modulating oostatic factor (TMOF) (OOSH).
OS Aedes aegypti (Yellowfever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
OX NCBI_TaxID=7159;
RN [1]
RP SEQUENCE.
RC STRAIN=Vero beach; TISSUE=Ovary;
RX MEDLINE=90367888; PubMed=2394318;
RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
RT "Mosquito oostatic factor: a novel decapeptide modulating
RT trypsin-like enzyme biosynthesis in the midgut.";
RL FASEB J. 4:3015-3020(1990).
RN [2]
RP SEQUENCE.
RC STRAIN=Vero beach; TISSUE=Ovary;
RX MEDLINE=93357794; PubMed=8353526;
RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
RT "Mass spectrometry and characterization of Aedes aegypti trypsin
RT modulating oostatic factor (TMOF) and its analogs.";
RL Insect Biochem. Mol. Biol. 23:703-712(1993).
CC -!- FUNCTION: HAS AN OOSTATIC ACTIVITY. INHIBITS TRYPSIN BIOSYNTHESIS
CC IN THE MIDGUT WHICH INDIRECTLY REDUCES THE VITELLOGENIN
CC CONCENTRATION IN THE HEMOLYPH RESULTING IN INHIBITION OF OOCYTE
CC DEVELOPMENT.
CC -!- DEVELOPMENTAL STAGE: SYNTHESIZED AND RELEASED FROM FOLLICULAR
CC EPITHELIUM 18-24 HRS AFTER A BLOOD MEAL. SYNTHESIS PEAKS AT
CC 36 HRS AND STOPS AT 56 HRS.
DR PIR; A36454; A36454.
KW Hormone.
FT DOMAIN 3 10 POLY-PRO.
FT VARIANT 1 2 YD -> DY (IN TMFO(B)).
SQ SEQUENCE 10 AA; 1047 MW; 236D0A7777776DC7 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
DB 5 PP 6

RESULT 43
UPA2_HUMAN STANDARD; PRT; 10 AA.
AC P30088;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 10) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;

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RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.4, ITS MW IS: 49 kDa.
DR SWISS-2DPAGE; P30088; HUMAN.
FT NON_TER 1 1
FT UNSURE 6 6
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1079 MW; 51AC54AAB77775B7 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
Db 5 PP 6

RESULT 44
UPA5_HUMAN STANDARD; PRT; 10 AA.
ID UPAS_HUMAN STANDARD; PRT; 10 AA.
AC P30091;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 13) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.85, ITS MW IS: 40 kDa.
CC -!- MISCELLANEOUS: THIS SPOT IS ON A POSITION THOUGHT TO BE THAT OF
CC ZN-ALPHA-2 GLYCOPROTEIN, BUT IT DOES NOT CORRESPOND TO THAT
CC PROTEIN.
DR SWISS-2DPAGE; P30091; HUMAN.
FT NON_TER 1 1
FT VARIANT 9 9 G -> Y.
FT NON_TER 10 10 /FTId=VAR_000002.
SQ SEQUENCE 10 AA; 1109 MW; C3DA94C732C32776 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
Db 3 QP 4

RESULT 45
URE3_MORMO STANDARD; PRT; 10 AA.
ID URE3_MORMO STANDARD; PRT; 10 AA.
AC P17339;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Urease gamma subunit (EC 3.5.1.5) (6 kDa subunit) (Urea
DE amidohydrolase) (Fragment).

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GN UREA.
OS Morganella morganii (Proteus morganii).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Morganella.
OX NCBI_TaxID=582;
RN [1]_
RP SEQUENCE.
RX MEDLINE=90264298; PubMed=2345135;
RT Hu L.-T., Nicholson E.B., Jones B.D., Lynch M.J., Mobley H.L.T.;
RT "Morganella morganii urease: purification, characterization, and
RT isolation of gene sequences.";
RL J. Bacteriol. 172:3073-3080(1990).
CC -!- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
CC -!- SUBUNIT: (ALPHA, BETA, GAMMA)(3) (BY SIMILARITY)
CC -!- SIMILARITY: BELONGS TO THE UREASE GAMMA SUBUNIT FAMILY.
DR PIR; C35389; C35389.
KW Hydrolase.
FT NON_TER 10 10
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1171 MW; 4B313BCB077771A7 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
Db 5 PP 6

RESULT 46
ASL1_BACSE STANDARD; PRT; 11 AA.
ID ASL1_BACSE STANDARD; PRT; 11 AA.
AC P83146;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acharan sulfate lyase 1 (EC 4.2.2.-) (Fragment).
OS Bacteroides stercoris.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=46506;
RN [1]_
RP SEQUENCE, FUNCTION, ENZYME REGULATION, AND SUBUNIT.
RC STRAIN=HJ-15;
RX MEDLINE=21223019; PubMed=11322884;
RA Kim B.-T., Hong S.-W., Kim W.-S., Kim Y.S., Kim D.-H.;
RT "Purification and characterization of acharan sulfate lyases, two
RT novel heparinases, from Bacteroides stercoris HJ-15.";
RL Eur. J. Biochem. 268:2635-2641(2001).
CC -!- FUNCTION: Degrades acharan sulfate and, to a lesser extent,
CC heparin and heparan sulfate.
CC -!- ENZYME REGULATION: Inhibited
CC Activated by reducing agents, such as DL-dithiothreitol and 2-
CC mercaptoethanol.
CC -!- SUBUNIT: Monomer.
CC -!- PTM: The N-terminus is blocked.
CC -!- MISCELLANEOUS: Has an isoelectric point of 8.6. Its optimum pH is
CC 7.2 and optimum temperature 45 degrees Celsius.
KW Lyase; Heparin-binding.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1395 MW; 01B2DAA241E865AB CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQ 5
Db 10 HQ 11

RESULT 47

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BPP3_BOTIN
ID _BPP3_BOTIN STANDARD; PRT; 11 AA.
AC P30423;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S4,3,2 (10C) (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; C37196; C37196
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1199 MW; 20B25813C7741777 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7
Db 4 PP 5

RESULT 48
BPP4_BOTIN
ID _BPP4_BOTIN STANDARD; PRT; 11 AA.
AC P30424;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S4,1,2 (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; D37196; D37196
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1143 MW; 20BBF13C7741777 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7
Db 4 PP 5

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Qy 6 PP 7
Db 4 PP 5

RESULT 49
BPPB_AKGHA
ID _BPPB_AKGHA STANDARD; PRT; 11 AA.
AC P01021;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide B (Angiotensin-converting
DE enzyme inhibitor).
OS Agkistrodon halys blomhoffi (Mamushi) (Gloydius blomhoffii).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Agkistrodon.
OX NCBI_TaxID=61300;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Kato H., Suzuki T.;
RT "Amino acid sequence of bradykinin-potentiating peptide isolated from
RT the venom of Agkistrodon halys blomhoffii.";
RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 46:176-181(1970).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; A01254; XASNBA.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1199 MW; 295CBF0627741777 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7
Db 4 PP 5

RESULT 50
BPP_AGKHP
ID _BPP_AGKHP STANDARD; PRT; 11 AA.
AC P04562;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide (Angiotensin-converting
DE enzyme inhibitor).
OS Agkistrodon halys pallas (Chinese water moccasin) (Gloydius halys
OS pallas).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Gloydius.
OX NCBI_TaxID=8714;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=86177022; PubMed=3008123;
RA Chi C.-W., Wang S.-Z., Xu L.-G., Wang M.-Y., Lo S.-S., Huang W.-D.;
RT "Structure-function studies on the bradykinin potentiating peptide
RT from Chinese snake venom (Agkistrodon halys pallas).";
RL Peptides 6 Suppl. 3:339-342(1985).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; JC0002; XAVIBH.

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KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1112 MW; 30BABF1277686777 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 0; Mismatches 0; Gaps 0;

QY 6 PP 7
DB 4 PP 5

RESULT 51
BRK MEGFL
ID BRK MEGFL STANDARD; PRT; 11 AA.
AC P12797;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Megascoliakinin ([Thr6]bradykinin-Lys-Ala) [Contains: Bradykinin-like
DE peptide ([Thr6]bradykinin)].
OS Megascolia flavifrons (Garden dagger wasp) (Solitary wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Scolioidea;
OC Scoliidae; Megascolia.
OX NCBI_TaxID=7437;
RN [1]_
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=87293024; PubMed=3617088;
RA Yasuhara T., Mantel P., Nakajima T., Piek T.;
RT "Two kinins isolated from an extract of the venom reservoirs of the
RT solitary wasp Megascolia flavifrons.";
RL Toxicon 25:527-535(1987).
RN [2]_
RP SEQUENCE.
RC TISSUE=Venom;
RA Nakajima T., Piek T., Yashuara T., Mantel P.;
RT "Two kinins isolated from the venom of Megascolia flavifrons.";
RL Toxicon 26:34-34(1988).
CC -!- FUNCTION: Both proteins have bradykinin-like, although lower
CC activities (e.g. smooth muscle contraction).
CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
DR PIR; B26744; B26744.
KW Bradykinin; Vasodilator.
FT PEPTIDE 1 11 MEGASCOLIAKININ.
FT PEPTIDE 1 9 BRADYKININ-LIKE PEPTIDE.
SQ SEQUENCE 11 AA; 1273 MW; 33867393D771A9C8 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 0; Mismatches 0; Gaps 0;

QY 6 PP 7
DB 2 PP 3

RESULT 52
CA31_LITCI
ID CA31_LITCI STANDARD; PRT; 11 AA.
AC P82089;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Caerulein 3.1/3.1Y4.
OS Litoria citropa (Australian blue mountains tree frog).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=94770;

[1]
RN SEQUENCE, AND MASS SPECTROMETRY.
RP TISSUE=Skin secretion;
RX MEDLINE=20057701; PubMed=10589099;
RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
RT "Caerulein-like peptides from the skin glands of the Australian blue
RT montana tree frog Litoria citropa. Part 1. Sequence determination
RT using electrospray mass spectrometry.";
RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
CC -!- FUNCTION: HYPOTENSIVE NEUROPEPTIDE (PROBABLE).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
CC -!- PTM: Isoform 3.1Y4 differs from isoform 3.1 in not being
CC sulfated.
CC -!- MASS SPECTROMETRY: MW=1407; METHOD=Electrospray.
CC -!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; FALSE NEG.
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
KW Pyrrolidone carboxylic acid. PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 1 1
FT MOD RES 4 4 SULFATION.
FT MOD RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1347 MW; 10DAB7D67861A86B CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WM 3
DB 8 WM 9

RESULT 53
CBP1_ACHFU STANDARD; PRT; 11 AA.
AC P22790;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Cardio-excitatory peptide-1 (ACEP-1).
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]_
RP SEQUENCE.
RC STRAIN=Perussac; TISSUE=Heart atrium;
RX MEDLINE=90211261; PubMed=2322251;
RA Fujimoto K., Ohta N., Yoshida M., Kubota I., Muneoka Y., Kobayashi M.;
RT "A novel cardio-excitatory peptide isolated from the atria of the
RT African giant snail, Achatina fulica.";
RL Biochem. Biophys. Res. Commun. 167:777-783(1990).
CC -!- FUNCTION: POTENTIATES THE BEAT OF THE VENTRICLE, AND HAS ALSO
CC EXCITATORY ACTIONS ON THE PENIS RETRACTOR MUSCLE, THE BUCCAL
CC MUSCLE AND THE IDENTIFIED NEURONS CONTROLLING THE BUCCAL MUSCLE
CC MOVEMENT OF ACHATINA.
CC -!- SIMILARITY: TO POSSIBLE PEPTIDE L5 FROM APLYSIA.
DR PIR; A34662; A34662.
KW Hormone; Amidation.
FT MOD RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1305 MW; 82D6D5B9C7741365 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
DB 4 SW 5

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RESULT 54  
LADD\_ONCMY STANDARD; PRT; 11 AA.  
AC P81018;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Ladderlectin (Fragment).  
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
OX NCBI\_TaxID=8022;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Blood;  
RX MEDLINE=97293418; PubMed=9149391;  
RA Jensen L.E., Thiel S., Petersen T.E., Jensenius J.C.;  
RT "A rainbow trout lectin with multimeric structure.";  
RL Comp. Biochem. Physiol. 116B:385-390(1997).  
CC -|- FUNCTION: LECTIN THAT BINDS SEPHAROSE.  
CC -|- COFACTOR: CALCIUM IS ESSENTIAL FOR SEPHAROSE BINDING.  
CC -|- SUBUNIT: MULTIMERIC.  
KW Lectin; Calcium.  
FT NOV 11 11  
SQ SEQUENCE 11 AA; 1163 MW; 0B26227FF6D45404 CRC64;  
Query Match 28.6%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 6 PP 7  
Db 9 PP 10

RESULT 55  
TKN1\_PSEGU STANDARD; PRT; 11 AA.  
AC P42986;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Kassinin-like peptide K-I (PG-KI).  
OS Pseudophryne guentheri (Guenther's toadlet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;  
OC Myobatrachinae; Pseudophryne.  
OX NCBI\_TaxID=30349;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=90287814; PubMed=2356157;  
RA Sannaco M., Severini C., de Biase D., Barra D., Bossa F.,  
RA Roberts J.D., Melchiorri P., Erspamer V.;  
RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
the Australian frog Pseudophryne guentheri.";  
RL Peptides 11:299-304(1990).  
CC -|- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,  
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND  
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH  
CC MUSCLES.  
CC -|- SUBCELLULAR LOCATION: Secreted.  
CC -|- TISSUE SPECIFICITY: Skin.  
CC -|- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.  
DR InterPro; IPR003580; Protachykinin.  
DR InterPro; IPR002040; Tachykinin.  
DR Pfam; PF02202; Tachykinin; 1.  
DR SMART; SM00203; TK; 1.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Euteleostomi;  
KW Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;  
OX NCBI\_TaxID=30349;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=90287814; PubMed=2356157;  
RA Sannaco M., Severini C., de Biase D., Barra D., Bossa F.,  
RA Roberts J.D., Melchiorri P., Erspamer V.;  
RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
the Australian frog Pseudophryne guentheri.";  
RL Peptides 11:299-304(1990).  
CC -|- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,  
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND  
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH  
CC MUSCLES.  
CC -|- SUBCELLULAR LOCATION: Secreted.  
CC -|- TISSUE SPECIFICITY: Skin.  
CC -|- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.  
DR PIR; B60409; B60409.  
DR InterPro; IPR003580; Protachykinin.  
DR InterPro; IPR002040; Tachykinin.  
DR Pfam; PF02202; Tachykinin; 1.  
DR SMART; SM00203; TK; 1.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
KW Pyrrolidone carboxylic acid.

FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1269 MW; 3DBA7C37C9CBIAB7 CRC64;  
Query Match 28.6%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 5 QP 6  
Db 1 QP 2

RESULT 56  
TKN1\_UPERU STANDARD; PRT; 11 AA.  
AC P08612;  
DT 01-AUG-1988 (Rel. 08, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Uperolein.  
OS Uperoleia rugosa (Wrinkled toadlet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;  
OC Myobatrachinae; Uperoleia.  
OX NCBI\_TaxID=8368;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=75131227; PubMed=1120493;  
RA Anastasi A., Erspamer V., Eudean R.;  
RT "Structure of uperolein, a physalaemin-like endecapeptide occurring  
in the skin of Uperoleia rugosa and Uperoleia marmorata.";  
RL Experientia 31:394-395(1975).  
CC -|- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,  
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND  
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH  
CC MUSCLES.  
CC -|- SUBCELLULAR LOCATION: Secreted.  
CC -|- TISSUE SPECIFICITY: Skin.  
CC -|- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.  
DR InterPro; IPR003580; Protachykinin.  
DR InterPro; IPR002040; Tachykinin.  
DR Pfam; PF02202; Tachykinin; 1.  
DR SMART; SM00203; TK; 1.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
KW Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1252 MW; 32B67C3E59CDP457 CRC64;  
Query Match 28.6%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 5 QP 6  
Db 1 QP 2

RESULT 57  
TKN2\_PSEGU STANDARD; PRT; 11 AA.  
AC P42987;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Kassinin-like peptide K-II (PG-KII).  
OS Pseudophryne guentheri (Guenther's toadlet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;  
OC Myobatrachinae; Pseudophryne.



OS Pseudophryne guentheri (Guenther's toadlet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;  
 OC Myobatrachinae; Pseudophryne.  
 OX NCBI\_TaxID=30349;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=90287814; PubMed=2356157;  
 RA Siamaco M., Severini C., de Biase D., Barra D., Bossa F.,  
 RA Roberts J.D., Melchiorri P., Erspamer V.;  
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
 RT the Australian frog Pseudophryne guntheri.";  
 RL Peptides 11:299-304(1990).  
 CC -|- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,  
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND  
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH  
 CC MUSCLES.  
 CC -|- SUBCELLULAR LOCATION: Secreted.  
 CC -|- TISSUE SPECIFICITY: Skin.  
 CC -|- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.  
 DR PIR; F60409; F60409.  
 DR InterPro; IPR003580; Protachykinin.  
 DR Pfam; PF02202; Tachykinin.  
 DR SMART; SM00203; TK; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 11 11 AMIDATION  
 FT SEQUENCE 11 AA; 1293 MW; 3A247C2CC9CB1457 CRC64;  
 QY Query Match 28.6%; Score 2; DB 1; Length 11;  
 DB Best Local Similarity 100.0%; Pred.No. 2.8e+03;  
 DB Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 61  
 TKNA ONCMY  
 ID TKNA ONCMY STANDARD; PRT; 11 AA.  
 AC P28499;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Substance P.  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 OX NCBI\_TaxID=8022;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=92298992; PubMed=1376687;  
 RA Jensen J., Conlon J.M.;  
 RT "Substance-P-related and neurokinin-A-related peptides from the brain  
 RT of the cod and trout.";  
 RL Eur. J. Biochem. 206:659-664(1992).  
 CC -|- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,  
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND  
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH  
 CC MUSCLES.  
 CC -|- SUBCELLULAR LOCATION: Secreted.  
 CC -|- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.  
 DR PIR; S23308; S23308.  
 DR InterPro; IPR003580; Protachykinin.  
 DR InterPro; IPR002040; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.

DR SMART; SM00203; TK; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.  
 FT MOD\_RES 11 11 AMIDATION (BY SIMILARITY).  
 SQ SEQUENCE 11 AA; 1358 MW; 214860DEC9D6D1F7 CRC64;  
 QY Query Match 28.6%; Score 2; DB 1; Length 11;  
 DB Best Local Similarity 100.0%; Pred.No. 2.8e+03;  
 DB Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 62  
 TKN ELEMO  
 ID TKN ELEMO STANDARD; PRT; 11 AA.  
 AC P01293;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Eleidoisin.  
 OS Eleidone moschata (Musky octopus) (Ozaena moschata), and  
 OS Eleidone cirrhosa (Curled octopus) (Ozaena cirrosa).  
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;  
 OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Eleidone.  
 OX NCBI\_TaxID=6641, 102876;  
 RN [1]  
 RP SEQUENCE.  
 RA Anastasi A., Erspamer V.;  
 RT "The isolation and amino acid sequence of eleidoisin, the active  
 RT endecapeptide of the posterior salivary glands of Eleidone.";  
 RL Arch. Biochem. Biophys. 101:56-65(1963).  
 CC -|- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,  
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND  
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH  
 CC MUSCLES.  
 CC -|- SUBCELLULAR LOCATION: Secreted.  
 CC -|- TISSUE SPECIFICITY: Skin.  
 CC -|- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.  
 DR PIR; A01561; EOCC.  
 DR PIR; B01561; EOCC.  
 DR PDB; LMQ; 18-FEB-03.  
 DR InterPro; IPR002040; Tachykinin.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Tachykinin; Neuropeptide; Amidation; Pyrrolidone carboxylic acid;  
 KW 3D-structure.  
 FT MOD\_RES 1 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 11 11 AMIDATION.  
 FT SEQUENCE 11 AA; 1206 MW; 570D7C2559CDDAA3 CRC64;  
 QY Query Match 28.6%; Score 2; DB 1; Length 11;  
 DB Best Local Similarity 100.0%; Pred.No. 2.8e+03;  
 DB Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 63  
 FAR7 PENMO  
 ID FAR7 PENMO STANDARD; PRT; 12 AA.  
 AC P83322;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE FRRamide-like neuropeptide FLP7 (GYRKPFPNGSIF-amide).  
 OS Penaeus monodon (Penaeid shrimp).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;  
 OC Penaeidae; Penaeus.

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OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigornkul P., Pupuem J., Krungkarn C., Longyant S.,
RA Chaivathangkura P., Sithigornkul W., Petsom A.;
RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk
of the giant tiger prawn Penaeus monodon."
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1381.4; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
CC Neuropeptide; Amidation.
FT MOD RES 12 12
SQ SEQUENCE 12 AA; 1383 MW; 31209192EF49D777 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
DB 5 PP 6

RESULT 64
FARI CALVO STANDARD; PRT; 12 AA.
AC P41869;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CallimyrFamide 1.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.P., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
neuropeptides (designated callimyrFamides) from the blowfly
Calliphora vomitoria."
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
CC PIR; E44787; E44787.
DR Neuropeptide; Amidation.
FT MOD RES 12 12
SQ SEQUENCE 12 AA; 1390 MW; 2DDDB316914AB5A7 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
DB 4 QP 5

RESULT 65
FIFI_SARBU STANDARD; PRT; 12 AA.
AC P83349;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

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DE Neb-FIRFamide 1.
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7385;
RN [1]
RP SEQUENCE, AMIDATION, AND FUNCTION.
RC TISSUE=CNS;
RX MEDLINE=22342733; PubMed=12438685;
RA Meusen T., Mertens I., Clynen E., Baggerman G., Nichols R.,
RA Nachman R.J., Huybrechts R., De Loof A., Schoofs L.;
RT "Identification in Drosophila melanogaster of the invertebrate G
protein-coupled FMRamide receptor."
RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).
CC -!- FUNCTION: Has modulatory actions at skeletal neuromuscular
junctions.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
CC Neuropeptide; Amidation.
FT MOD RES 12 12
SQ SEQUENCE 12 AA; 1389 MW; 2DC45519C14AB5A7 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
DB 2 PP 3

RESULT 66
HS9A RAT STANDARD; PRT; 12 AA.
AC P82955;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Heat shock protein HSP 90-alpha (Fragment).
GN HSPCA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=21589773; PubMed=11732320;
RA Langer T., Fasold H.;
RT "Isolation and quantification of the heat shock protein 90 alpha and
beta isoforms from rat liver."
RL Proteolipoma 218:54-56(2001).
CC -!- FUNCTION: MOLECULAR CHAPERONE. HAS ATPASE ACTIVITY
(BY SIMILARITY).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY.
DR InterPro; IPR001404; Hsp90.
DR PROSITE; PS00298; HSP90; PARTIAL.
KW Chaperone; ATP-binding; Heat shock; Phosphorylation.
FT MOD RES 4 4
FT MOD_RES 6 6
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1432 MW; DE47C322CAB6C1B6 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      5 QP 6
DB      9 QP 10

RESULT 67
TKN2 KASMA
ID _TKN2_KASMA STANDARD; PRT; 12 AA.
AC P06614;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hylambatin.
OS Kassina maculata (African rhacophorid frog) (Hylambates maculatus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Hyperoliidae;
OC Kassina.
OX NCBI_TaxID=8414;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Yasuhara T., Nakajima T., Erspamer G.F., Erspamer V.;
RT "New tachykinins, Glu2, Pro5-kassinin (hylambates-kassinin) and
RT hylambatin, in the skin of the African rhacophorid frog Hylambates
RT maculatus.";
RL Biomed. Res. 2:613-617(1981).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOLVE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; S07436; S07436.
DR InterPro; IPR002040; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 12 12 AMIDATION.
SQ SEQUENCE 12 AA; 1441 MW; 3287CD2F0DD40AB7 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 PP 7
DB      2 PP 3

RESULT 68
ACT7 -SOYEN
ID _ACT7_SOYEN STANDARD; PRT; 13 AA.
AC F15987;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Actin 7 (Fragment).
GN SAC7.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Wayne; PubMed-2102831;
RX MEDLINE-91346640;
RA Pearson L., Mesgher R.B.;
RT "Diverse soybean actin transcripts contain a large intron in the 5',
RT untranslated leader: structural similarity to vertebrate muscle actin
RT genes.";
RL Plant Mol. Biol. 14:513-526(1990).

QY      5 QP 6
DB      9 QP 10

RESULT 69
AH4 PRUSE
ID _AH4_PRUSE STANDARD; PRT; 13 AA.
AC P29262;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Amygdalin beta-glucosidase II' (EC 3.2.1.117) (Amygdalin hydrolase
DE isozyme II') (AH II') (Fragment).
OS Prunus serotina (Black cherry).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=23207;
RN [1]
RP SEQUENCE.
RC TISSUE=Seed;
RA Li C.P., Swain E., Poulton J.E.;
RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase.";
RL Plant Physiol. 100:282-290(1992).
CC -!- CATALYTIC ACTIVITY: (R)-amygdalin + H(2)O = (R)-prunasin + D-
CC glucose.
CC -!- SUBUNIT: Monomer.
CC -!- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS
CC UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COTYLEDON
CC DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR
CC EMBRYONAL TISSUES.
CC -!- PTM: GLYCOSYLATED.
KW Glycosidase; Hydrolase; Glycoprotein; Multigene family.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1417 MW; F7CC4FA921B9D051 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 QP 6
DB      8 QP 9

Query Match 28.6%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC -!- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED
CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE USUALLY EXPRESSED
CC IN ALL EUKARYOTIC CELLS.
CC -!- FUNCTION: ESSENTIAL COMPONENT OF CELL CYTOSKELETON; PLAYS AN
CC IMPORTANT ROLE IN CYTOPLASMIC STREAMING, CELL SHAPE DETERMINATION,
CC CELL DIVISION, ORGANELLE MOVEMENT AND EXTENSION GROWTH.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- MISCELLANEOUS: THERE ARE AT LEAST 16 ACTIN GENES IN SOYBEAN.
CC -!- SIMILARITY: Belongs to the actin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X17120; CAA34980.1; --
CC PIR; S15755; S15755.
CC InterPro; IPR004001; Actin.
CC DR PROSITE; PS00406; ACTINS_1; PARTIAL.
CC DR PROSITE; PS00432; ACTINS_2; PARTIAL.
CC DR PROSITE; PS01132; ACTINS_ACT LIKE; PARTIAL.
KW Structural protein; Multigene family.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1420 MW; 8BEFF3C36D4FD05A CRC64;

Query Match 28.6%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 QP 6
DB      8 QP 9

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Qy      6 PP 7
      ||
Db      3 PP 4

RESULT 70
BPPI_BOTJA
ID BPPI_BOTJA STANDARD; PRT; 13 AA.
AC P01020; P30421;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S3.1 (13A) (Angiotensin-converting
enzyme inhibitor V-9).
OS Bothrops jararaca (Jararaca), and
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724, 8723;
RN [1]
RP SEQUENCE.
RC SPECIES=B.jararaca; TISSUE=Venom;
RX MEDLINE=72118526; PubMed=4334402;
RA Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R.,
RA Kocy O.;
RT "Angiotensin-converting enzyme inhibitors from the venom of Bothrops
jararaca. Isolation, elucidation of structure, and synthesis.";
RL Biochemistry 10:4033-4039(1971).
RN [2]
RP SEQUENCE.
RC SPECIES=B.insularis; TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; A01253; XAV19B.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 13 AA; 1388 MW; 6824FC97D83D6774 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 PP 7
      ||
Db     12 PP 13

RESULT 71
BRK_PARD
ID BRK_PARD STANDARD; PRT; 13 AA.
AC P42717;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Waspkinin.
OS Parapolybia indica.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Polistinae; Parapolybia.
OX NCBI_TaxID=31921;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Toki T., Yasuhara T., Nakajima T.;
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RT "Isolation and sequential analysis of peptides on the venom sac of
RL Parapolybia indica.";
RL Eisei Dobutsu 39:105-111(1988).
CC -!- FUNCTION: Induces smooth muscle contraction.
CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
KW Bradykinin; Vasodilator; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 13 AA; 1573 MW; 2673CE3D83ECC867 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 PP 7
      ||
Db      5 PP 6

RESULT 72
EIZ2_LITRU
ID EIZ2_LITRU STANDARD; PRT; 13 AA.
AC P82098;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Electrin 2.2.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
Litoria rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1598 MW; C1808EF3B3857322 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 QP 6
      ||
Db      9 QP 10

RESULT 73
EP65_HUMAN
ID EP65_HUMAN STANDARD; PRT; 13 AA.
AC P54963;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Erythrocyte 65 kDa protein (P65) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE.
RX MEDLINE=90004678; PubMed=2507249;
RA Hart G.W., Haliwanger R.S., Holt G.D., Kelly W.G.;
RT "Nucleoplasmic and cytoplasmic glycoproteins.";
RL Ciba Found. Symp. 145:102-118(1989).
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CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
DR GO: 0005737; C:cytoplasm; NAS.
KW Glycoprotein.
FT NON_TER 1 1 O-LINKED (GLCNAC).
FT CARBOHYD 2 2
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1300 MW; DOB873344C61A776 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
Db 6 QP 7

RESULT 74
LMT4 LOCMI STANDARD; PRT; 13 AA.
AC P41430;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Locustamyotropin 4 (LOM-MT-4).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,
RT de Loof A.;
RT "Isolation, identification and synthesis of locustamyotropin III and
RT IV, two additional neuropeptides of Locusta migratoria: members of the
RT locustamyotropin peptide family.";
RL Insect Biochem. Mol. Biol. 22:447-452(1992).
CC -!- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY). LOM-MT IV SEEMS TO BE A MORE POTENT MUSCLE
CC STIMULATOR THAN LOM-MT I, II AND III.
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR PIR; B61620; B61620.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1553 MW; 20861943824D6698 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQ 5
Db 3 HQ 4

RESULT 75
MPI_MICOC STANDARD; PRT; 13 AA.
AC P81532;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE MPI protein (Fragments).
OS Microplitis ocellatae (Braconid wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonidae;
OC Braconidae; Microgasterinae; Microplitis.
OX NCBI_TaxID=99573;
RN [1]

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RP SEQUENCE.
RC TISSUE=Larva;
RA Takahashi M., Quicke D.L.J.;
RL Submitted (OCT-1998) to the SWISS-PROT data bank.
CC -!- TISSUE SPECIFICITY: SALIVARY GLANDS.
CC -!- DEVELOPMENTAL STAGE: LARVAL.
FT NON_CONS 10 11
SQ SEQUENCE 13 AA; 1595 MW; 0C0786C9DD82777B CRC64;

Query Match 28.6%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
Db 7 PP 8

Search completed: November 25, 2003, 19:28:23
Job time : 3.55399 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:25:50 ; Search time 13.1453 Seconds  
(without alignments)  
137.415 Million cell updates/sec

Title: US-09-641-801-24

Perfect score: 7

Sequence: 1 SWMHQPP 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phase.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_rviro.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	3	42.9	9	10	P82429
2	3	42.9	9	16	Q935G1
3	3	42.9	11	2	Q47569
4	3	42.9	11	13	Q80UP1
5	3	42.9	13	5	Q9U5U2
6	3	42.9	13	12	Q67604
7	3	42.9	15	10	Q9S8N8
8	3	42.9	16	11	Q9JHB6
9	3	42.9	17	3	Q06800
10	3	42.9	17	4	Q14001
11	3	42.9	18	11	Q9JIE9
12	3	42.9	19	13	Q9PRT0
13	3	42.9	19	13	Q9PRN4
14	3	42.9	20	16	Q8EGY4
15	2	28.6	7	2	P72081
16	2	28.6	7	6	Q28742

17	2	28.6	7	8	P92214	P92214 amblyopyrum
18	2	28.6	7	8	P92393	P92393 hordeum vul
19	2	28.6	7	8	P92403	P92403 lophopyrum
20	2	28.6	7	8	P92427	P92427 peridictyon
21	2	28.6	7	8	P92430	P92430 aegilops ta
22	2	28.6	7	8	P92221	P92221 bromus iner
23	2	28.6	7	8	P92425	P92425 pseudoroegn
24	2	28.6	7	8	P92381	P92381 hordeum bra
25	2	28.6	7	8	P92387	P92387 henrardia p
26	2	28.6	7	8	P92210	P92210 agropyron c
27	2	28.6	7	8	P92440	P92440 thinopyrum
28	2	28.6	7	8	P92218	P92218 australopyr
29	2	28.6	7	8	P92390	P92390 heteranthel
30	2	28.6	7	8	P92372	P92372 haynaldia v
31	2	28.6	7	8	P92442	P92442 taeniatheru
32	2	28.6	7	8	P92226	P92226 crithopsis
33	2	28.6	7	8	P92385	P92385 hordeum mar
34	2	28.6	7	8	P92421	P92421 psathyrosta
35	2	28.6	7	8	Q16468	Q16468 homo sapien
36	2	28.6	8	5	P82685	P82685 periplaneta
37	2	28.6	8	5	P82686	P82686 periplaneta
38	2	28.6	8	5	P82687	P82687 periplaneta
39	2	28.6	8	5	P82688	P82688 periplaneta
40	2	28.6	8	5	P82689	P82689 periplaneta
41	2	28.6	8	6	Q9GMH3	Q9GMH3 lagenorhync
42	2	28.6	8	6	Q28866	Q28866 megaptera n
43	2	28.6	8	12	Q9J205	Q9J205 hepatitis c
44	2	28.6	8	12	Q64971	Q64971 alfalfa mos
45	2	28.6	9	2	Q53914	Q53914 streptomyce
46	2	28.6	9	2	Q43960	Q43960 azotobacter
47	2	28.6	9	2	Q93193	Q93193 pseudomonas
48	2	28.6	9	4	Q9UKJ6	Q9UKJ6 homo sapien
49	2	28.6	9	4	Q9UCS8	Q9UCS8 homo sapien
50	2	28.6	9	4	Q15891	Q15891 homo sapien
51	2	28.6	9	4	Q16386	Q16386 homo sapien
52	2	28.6	9	5	Q9TWV0	Q9TWV0 anthopleura
53	2	28.6	9	6	Q9GJV2	Q9GJV2 lagenorhync
54	2	28.6	9	6	Q9T777	Q9T777 bos taurus
55	2	28.6	9	6	Q9GJV3	Q9GJV3 lagenorhync
56	2	28.6	9	6	Q9GJV1	Q9GJV1 lagenorhync
57	2	28.6	9	8	Q8WFT4	Q8WFT4 diadema ant
58	2	28.6	9	10	P82440	P82440 nicotiana t
59	2	28.6	9	11	Q08979	Q08979 mus musculu
60	2	28.6	9	12	Q90350	Q90350 hepatitis g
61	2	28.6	9	12	Q71069	Q71069 canine dist
62	2	28.6	9	12	Q92766	Q92766 canine dist
63	2	28.6	9	12	Q71066	Q71066 canine dist
64	2	28.6	9	13	Q9PRJ4	Q9PRJ4 lepisosteus
65	2	28.6	9	13	Q8AYL5	Q8AYL5 carassius a
66	2	28.6	10	2	Q8AUM7	Q8AUM7 carassius a
67	2	28.6	10	2	Q9R5T2	Q9R5T2 acetobacter
68	2	28.6	10	2	P83062	P83062 bacillus ce
69	2	28.6	10	4	Q14096	Q14096 homo sapien
70	2	28.6	10	4	Q15342	Q15342 homo sapien
71	2	28.6	10	4	Q9UCR0	Q9UCR0 homo sapien
72	2	28.6	10	4	Q9UE86	Q9UE86 homo sapien
73	2	28.6	10	8	Q8WFT6	Q8WFT6 diadema ant
74	2	28.6	10	8	Q8WFT5	Q8WFT5 diadema ant
75	2	28.6	10	8	Q8SHA8	Q8SHA8 rhampholeon
76	2	28.6	10	8	Q8LLJ0	Q8LLJ0 oryza sativ
77	2	28.6	10	10	Q92213	Q92213 aegilops sq
78	2	28.6	10	10	P81898	P81898 prunus dulc
79	2	28.6	10	10	P81899	P81899 prunus dulc
80	2	28.6	10	11	Q91WZ3	Q91WZ3 rattus sp.
81	2	28.6	10	11	Q9QVFO	Q9QVFO mus sp. pro
82	2	28.6	10	11	Q9QVK7	Q9QVK7 mus sp. nep
83	2	28.6	10	11	Q8VHM9	Q8VHM9 mus musculu
84	2	28.6	10	11	Q9QVE9	Q9QVE9 mus sp. pro
85	2	28.6	10	11	Q8CJEO	Q8CJEO rattus norv
86	2	28.6	10	12	Q9Q0W9	Q9Q0W9 polyomaviru
87	2	28.6	10	12	Q8JTV0	Q8JTV0 polyomaviru
88	2	28.6	10	12	Q9Q0W1	Q9Q0W1 polyomaviru
89	2	28.6	10	12	Q8JTV68	Q8JTV68 polyomaviru

90 O90348 hepatitis g  
 91 Q9Q0V9 polyomaviru  
 92 Q8JVB4 polyomaviru  
 93 Q9Q0W7 polyomaviru  
 94 Q8JVB6 polyomaviru  
 95 Q9Q0V7 polyomaviru  
 96 Q8JVB2 polyomaviru  
 97 Q8JVB7 polyomaviru  
 98 P90391 tomato yell  
 99 Q8JVB4 polyomaviru  
 100 Q8JVB7 polyomaviru

ID P82429 PRELIMINARY; PRT; 9 AA.  
 AC P82429;  
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE 44 kDa cell wall protein (Fragment).  
 OS Nicotiana tabacum (Common tobacco).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.  
 OX NCBI\_TaxID=4097;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=cv. PETIT HAVANA;  
 RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,  
 RA Wojtaszek P., Bolwell G.P.;  
 RT "Proteomic study of secondary cell wall proteins from transformed  
 RT tobacco culture";  
 RL Planta 0-0-0(2000).  
 CC -!- SUBCELLULAR LOCATION: CELL WALL.  
 CC -!- TISSUE SPECIFICITY: XYLEM.  
 KW Cell wall.  
 FT NON TER 9  
 SQ SEQUENCE 9 AA; 986 MW; C22CCACADG6C7776 CRC64;

## ALIGNMENTS

RESULT 1  
 P82429  
 ID P82429 PRELIMINARY; PRT; 9 AA.  
 AC P82429;  
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE 44 kDa cell wall protein (Fragment).  
 OS Nicotiana tabacum (Common tobacco).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.  
 OX NCBI\_TaxID=4097;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=cv. PETIT HAVANA;  
 RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,  
 RA Wojtaszek P., Bolwell G.P.;  
 RT "Proteomic study of secondary cell wall proteins from transformed  
 RT tobacco culture";  
 RL Planta 0-0-0(2000).  
 CC -!- SUBCELLULAR LOCATION: CELL WALL.  
 CC -!- TISSUE SPECIFICITY: XYLEM.  
 KW Cell wall.  
 FT NON TER 9  
 SQ SEQUENCE 9 AA; 986 MW; C22CCACADG6C7776 CRC64;

Query Match 42.9%; Score 3; DB 10; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7  
 Db 2 QPP 4

RESULT 2  
 Q935G1  
 ID Q935G1 PRELIMINARY; PRT; 9 AA.  
 AC Q935G1;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Putative membrane protein (Fragment).  
 GN HCM1.O1C.  
 OS Salmonella typhi.  
 OG Plasmid pHCM1.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Salmonella.  
 OX NCBI\_TaxID=601;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CT18;  
 RX MEDLINE=21534947; PubMed=11677608;  
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.,  
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,  
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,

RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,  
 RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jegels K.,  
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,  
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,  
 RA Whitehead S., Barrell B.G.;  
 RT "Complete genome sequence of a multiple drug resistant Salmonella  
 RT enterica serovar Typhi CT18";  
 RL Nature 413:848-852(2001).  
 DR EMBL; ALS13383; CAD09867.1; -.  
 KW Plasmid; Complete proteome.  
 FT NON TER 9  
 SQ SEQUENCE 9 AA; 904 MW; 5FCDCT7776D86767 CRC64;

Query Match 42.9%; Score 3; DB 16; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7  
 Db 5 QPP 7

RESULT 3  
 Q47569  
 ID Q47569 PRELIMINARY; PRT; 11 AA.  
 AC Q47569;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-JAN-1999 (TrEMBLrel. 09, Last annotation update)  
 DE Hypothetical 1.3 kDa protein (Fragment).  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K-12;  
 RX MEDLINE=94162733; PubMed=7764507;  
 RA Yamada M., Yanai S., Talkuder A.;  
 RT "Analysis of products of the Escherichia coli genomic genes and  
 RT regulation of their expressions: an applicable procedure for genomic  
 RT analysis of other microorganisms";  
 RL Biosci. Biotechnol. Biochem. 58:117-120(1994).  
 DR EMBL; D21156; BAA04692.1; -.  
 KW Hypothetical protein.  
 FT NON TER 11  
 SQ SEQUENCE 11 AA; 1322 MW; C0BBE40E37672732 CRC64;

Query Match 42.9%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.8e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MHQ 5  
 Db 1 MHQ 3

RESULT 4  
 Q8UUP1  
 ID Q8UUP1 PRELIMINARY; PRT; 11 AA.  
 AC Q8UUP1;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Beta-TrCP protein (Fragment).  
 GN BETA-TRCP.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.

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RA Carnevali P.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Ballarino M.;
RT "Analisi strutturale e funzionale del gene beta-TrCP in Xenopus laevis.";
RL Thesis (2001), Department of Genetica e Biologia Molecolare, University of Rome La Sapienza, Rome, Italy.
DR ENBL; AJ428930; CAD21927.1; -.
FT NON TER 11 11
SQ SEQUENCE 11 AA; 1195 MW; CEB938EE35BEA5B9 CRC64;

Query Match 42.9%; Score 3; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
Db 9 QPP 11

RESULT 5
Q9U5J2 PRELIMINARY; PRT; 13 AA.
AC Q9U5J2
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE GPI-phospholipase C (Fragment).
GN GPI-PLC.
OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=3691;
RN [1]
RP SEQUENCE FROM N.A.
RA Webb H.D., Gaud A.F., Carrington M.;
RT "The trypanosoma brucei GPI-PLC gene is not linked to functionally related genes or to genes showing the same developmentally regulated expression.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR ENBL; AJ250727; CAB60093.1; -.
DR InterPro: IPR003633; Varsurf_glyc_PPLC.
DR Pfam: PF03490; Varsurf_PPLC; 1.
FT NON TER 13 13
SQ SEQUENCE 13 AA; 1541 MW; 535AA96B464CA373 CRC64;

Query Match 42.9%; Score 3; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SWM 3
Db 11 SWM 13

RESULT 6
Q67604 PRELIMINARY; PRT; 13 AA.
AC Q67604;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Movement protein (Fragment).
GN BCL.
OS Squash leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10829;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Los Mochis 1;
RA Loniello A.O., Ford R.E., Salinas R.A., Morales F.J., Maxwell D.P.;

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RT "Diversity among geminiviruses associated with vegetables from Valle del Fuerte, Sinaloa, Mexico.";
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
DR ENBL; L27273; AAA47820.1; -.
FT NON TER 1 1
SQ SEQUENCE 13 AA; 1376 MW; D471DB4D634E76C2 CRC64;

Query Match 42.9%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
Db 7 QPP 9

RESULT 7
Q9S8N8 PRELIMINARY; PRT; 15 AA.
AC Q9S8N8
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Protein E-22 (Fragment).
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE
RX MEDLINE=94170739; PubMed=8125056;
RA Flensrud R.;
RT "Separation of acidic barley endosperm proteins by two-dimensional electrophoresis.";
RL Electrophoresis 14:1060-1066 (1993).
SQ SEQUENCE 15 AA; 1752 MW; C7D693937E908B9E CRC64;

Query Match 42.9%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
Db 4 QPP 6

RESULT 8
Q9JHB6 PRELIMINARY; PRT; 16 AA.
AC Q9JHB6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Meprin 1 beta (Fragment).
GN MEP1B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96147211; PubMed=8567689;
RA Dietrich J.M., Jiang W., Bond J.S.;
RT "A novel meprin beta' mRNA in mouse embryonal and human colon carcinoma cells.";
RL J. Biol. Chem. 271:2271-2278 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Jiang W., Kumar J.M., Bond J.S.;
RT "Structure of the mouse metalloprotease meprin beta gene (Meplb): alternative splicing in cancer cells.";

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RL Submitted (JUN-1999) to the EMBL/GenBank/DBSJ databases.  
 DR EMBL; AF160982; AAF80401.1; -.  
 DR MGI; MGI:96964; Mep1b.  
 FT NON\_TER 16  
 SQ SEQUENCE 16 AA; 1979 MW; EB9785A3F6189622 CRC64;

Query Match 42.9%; Score 3; DB 11; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HOP 6  
 DB 5 HOP 7

## RESULT 9

Q06800 PRELIMINARY; PRT; 17 AA.  
 AC Q06800;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
 DE N1780.  
 GN N1780.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96287653; PubMed=8686380;  
 RA Nasr F., Becam A.M., Herbert C.J.;  
 RT "The sequence of 36.8 kb from the left arm of chromosome XIV reveals  
 RT 24 complete open reading frames: 18 correspond to new genes, one of  
 RT which encodes a protein similar to the human myotonic dystrophy  
 RT kinase.";  
 RL Yeast 12:169-175(1996).  
 DR EMBL; X92517; CAA63292.1; -.  
 SQ SEQUENCE 17 AA; 2139 MW; BD7E9AFAADF754AF CRC64;

Query Match 42.9%; Score 3; DB 3; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHQ 5  
 DB 1 MHQ 3

## RESULT 10

Q14001 PRELIMINARY; PRT; 17 AA.  
 AC Q14001;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Cyclic nucleotide phosphodiesterase (Fragment).  
 GN CGIPDEL.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97079687; PubMed=8921398;  
 RA Loebert R.W., Winterpacht A., Seipel B., Zabel B.U.;  
 RT "Molecular cloning and chromosomal assignment of the human homologue  
 RT of the rat cGMP-inhibited phosphodiesterase 1 (PDE3A)-A gene involved  
 RT in fat metabolism located at 11p15.1.";  
 RL Genomics 37:211-218(1996).  
 DR EMBL; X95522; CAA64776.1; -.  
 FT NON\_TER 17  
 SQ SEQUENCE 17 AA; 2057 MW; 69D117C4FAE11540 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 OPP 7  
 DB 15 OPP 17

## RESULT 11

Q9JIE9 PRELIMINARY; PRT; 18 AA.  
 AC Q9JIE9;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Protein arginine N-methyltransferase 1 (Fragment).  
 GN MRMT1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20307889; PubMed=10848611;  
 RA Pawlak M.R., Scherer C.A., Chen J., Roshon M.J., Ruley H.E.;  
 RT "Arginine N-methyltransferase 1 is required for early postimplantation  
 RT mouse development, but cells deficient in the enzyme are viable.";  
 RL Mol. Cell. Biol. 20:4859-4869(2000).  
 DR EMBL; AF32718; AAF37294.1; -.  
 KW Methyltransferase; Transferase.  
 FT NON\_TER 18  
 FT NON\_TER 1  
 SQ SEQUENCE 18 AA; 1931 MW; 392B2C312C4A8372 CRC64;

Query Match 42.9%; Score 3; DB 11; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 OPP 7  
 DB 13 OPP 15

## RESULT 12

Q9PRT0 PRELIMINARY; PRT; 19 AA.  
 AC Q9PRT0;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
 DE 23A7 antigen (Fragment).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=95332492; PubMed=7608337;  
 RA Denburg J.L., Caldwell R.T., Warner J.M.;  
 RT "Developmental changes in epitope accessibility as an indicator of  
 RT multiple states of an immunoglobulin-like neural cell adhesion  
 RT molecule.";  
 RL J. Comp. Neurol. 354:533-550(1995).

SQ SEQUENCE 19 AA; 2051 MW; 83E67BEE484EBD03 CRC64;

Query Match 42.9%; Score 3; DB 13; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 OPP 7

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Db          15 QPP 17
||||
RESULT 13
Q9PRN4      PRELIMINARY;      PRT;      19 AA.
AC Q9PRN4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Melanotropin MSH-A.
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
OX NCBI_TaxID=7757;
RN [1]
RP SEQUENCE.
RX MEDLINE=96112167; PubMed=8537171;
RA Takahashi A., Amemiya Y., Nozaki M., Sower S.A., Joss J., Gorbman A.,
RA Kawauchi H.,
RT "Isolation and characterization of melanotropins from lamprey
RT pituitary glands."
RL Int. J. Pept. Protein Res. 46:197-204(1995).
SQ SEQUENCE 19 AA; 2400 MW; 0F4CD35F7E0BC340 CRC64;

Query Match      42.9%; Score 3; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
|||
Db          14 QPP 16

RESULT 14
Q8RGY4      PRELIMINARY;      PRT;      20 AA.
AC Q8RGY4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein FN0141.
GN FN0141.
OS Fusobacterium nucleatum (subsp. nucleatum).
OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;
OC Fusobacterium.
OX NCBI_TaxID=76856;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 25586;
RX MEDLINE=21866394; PubMed=11889109;
RA Kapatal V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
RA Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
RA Vasteva O., Chu L., Kogan Y., Chaga O., Goltzman E., Bernal A.,
RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
RA Ponstein M., Kyrpides N., Overbeek R.;
RT "Genome sequence and analysis of the oral bacterium Fusobacterium
RT nucleatum strain ATCC 25586."
RL J. Bacteriol. 184:2005-2018(2002).
RW EMBL; A2010528; AAL94347.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 20 AA; 2542 MW; 15BD7516B34C2A14 CRC64;

Query Match      42.9%; Score 3; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
|||
Db          12 QPP 14

RESULT 15
P72081      PRELIMINARY;      PRT;      7 AA.
AC P72081;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 3'-methylcephem hydroxylase (Fragment).
GN CEFF.
OS Nocardia lactamdurans.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Pseudonocardiaceae; Pseudonocardiaceae; Amycolatopsis.
OX NCBI_TaxID=1913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96009872; PubMed=7557411;
RA Coque J., Perez-Llarena F.J., Enguita F.J., Fuente J.L., Martin J.F.,
RA Liras P.;
RT "Characterization of the cmcH genes of Nocardia lactamdurans and
RT Streptomyces clavuligerus encoding a functional 3'-hydroxymethylcephem
RT O-carbamoyltransferase for cephamycin biosynthesis."
RL Gene 162:21-27(1995).
DR EMBL; Z21682; CAA79797.1; -.
FT NON TER 1
SQ SEQUENCE 7 AA; 746 MW; 75A1B2CDD1E681C0 CRC64;

Query Match      28.6%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MH 4
|||
Db          2 MH 3

RESULT 16
Q28742      PRELIMINARY;      PRT;      7 AA.
AC Q28742;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Alpha-myosin heavy chain (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84221901; PubMed=6328491;
RA Friedman D.J., Umeda P.K., Sinha A.M., Heu H.-J., Jokovic S.,
RA Rabinowitz M.;
RT "Characterization of genomic clones specifying rabbit alpha- and beta-
RT ventricular myosin heavy chains."
RL Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048(1984).
DR EMBL; K01698; AAA31415.1; -.
FT NON TER 1
SQ SEQUENCE 7 AA; 916 MW; 6B1B1AA1E69326B0 CRC64;

Query Match      28.6%; Score 2; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MH 4
|||
Db          3 MH 4

RESULT 17
P92214      PRELIMINARY;      PRT;      7 AA.
AC P92214;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)

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DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Ribosomal protein 11 (Fragment).  
 GN RPS11.  
 OS Amblyopyrum muticum.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Amblyopyrum.  
 OC NCBI\_TaxID=4595;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H5572; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data.";  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77756; CAB01346.1; -.  
 KW Chloroplast.  
 FT NON TER  
 SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;  
  
 Query Match 28.6%; Score 2; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 6 PP 7  
 DB 1 PP 2  
  
 RESULT 18  
 P92393  
 ID P92393 PRELIMINARY; PRT; 7 AA.  
 AC P92393;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Ribosomal protein 11 (Fragment).  
 GN RPS11.  
 OS Hordeum vulgare (Barley).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Hordeum.  
 OC NCBI\_TaxID=4513;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H3139; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data.";  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77764; CAB01370.1; -.  
 KW Chloroplast.  
 FT NON TER  
 SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;  
  
 Query Match 28.6%; Score 2; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 6 PP 7  
 DB 1 PP 2  
  
 RESULT 19  
 P92403  
 ID P92403 PRELIMINARY; PRT; 7 AA.  
 AC P92403;

DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Ribosomal protein 11 (Fragment).  
 GN RPS11.  
 OS Lophopyrum elongatum (Tall wheatgrass) (Argopyrum elongatum).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Lophopyrum.  
 OC NCBI\_TaxID=4588;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H6692; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data.";  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77743; CAB01307.1; -.  
 KW Chloroplast.  
 FT NON TER  
 SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;  
  
 Query Match 28.6%; Score 2; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 6 PP 7  
 DB 1 PP 2  
  
 RESULT 20  
 P92427  
 ID P92427 PRELIMINARY; PRT; 7 AA.  
 AC P92427;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Ribosomal protein (Fragment).  
 GN RPS11.  
 OS Peridictyon sanctum.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Peridictyon.  
 OC NCBI\_TaxID=37683;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H5575; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data.";  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77749; CAB01325.1; -.  
 KW Chloroplast.  
 FT NON TER  
 SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;  
  
 Query Match 28.6%; Score 2; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 6 PP 7  
 DB 1 PP 2  
  
 RESULT 21  
 P92430  
 ID P92430 PRELIMINARY; PRT; 7 AA.

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AC P92430;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Aegilops tauschii (Aegilops squarrosa).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Aegilops.
OX NCBI_TaxID=37682;
RN [1]_TaxID=37682;
RP SEQUENCE FROM N.A.
RC STRAIN=H6688; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77758; CAB01352.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
DB 1 PP 2

RESULT 22
P92221
ID P92221 PRELIMINARY; PRT; 7 AA.
AC P92221;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Bromus inermis (Smooth brome grass).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Bromae; Bromus.
OX NCBI_TaxID=15371;
RN [1]_TaxID=15371;
RP SEQUENCE FROM N.A.
RC STRAIN=OSA414; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77759; CAB01355.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
DB 1 PP 2

RESULT 23
P92425
ID P92425 PRELIMINARY; PRT; 7 AA.
AC P92425;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Pseudoroegneria spicata (Bluebunch wheatgrass) (Agropyron spicatum).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Pseudoroegneria.
OX NCBI_TaxID=4604;
RN [1]_TaxID=4604;
RP SEQUENCE FROM N.A.
RC STRAIN=H9082; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77744; CAB01310.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
DB 1 PP 2

RESULT 24
P92381
ID P92381 PRELIMINARY; PRT; 7 AA.
AC P92381;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Hordeum brachyantherum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=52712;
RN [1]_TaxID=52712;
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77761; CAB01361.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
DB 1 PP 2

RESULT 25
P92425
ID P92425 PRELIMINARY; PRT; 7 AA.
AC P92425;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Pseudoroegneria spicata (Bluebunch wheatgrass) (Agropyron spicatum).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Pseudoroegneria.
OX NCBI_TaxID=4604;
RN [1]_TaxID=4604;
RP SEQUENCE FROM N.A.
RC STRAIN=H9082; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77744; CAB01310.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
DB 1 PP 2

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P92387
ID P92387 PRELIMINARY; PRT; 7 AA.
AC P92387;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Henrardia persica.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Henrardia.
OX NCBI_TaxID=37678;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H5556; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77748; CAB01322.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 1 1 894 MW; 6734140333277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
DB 1 PP 2

RESULT 26
P92210
ID P92210 PRELIMINARY; PRT; 7 AA.
AC P92210;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Agropyron cristatum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Agropyron.
OX NCBI_TaxID=4593;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H4349; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77771; CAB01391.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 1 1 894 MW; 6734140333277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
DB 1 PP 2

P92387
ID P92387 PRELIMINARY; PRT; 7 AA.
AC P92387;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Henrardia persica.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Henrardia.
OX NCBI_TaxID=37678;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H5556; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77748; CAB01322.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 1 1 894 MW; 6734140333277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
DB 1 PP 2

P92210
ID P92210 PRELIMINARY; PRT; 7 AA.
AC P92210;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Agropyron cristatum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Agropyron.
OX NCBI_TaxID=4593;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H4349; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77771; CAB01391.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 1 1 894 MW; 6734140333277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
DB 1 PP 2

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RESULT 27
P92440
ID P92440 PRELIMINARY; PRT; 7 AA.
AC P92440;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Thinopyrum bessarabicum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Thinopyrum.
OX NCBI_TaxID=4601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H6725; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77769; CAB01385.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 1 1 894 MW; 6734140333277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
DB 1 PP 2

RESULT 28
P92218
ID P92218 PRELIMINARY; PRT; 7 AA.
AC P92218;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Ribosomal protein 11 (Fragment).
GN RPS11.
OS Australopyrum retrofractum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Australopyrum.
OX NCBI_TaxID=4597;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H6723; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G., Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77767; CAB01379.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 1 1 894 MW; 6734140333277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
DB 1 PP 2

```

RESULT 29									
ID	P92390	PRELIMINARY;	PRT;	7 AA.					
AC	P92390;								
DT	01-MAY-1997 (TrEMBLrel. 03, Created)								
DT	01-MAY-1997 (TrEMBLrel. 03, Last sequence update)								
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)								
DE	Ribosomal protein 11 (Fragment).								
GN	RPS11.								
OS	Heterantherium piliferum.								
OG	Chloroplast.								
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;								
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;								
OC	Triticeae; Heterantherium.								
OX	NCBI_TaxID=37679;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	STRAIN=H5557; TISSUE=Leaf;								
RX	MEDLINE=97271648; PubMed=9126564;								
RA	Petersen G., Seberg O.;								
RT	"Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA								
RT	sequence data.";								
RL	Mol. Phylogenet. Evol. 7:217-230(1997).								
DR	EMBL; Z77750; CAB01328.1; --								
KW	Chloroplast.								
FT	NON_TER	1	1						
SQ	SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;								
Query Match 28.6%; Score 2; DB 8; Length 7;									
Best Local Similarity 100.0%; Pred. No. 8.3e+05;									
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	6 PP 7								
Db	1 PP 2								
RESULT 30									
ID	P92372	PRELIMINARY;	PRT;	7 AA.					
AC	P92372;								
DT	01-MAY-1997 (TrEMBLrel. 03, Created)								
DT	01-MAY-1997 (TrEMBLrel. 03, Last sequence update)								
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)								
DE	Ribosomal protein 11 (Fragment).								
GN	RPS11.								
OS	Haynaldia villosa.								
OG	Chloroplast.								
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;								
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;								
OC	PACAD clade; Panicoideae; Andropogoneae; Haynaldia.								
OX	NCBI_TaxID=40247;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	STRAIN=H5561; TISSUE=Leaf;								
RX	MEDLINE=97271648; PubMed=9126564;								
RA	Petersen G., Seberg O.;								
RT	"Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA								
RT	sequence data.";								
RL	Mol. Phylogenet. Evol. 7:217-230(1997).								
DR	EMBL; Z77741; CAB01301.1; --								
KW	Chloroplast.								
FT	NON_TER	1	1						
SQ	SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;								
Query Match 28.6%; Score 2; DB 8; Length 7;									
Best Local Similarity 100.0%; Pred. No. 8.3e+05;									
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	6 PP 7								
Db	1 PP 2								

RESULT 31									
ID	P92442	PRELIMINARY;	PRT;	7 AA.					
AC	P92442;								
DT	01-MAY-1997 (TrEMBLrel. 03, Created)								
DT	01-MAY-1997 (TrEMBLrel. 03, Last sequence update)								
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)								
DE	Ribosomal protein 11 (Fragment).								
GN	RPS11.								
OS	Taeniatherum caput-medusae (Medusahead).								
OG	Chloroplast.								
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;								
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;								
OC	Triticeae; Taeniatherum.								
OX	NCBI_TaxID=37687;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	STRAIN=H10254; TISSUE=Leaf;								
RX	MEDLINE=97271648; PubMed=9126564;								
RA	Petersen G., Seberg O.;								
RT	"Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA								
RT	sequence data.";								
RL	Mol. Phylogenet. Evol. 7:217-230(1997).								
DR	EMBL; Z77760; CAB01358.1; --								
KW	Chloroplast.								
FT	NON_TER	1	1						
SQ	SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;								
Query Match 28.6%; Score 2; DB 8; Length 7;									
Best Local Similarity 100.0%; Pred. No. 8.3e+05;									
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	6 PP 7								
Db	1 PP 2								
RESULT 32									
ID	P92226	PRELIMINARY;	PRT;	7 AA.					
AC	P92226;								
DT	01-MAY-1997 (TrEMBLrel. 03, Created)								
DT	01-MAY-1997 (TrEMBLrel. 03, Last sequence update)								
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)								
DE	Ribosomal protein 11 (Fragment).								
GN	RPS11.								
OS	Critopsis delileana.								
OG	Chloroplast.								
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;								
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;								
OC	Triticeae; Critopsis.								
OX	NCBI_TaxID=37674;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	STRAIN=H5558; TISSUE=Leaf;								
RX	MEDLINE=97271648; PubMed=9126564;								
RA	Petersen G., Seberg O.;								
RT	"Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA								
RT	sequence data.";								
RL	Mol. Phylogenet. Evol. 7:217-230(1997).								
DR	EMBL; Z77751; CAB01331.1; --								
KW	Chloroplast.								
FT	NON_TER	1	1						
SQ	SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;								
Query Match 28.6%; Score 2; DB 8; Length 7;									
Best Local Similarity 100.0%; Pred. No. 8.3e+05;									
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	6 PP 7								
Db	1 PP 2								

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Db          1 PP 2

RESULT 33
P32385
ID P92385 PRELIMINARY; PRT; 7 AA.
AC P92385; P92383;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-MAY-2002 (TReMBLrel. 20, Last annotation update)
DE Ribosomal protein 11 (Fragment).
OS Homo sapiens (Human).
NCBI_TaxID=4519;
GN RPS11.
OS Hordeum marinum (Seaside barley).
OS Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4519;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=H299, and H801; TISSUE=Leaf;
RA Petersen G., Seberg O.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; 277763; CAB01367.1; -.
DR EMBL; 277762; CAB01364.1; -.
KW Chloroplast; Ribosomal protein.
FT NON_TER 1
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
DB 1 PP 2

RESULT 34
P32421
ID P92421 PRELIMINARY; PRT; 7 AA.
AC P92421; P92419;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-MAY-2002 (TReMBLrel. 20, Last annotation update)
DE Ribosomal protein 11 (Fragment).
OS Homo sapiens (Human).
NCBI_TaxID=37729;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=H4372, and H917; TISSUE=Leaf;
RA Petersen G., Seberg O.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; 277753; CAB01337.1; -.
DR EMBL; 277752; CAB01334.1; -.
KW Chloroplast; Ribosomal protein.
FT NON_TER 1
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 28.6%; Score 2; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
DB 1 PP 2

RESULT 35
Q16468
ID Q16468 PRELIMINARY; PRT; 8 AA.
AC Q16468;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE DNA for cosmid cCl3-1134 PCR primer 1 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RC MEDLINE=96435920; PubMed=9838806;
RA James L.A., Ogilvie D.J., Yamakawa K., Nakamura Y., Stirling C.J.,
RA Anand R.;
RT "Walking, cloning and mapping with YACs in 3q27. Localisation of 5
RT ESTs including 3 members of the Cystatin gene family and
RT identification of CpG islands.";
RL Genomics 32:425-430(1996).
DR EMBL; X88976; CAA61407.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 925 MW; FD5411A7376871E6 CRC64;

Query Match 28.6%; Score 2; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MH 4
DB 1 MH 2

RESULT 36
P82685
ID P82685 PRELIMINARY; PRT; 8 AA.
AC P82685;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE Kinin-1 (PEA-K-1).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]_
RP SEQUENCE, AND FUNCTION.
RC TISSUE=CORPORA CARDIACA;
RX MEDLINE=98010462; PubMed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kinins from the
RT retrocerebral complex of the American cockroach, Periplaneta
RT americana.";
RL Regul. Pept. 71:199-205(1997).
CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -1- SIMILARITY: BELONGS TO THE KININ FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 950 MW; 326365B449D5A774 CRC64;

Query Match 28.6%; Score 2; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
DB 6 SW 7

RESULT 37

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P82686
ID P82686 PRELIMINARY; PRT; 8 AA.
AC P82686;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE Kinin-2 (PEA-K-2).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=CORPORA CARDIACA;
RX MEDLINE=98010462; PubMed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kinins from the
RT retrocerebral complex of the American cockroach, Periplaneta
RT americana."
RL Regul. Pept. 71:199-205(1997).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC -!- (MYOTROPIC ACTIVITY).
CC -!- SIMILARITY: BELONGS TO THE KININ FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 8
SQ SEQUENCE 8 AA; 856 MW; DC6365A5B9D5BDDA CRC64;

Query Match 28.6%; Score 2; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
Db 6 SW 7

RESULT 38
P82687
ID P82687 PRELIMINARY; PRT; 8 AA.
AC P82687;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE Kinin-3 (PEA-K-3).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=CORPORA CARDIACA;
RX MEDLINE=98010462; PubMed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kinins from the
RT retrocerebral complex of the American cockroach, Periplaneta
RT americana."
RL Regul. Pept. 71:199-205(1997).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC -!- (MYOTROPIC ACTIVITY).
CC -!- SIMILARITY: BELONGS TO THE KININ FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 8
SQ SEQUENCE 8 AA; 909 MW; DC6365B449D5A76A CRC64;

Query Match 28.6%; Score 2; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
Db 6 SW 7

P82688
ID P82688 PRELIMINARY; PRT; 8 AA.
AC P82688;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE Kinin-4 (PEA-K-4).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=CORPORA CARDIACA;
RX MEDLINE=98010462; PubMed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kinins from the
RT retrocerebral complex of the American cockroach, Periplaneta
RT americana."
RL Regul. Pept. 71:199-205(1997).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC -!- (MYOTROPIC ACTIVITY).
CC -!- SIMILARITY: BELONGS TO THE KININ FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 8
SQ SEQUENCE 8 AA; 839 MW; 736365A5B9D6DD8 CRC64;

Query Match 28.6%; Score 2; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
Db 6 SW 7

RESULT 40
P82689
ID P82689 PRELIMINARY; PRT; 8 AA.
AC P82689;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE Kinin-5 (PEA-K-5).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=CORPORA CARDIACA;
RX MEDLINE=98010462; PubMed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of eight kinins from the
RT retrocerebral complex of the American cockroach, Periplaneta
RT americana."
RL Regul. Pept. 71:199-205(1997).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC -!- (MYOTROPIC ACTIVITY).
CC -!- SIMILARITY: BELONGS TO THE KININ FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 8
SQ SEQUENCE 8 AA; 865 MW; C76365B449DC775 CRC64;

Query Match 28.6%; Score 2; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2
Db 6 SW 7

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QY      1 SW 2
Db      6 SW 7

RESULT 41
Q9GMH3
ID Q9GMH3 PRELIMINARY; PRT; 8 AA.
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Actin (Fragment).
OS Lagenorhynchus obscurus (Dusky dolphin).
OC Eukaryota; Metazoa; Chordata; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC Lagenorhynchus.
OX NCBI_TaxID=27611;
RN [1]
RP SEQUENCE FROM N.A.
RA Hare M.P., Cipriano F., Palumbi S.R.;
RT "Slow Evolution of Genetic Monophyly in Dolphins: Implications for
RT Speciation, Systematics and Conservation.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF140833; AAF98686.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 962 MW; 5BD1F417740862C0 CRC64;

Query Match 28.6%; Score 2; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 HQ 5
Db      7 HQ 8

RESULT 42
Q28866
ID Q28866 PRELIMINARY; PRT; 8 AA.
AC Q28866;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE Actin protein (Fragment).
GN ACTIN.
OS Megaptera novaeangliae (Humpback whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
OC Balaeopteridae; Megaptera.
OX NCBI_TaxID=9773;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94285813; PubMed=7912407;
RA Palumbi S.R., Baker C.S.;
RT "Contrasting population structure from nuclear intron sequences and
RT mtDNA of humpback whales.";
RL Mol. Biol. Evol. 11:426-435(1994).
DR EMBL; S73467; AAD14118.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 906 MW; 69C866D1F4177408 CRC64;

Query Match 28.6%; Score 2; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 HQ 5
Db      5 HQ 6

RESULT 43

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Q9J205
ID Q9J205 PRELIMINARY; PRT; 8 AA.
AC Q9J205;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Truncated polyprotein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RA Pan X., Disisceglie A.M.;
RT "Identification of liver-specific quasispecies of the hepatitis C
RT virus in chronically infected patients.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF211054; AAF30114.1; -.
KW Polyprotein.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 917 MW; B1D41AF7776DCA CRC64;

Query Match 28.6%; Score 2; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 PP 7
Db      3 PP 4

RESULT 44
Q64971
ID Q64971 PRELIMINARY; PRT; 8 AA.
AC Q64971;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Putative ORF (Fragment).
OS Alfalfa mosaic virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Alfamovirus.
OX NCBI_TaxID=12321;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81124289; PubMed=6927843;
RA Koper-Zwarthoff E.C., Brederode F.T.M., Veeneman G., van Boom J.H.,
RA Bol J.F.;
RT "Nucleotide sequences at the 5'-termini of the alfalfa mosaic virus
RT RNAs and the intercistronic junction in RNA 3.";
RL Nucleic Acids Res. 8:5635-5647(1980).
DR EMBL; V00047; CAA23416.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 917 MW; 69D40B0775A365B8 CRC64;

Query Match 28.6%; Score 2; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SW 2
Db      2 SW 3

RESULT 45
Q53914
ID Q53914 PRELIMINARY; PRT; 9 AA.
AC Q53914;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Curd protein (Fragment).

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OS Streptomyces cyaneus (Streptomyces curacoi).  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomycineae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=1904;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Bergh S.T., Uhlen M.;  
 RT "Cloning, analysis and heterologous expression of the polyketides  
 synthesis genes of Streptomyces curacoi";  
 RL Submitted (JUN-1990) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; M33704; AAA26724.1; -.  
 FT NON-TER 1  
 SQ SEQUENCE 9 AA; 1027 MW; 995BDDDC4140AB1 CRC64;

Query Match 28.6%; Score 2; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QP 6  
 Db 8 QP 9

RESULT 46  
 Q43960 PRELIMINARY; PRT; 9 AA.  
 AC Q43960;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Hydrogenase-related protein (Fragment).  
 GN HUPA.  
 OS Azotobacter chroococcum.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Azotobacter.  
 OX NCBI\_TaxID=353;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MCD1.  
 RX MEDLINE=95055698; PubMed=7966281;  
 RA Du L., Tibelius K.H., Souza E.M., Garg R.P., Yates M.G.;  
 RT "Sequences, organization and analysis of the hupZMNQORTV genes from  
 the Azotobacter chroococcum hydrogenase gene cluster";  
 RL J. Mol. Biol. 243:549-557(1994).  
 DR EMBL; L25315; AAA64455.1; -.  
 FT NON-TER 9  
 SQ SEQUENCE 9 AA; 1004 MW; EF421DD045B69B11 CRC64;

Query Match 28.6%; Score 2; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MH 4  
 Db 1 MH 2

RESULT 47  
 Q99193 PRELIMINARY; PRT; 9 AA.  
 AC Q99193;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE RpoB beta-subunit of RNA polymerase (Fragment).  
 OS Pseudomonas putida.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxID=303;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Borodin A.M., Danilovich A.V., Allikmets R.L., Rostapshov V.M.,  
 RA Chernov I.P., Azhikina T.L., Monastyrskaya S., Sverdlov D.;

RT "Nucleotide sequence of the rpoB gene coding for the beta-subunit of  
 RT RNA polymerase in Pseudomonas putida";  
 RL Dokl. Biochem. 302:1261-1265(1988).  
 DR EMBL; X15849; CAA33847.1; -.  
 FT NON-TER 9  
 SQ SEQUENCE 9 AA; 852 MW; 5B416776DC76727 CRC64;

Query Match 28.6%; Score 2; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7  
 Db 6 PP 7

RESULT 48  
 Q9UKJ6 PRELIMINARY; PRT; 9 AA.  
 AC Q9UKJ6;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE Androgen receptor (Fragment).  
 GN AR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Zhang W., Li X.Q., Wu Q.F.;  
 RT "A splice-site mutation in Androgen Receptor gene";  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF159087; AAF04001.1; -.  
 FT NON-TER 1  
 SQ SEQUENCE 9 AA; 1272 MW; 6F2B8415B331E684 CRC64;

Query Match 28.6%; Score 2; DB 4; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MH 4  
 Db 3 MH 4

RESULT 49  
 Q9UCS8 PRELIMINARY; PRT; 9 AA.  
 AC Q9UCS8;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Apolipoprotein A-I (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RA MEDLINE=92075698; PubMed=1742316;  
 RA Ethnholm C., Bozas S.E., Tenkanen H., Kirsbaum L., Metsa J.,  
 RA Murphy B., Walker I.D.;  
 RT "The apolipoprotein A-I binding protein of placenta and the SP-40,40  
 protein of human blood are different proteins which both bind to  
 apolipoprotein A-I";  
 RL Biochim. Biophys. Acta 1086:255-260(1991).  
 FT NON-TER 1  
 SQ SEQUENCE 9 AA; 981 MW; 7FE37775A6C776B CRC64;

Query Match 28.6%; Score 2; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7  
DB 3 PP 4

RESULT 50  
Q15891 ID Q15891 PRELIMINARY; PRT; 9 AA.  
AC Q15891;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE (Clone XP2EBB) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,  
RA Coolbaugh M.I., Chinsault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,  
RA Caskey C.T.H.;  
RT "Isolation of chromosome-specific genes by reciprocal probing of  
RT arrayed cDNAs and cosmid libraries.";  
RL Hum. Mol. Genet. 0:0-0(1995).  
DR EMBL; L32131; AAA73881.1; -.  
FT NON\_TER 1 1  
FT NON\_TER 9 9  
SQ SEQUENCE 9 AA; 1030 MW; E56635A1A33686D1 CRC64;

Query Match 28.6%; Score 2; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQ 5  
DB 2 HQ 3

RESULT 51  
Q16386 ID Q16386 PRELIMINARY; PRT; 9 AA.  
AC Q16386;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE Mex40 protein (Fragment).  
GN MEX40.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95400293; PubMed=7670464;  
RA Budarf M.L., Collins J., Gong W., Roe B., Wang Z., Bailey L.C.,  
RA Sellinger B., Michaud D., Briscoil D.A., Emanuel B.S.;  
RT "Cloning a balanced translocation associated with DiGeorge syndrome  
RT and identification of a disrupted candidate gene.";  
RL Nat. Genet. 10:269-278(1995).  
DR EMBL; S79485; AAD14301.1; -.  
FT NON\_TER 1 1  
FT NON\_TER 9 9  
SQ SEQUENCE 9 AA; 1137 MW; 734911A69446837B CRC64;

Query Match 28.6%; Score 2; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WM 3  
DB 3 WM 4

RESULT 52  
Q9TWV0 ID Q9TWV0 PRELIMINARY; PRT; 9 AA.  
AC Q9TWV0;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
DE Antho-RPAMIDB-NEUROPEPTIDE.  
OS Anthopleura elegantissima (Sea anemone).  
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;  
OC Nynanthaeae; Actiniidae; Anthopleura.  
OX NCBI\_TaxID=6110;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=93126143; PubMed=1480510;  
RA Carstensen K., Rinehart K.L., McFarlane I.D., Grimmelikhuijzen C.J.;  
RT "Isolation of Leu-Pro-Gly-Pro-Leu-Pro-Arg-Pro-NH2 (Antho-RPamide),  
RT an N-terminally protected, biologically active neuropeptide from sea  
RT anemones.";  
RL Peptides 13:851-857(1992).  
SQ SEQUENCE 9 AA; 943 MW; 2908176737686777 CRC64;

Query Match 28.6%; Score 2; DB 5; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7  
DB 2 PP 3

RESULT 53  
Q9GJV2 ID Q9GJV2 PRELIMINARY; PRT; 9 AA.  
AC Q9GJV2;  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
DE Actin (Fragment).  
OS Lagenorhynchus obliquidens (Pacific white-sided dolphin).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;  
OC Lagenorhynchus.  
OX NCBI\_TaxID=90247;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hare M.P., Cipriano F., Palumbi S.R.;  
RT "Slow Evolution of Genetic Monophyly in Dolphins: Implications for  
RT Speciation, Systematics and Conservation.";  
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF140811; AAF98684.1; -.  
DR EMBL; AF140826; AAF98679.1; -.  
DR EMBL; AF140827; AAF98680.1; -.  
DR EMBL; AF140828; AAF98681.1; -.  
DR EMBL; AF140829; AAF98682.1; -.  
DR EMBL; AF140830; AAF98683.1; -.  
FT NON\_TER 1 1  
FT NON\_TER 9 9  
SQ SEQUENCE 9 AA; 1049 MW; 1D0EF417740862C0 CRC64;

Query Match 28.6%; Score 2; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQ 5  
DB 8 HQ 9

```

RESULT 54
Q9T77
ID Q9T77 PRELIMINARY; PRT; 9 AA.
AC Q9T77;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Wilm's tumor protein 1 (Fragment).
GN WTL.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21015404; PubMed=11130975;
RA Brouillette J.A., Andrew J.R., Venta P.J.;
RT "Estimate of nucleotide diversity in dogs with a pool-and-sequence
method."
RL Mamm. Genome 11:1079-1086(2000).
DR EMBL; AF202074; AAF20919.1; -.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 1231 MW; 58DDF41416D1F403 CRC64;

Query Match 28.6%; Score 2; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQ 5
Db 4 HQ 5

RESULT 55
Q9GVJ3
ID Q9GVJ3 PRELIMINARY; PRT; 9 AA.
AC Q9GVJ3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Actin (Fragment).
OS Lagenorhynchus obscurus (Dusky dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC Lagenorhynchus.
OX NCBI_TaxID=27611;
RN [1]
RP SEQUENCE FROM N.A.
RX Hare M.P., Cipriano F., Palumbi S.R.;
RT "Slow Evolution of Genetic Monophyly in Dolphins: Implications for
Speciation, Systematics and Conservation."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF140834; AAF98687.1; -.
DR EMBL; AF140832; AAF98685.1; -.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 1049 MW; 1D0EF417740862C0 CRC64;

Query Match 28.6%; Score 2; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQ 5
Db 8 HQ 9

RESULT 56
Q9GVJ1
ID Q9GVJ1 PRELIMINARY; PRT; 9 AA.
AC Q9GVJ1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Actin (Fragment).
OS Lagenorhynchus acutus (Atlantic white-sided dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC Lagenorhynchus.
OX NCBI_TaxID=90246;
RN [1]
RP SEQUENCE FROM N.A.
RX Hare M.P., Cipriano F., Palumbi S.R.;
RT "Slow Evolution of Genetic Monophyly in Dolphins: Implications for
Speciation, Systematics and Conservation."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF140825; AAF98678.1; -.
DR EMBL; AF140822; AAF98675.1; -.
DR EMBL; AF140823; AAF98676.1; -.
DR EMBL; AF140824; AAF98677.1; -.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 1049 MW; 1D0EF417740862C0 CRC64;

Query Match 28.6%; Score 2; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQ 5
Db 8 HQ 9

RESULT 57
Q8WFT4
ID Q8WFT4 PRELIMINARY; PRT; 9 AA.
AC Q8WFT4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Cytochrome oxidase subunit II (Fragment).
GN COII.
OS Diadema antillarum.
OC Mitochondrion.
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinozoa; Euechinozoa; Diadematozoa; Diadematozoa; Diadematozoa;
OC Diadema.
OX NCBI_TaxID=105358;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=DCA3;
RC MEDLINE=21323357; PubMed=11430656;
RA Lessios H.A., Kessing B.D., Pearce J.S.;
RT "Population structure and speciation in tropical seas: global
phylogeography of the sea urchin Diadema."
RL Evolution 55:955-975(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=DCA3;
RC MEDLINE=21561594; PubMed=11703875;
RA Lessios H.A., Garrido M.J., Kessing B.D.;
RT "Demographic history of Diadema antillarum, a keystone herbivore on
Caribbean reefs."
RL Proc. R. Soc. Lond., B, Biol. Sci. 268:2347-2353(2001).
DR EMBL; AY012858; AAL33832.2; -.
KW Mitochondrion.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 1115 MW; EDF8DB1B173B46CA CRC64;

Query Match 28.6%; Score 2; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQ 5
Db 8 HQ 9

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QY 5 QP 6  
||  
Db 8 QP 9

## RESULT 58

P82440  
ID P82440 PRELIMINARY; PRT; 9 AA.  
AC P82440;  
DT 01-JUN-2000 (TrEMBLrel. 14, Created)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE 42 KDa cell wall protein (Fragment).  
OS Nicotiana tabacum (Common tobacco).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.  
OX NCBI\_TaxID=4097;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=cv. PETIT HAVANA;  
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,  
RA Wojtaszek P., Bolwell G.P.;  
RT "Proteomic study of secondary cell wall proteins from transformed  
RT tobacco culture."  
RL Planta 0:0-0(2000).  
CC -!- SUBCELLULAR LOCATION: CELL WALL.  
CC -!- TISSUE SPECIFICITY: XYLEM.  
KW Cell wall.  
FT NON-TER  
SQ SEQUENCE 9 AA; 1053 MW; 298CC9D2D5B1B07 CRC64;

Query Match 28.6%; Score 2; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6  
||  
Db 1 QP 2

## RESULT 59

O08979  
ID O08979 PRELIMINARY; PRT; 9 AA.  
AC O08979;  
DT 01-JUL-1997 (TrEMBLrel. 04, Created)  
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE AML1 protein (Fragment).  
GN AML1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NMRI; TISSUE=Tumor;  
RA MEDLINE=97332339; PubMed=9188573;  
RA Amtoft H.W., Sorensen A.B., Bareil C., Schmidt J., Luz A.,  
RA Pedersen F.S.;  
RT "Stability of AML1 (core) site enhancer mutations in T-lymphomas  
RT induced by attenuated SL3-3 murine leukemia virus mutants.";  
RL J. Virol. 71:5080-5087(1997).  
DR EMBL; Y11802; CAA72496.1; --  
FT NON-TER 1  
FT NON-TER 9  
SQ SEQUENCE 9 AA; 981 MW; 293E01E865A776D8 CRC64;

Query Match 28.6%; Score 2; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6  
||  
Db 3 QP 4

## RESULT 60

O90350  
ID O90350 PRELIMINARY; PRT; 9 AA.  
AC O90350;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Polyprotein (Fragment).  
OS Hepatitis G virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
OC GBV-C/HGV group.  
OX NCBI\_TaxID=45255;  
RN [1]\_TaxID=45255;  
RP SEQUENCE FROM N.A.  
RC STRAIN=SG3419;  
RX MEDLINE=99266893; PubMed=10335862;  
RA Wong S.B.J., Chan S.H., Ren E.C.;  
RT "Diversity of GB virus C/hepatitis G virus isolates in Singapore:  
RT predominance of group 2a and the Asian group 3 variant.";  
RL J. Med. Virol. 58:145-153(1999).  
DR EMBL; AF078065; AAC32371.1; --  
FT NON-TER 9  
SQ SEQUENCE 9 AA; 989 MW; D95CA5A5BEB9CDDD CRC64;

Query Match 28.6%; Score 2; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SW 2  
||  
Db 8 SW 9

## RESULT 61

O71069  
ID O71069 PRELIMINARY; PRT; 9 AA.  
AC O71069;  
DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Fusion protein (Fragment).  
GN F.  
OS Canine distemper virus.  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.  
OX NCBI\_TaxID=11232;  
RN [1]\_TaxID=11232;  
RP SEQUENCE FROM N.A.  
RC STRAIN=Dog EPM;  
RA Liemann H., Harder T., Haas L.;  
RT "Genetic analysis of the central untranslated genome region and the  
RT proximal coding part of the F gene of wild-type and vaccine distemper  
RT morbilliviruses.";  
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF026238; AAC09168.1; --  
FT NON-TER 9  
SQ SEQUENCE 9 AA; 984 MW; F29CB32760587331 CRC64;

Query Match 28.6%; Score 2; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MH 4  
||  
Db 1 MH 2

## RESULT 62

O92766  
ID O92766 PRELIMINARY; PRT; 9 AA.  
AC O92766;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
DE Fusion protein (Fragment).  
F.  
GN Canine distemper virus.  
OS Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.  
OC NCBI\_TaxID=11232;  
OX [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Dog #5526/89;  
RA Liemann H., Harder T., Haas L.;  
RT "Genetic analysis of the central untranslated genome region and the  
RT proximal coding part of the F gene of wild-type and vaccine distemper  
RT morbilliviruses."  
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF026237; AAC09167.1; -.  
FT NON\_TER 9  
SQ SEQUENCE 9 AA; 1011 MW; F281732760533441 CRC64;  
Query Match 28.6%; Score 2; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 3 MH 4  
Db 1 MH 2  
RESULT 63  
O71066  
ID O71066 PRELIMINARY; PRT; 9 AA.  
AC O71066;  
DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Fusion protein (Fragment).  
F.  
GN Canine distemper virus.  
OS Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.  
OC NCBI\_TaxID=11232;  
OX [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Dog #10757/96;  
RA Liemann H., Harder T., Haas L.;  
RT "Genetic analysis of the central untranslated genome region and the  
RT proximal coding part of the F gene of wild-type and vaccine distemper  
RT morbilliviruses."  
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF026234; AAC09164.1; -.  
FT NON\_TER 9  
SQ SEQUENCE 9 AA; 1124 MW; F29D04576044041 CRC64;  
Query Match 28.6%; Score 2; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 3 MH 4  
Db 1 MH 2  
RESULT 64  
Q9PRJ4  
ID Q9PRJ4 PRELIMINARY; PRT; 9 AA.  
AC Q9PRJ4;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE Bradykinin.  
OS Lepisosteus osseus (Long-nosed gar), and  
OS Amla calva (Bowfin).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Semionotiformes; Lepisosteidae;  
OC Lepisosteus  
OX NCBI\_TaxID=34771, 7924;  
GN [1]  
RP SEQUENCE.  
RX MEDLINE=95380361; PubMed=7651903;  
RA Conlon J.M., Platzack B., Marra L.E., Youson J.H., Olson K.R.;  
RT "Isolation and biological activity of [Trp5]bradykinin from the plasma  
RT of the phylogenetically ancient fish, the bowfin and the longnosed  
RT gar."  
RL Peptides 16:485-489(1995).  
SQ SEQUENCE 9 AA; 1099 MW; 3393D775A3786777 CRC64;  
Query Match 28.6%; Score 2; DB 13; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 6 PP 7  
Db 2 PP 3  
RESULT 65  
Q8AYL5  
ID Q8AYL5 PRELIMINARY; PRT; 9 AA.  
AC Q8AYL5  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Cytochrome P450 aromatase (Fragment).  
GN CYP19A.  
OS Carassius auratus (Goldfish).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Carassius.  
OX NCBI\_TaxID=7957;  
GN [1]  
RP SEQUENCE FROM N.A.  
RA Tchoudakova A.V., Kishida M., Wood E., Callard G.V.;  
RT "Promoter characteristics of two CYP19 genes differentially expressed  
RT in the brain and ovary of teleost fish."  
RL J. Steroid Biochem. Mol. Biol. 0:0-0(2001).  
DR EMBL; AF324897; AAN32618.1; -.  
FT NON\_TER 9  
SQ SEQUENCE 9 AA; 1060 MW; C49E76D7272B040D CRC64;  
Query Match 28.6%; Score 2; DB 13; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 5 QP 6  
Db 7 QP 8  
RESULT 66  
Q8AUM7  
ID Q8AUM7 PRELIMINARY; PRT; 9 AA.  
AC Q8AUM7;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Cytochrome P450 aromatase (Fragment).  
GN CYP19A.  
OS Carassius auratus (Goldfish).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Carassius.

```

OX  NCBI_TaxID=7957;
RN  [1]_TaxID=7957;
RP  SEQUENCE FROM N.A.
RA  Tchoudakova A.V., Kishida M., Wood E., Callard G.V.;
RT  "Promoter characteristics of two CYP19 genes differentially expressed
RL  in the brain and ovary of teleost fish.";
RL  J. Steroid Biochem. Mol. Biol. 0:0-0(2001).
DR  EMBL; AF324895; AN32616.1; -.
DR  EMBL; AF324896; AN32617.1; -.
FT  NON_TER
SQ  SEQUENCE 9 AA; 961 MW; C49E76D7272B187D CRC64;

Query Match      28.6%; Score 2; DB 13; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  5 QP 6
    ||
Db  7 QP 8

RESULT 67
ID  Q9R5T2      PRELIMINARY;      PRT;      10 AA.
AC  Q9R5T2;
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE  NADP-linked glucose-6-phosphate dehydrogenase (Fragment).
OS  Acetobacter hansenii.
OC  Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC  Acetobacteraceae; Gluconacetobacter.
OX  NCBI_TaxID=436;
RN  [1]
RP  SEQUENCE.
RX  MEDLINE=92027789; PubMed=1929428;
RA  Levy H.R., Cook C.;
RT  "Purification and properties of NADP-linked glucose-6-phosphate
RT  dehydrogenase from Acetobacter hansenii (Acetobacter xylinum).";
RL  Arch. Biochem. Biophys. 291:161-167(1991).
FT  NON_TER 1
FT  NON_TER 10
SQ  SEQUENCE 10 AA; 1111 MW; 5D91D4AAB2D77767 CRC64;

Query Match      28.6%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  6 PP 7
    ||
Db  4 PP 5

RESULT 68
ID  P83062      PRELIMINARY;      PRT;      10 AA.
AC  P83062;
DT  01-OCT-2001 (TrEMBLrel. 18, Created)
DT  01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DE  92 kDa protein (Fragment).
OS  Bacillus cereus.
OC  Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX  NCBI_TaxID=1396;
RN  [1]
RP  SEQUENCE.
RC  STRAIN=NCIMB 11796;
RA  Browne N., Dowds B.C.A.;
RL  Submitted (JUL-2001) to the SWISS-PROT data bank.
FT  NON_TER 10
SQ  SEQUENCE 10 AA; 1044 MW; 36E840B73AEB0777 CRC64;

Query Match      28.6%; Score 2; DB 2; Length 10;

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Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  6 PP 7
    ||
Db  3 PP 4

RESULT 69
ID  Q14096      PRELIMINARY;      PRT;      10 AA.
AC  Q14096;
DT  01-NOV-1996 (TrEMBLrel. 01, Created)
DT  01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE  CYP2B6 gene cryptic exon 3A of cytochrome P450IIB6.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=90174922; PubMed=2308828;
RA  Miles J.S., McLaren A.W., Gonzalez F.J., Wolf C.R.;
RT  "Alternative splicing in the human cytochrome P450IIB6 gene: use of a
RT  cryptic exon within intron 3 and splice acceptor site within exon 4.";
RL  Nucleic Acids Res. 18:189-189(1990).
DR  EMBL; X16864; CAA34754.1; -.
SQ  SEQUENCE 10 AA; 885 MW; 4181B9D87DC77767 CRC64;

Query Match      28.6%; Score 2; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  6 PP 7
    ||
Db  4 PP 5

RESULT 70
ID  Q15342      PRELIMINARY;      PRT;      10 AA.
AC  Q15342;
DT  01-NOV-1996 (TrEMBLrel. 01, Created)
DT  01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE  Aml1 protein (Fragment).
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=96226397; PubMed=8634147;
RA  Levanon D., Bernstein Y., Negraru V., Ghozi M.C., Bar-Am I.,
RA  Aloya R., Goldenberg D., Lotem J., Groner Y.;
RT  "A large variety of alternatively spliced and differentially expressed
RT  mRNAs are encoded by the human acute myeloid leukemia gene AML1.";
RL  DNA Cell Biol. 15:175-185(1996).
DR  EMBL; X90978; CAA62465.1; -.
FT  NON_TER 1
FT  NON_TER 1
SQ  SEQUENCE 10 AA; 1254 MW; 8D99287B441AF365 CRC64;

Query Match      28.6%; Score 2; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 SW 2
    ||
Db  3 SW 4

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RESULT 71
Q9UCR0      PRELIMINARY;      PRT;      10 AA.
AC Q9UCR0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE AUTOTAXIN (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=92129337; PubMed=1733949;
RA Stracke M.L., Krutzsch H.C., Unsworth E.J., Arestad A., Cioce V.,
RA Schiffman E., Liotta L.A.;
RT "Identification, purification, and partial sequence analysis of
RT autotaxin, a novel motility-stimulating protein.";
RL J. Biol. Chem. 267:2524-2529(1992).
FT NON_TER 1
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1193 MW; 3E01FB40544B19D7 CRC64;

Query Match      28.6%; Score 2; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7
Db 2 PP 3

RESULT 72
Q9UE86      PRELIMINARY;      PRT;      10 AA.
AC Q9UE86;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Collagen alpha 1(I) chain (Fragment).
GN COL1A1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92042176; PubMed=1939261;
RA Hawkins J.R., Superti-Furga A., Steinmann B., Dalglish R.;
RT "A 9-base pair deletion in COL1A1 in a lethal variant of osteogenesis
RT imperfecta.";
RL J. Biol. Chem. 266:22370-22374(1991).
DR EMBL; S66556; AAB20361.1; -.
FT NON_TER 1
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 777 MW; 2D20F6D8676DD867 CRC64;

Query Match      28.6%; Score 2; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PP 7
Db 2 PP 3

RESULT 73
Q8WFT6      PRELIMINARY;      PRT;      10 AA.
AC Q8WFT6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

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DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Cytochrome oxidase subunit II (Fragment).
GN COII.
OS Diadema antillarum.
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Diadematacea; Diadematoidea; Diademataidae;
OC Diadema.
OX NCBI_TaxID=105358;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=DCA1;
RX MEDLINE=21323357; PubMed=11430656;
RA Lessios H.A., Kessing B.D., Pearse J.S.;
RT "Population structure and speciation in tropical seas: global
RT phylogeography of the sea urchin Diadema.";
RL Evolution 55:955-975(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=DCA1;
RX MEDLINE=21561594; PubMed=11703875;
RA Lessios H.A., Garrido M.J., Kessing B.D.;
RT "Demographic history of Diadema antillarum, a keystone herbivore on
RT Caribbean reefs.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 268:2347-2353(2001).
DR EMBL; AY012856; AAL33830.2; -.
KW Mitochondrion.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 10 AA; 1301 MW; EDBB101B173B46CA CRC64;

Query Match      28.6%; Score 2; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QP 6
Db 9 QP 10

RESULT 74
Q8WFT5      PRELIMINARY;      PRT;      10 AA.
AC Q8WFT5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Cytochrome oxidase subunit II (Fragment).
GN COII.
OS Diadema antillarum.
OC Mitochondrion.
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Diadematacea; Diadematoidea; Diademataidae;
OC Diadema.
OX NCBI_TaxID=105358;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=DCA2;
RX MEDLINE=21323357; PubMed=11430656;
RA Lessios H.A., Kessing B.D., Pearse J.S.;
RT "Population structure and speciation in tropical seas: global
RT phylogeography of the sea urchin Diadema.";
RL Evolution 55:955-975(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=DCA2;
RX MEDLINE=21561594; PubMed=11703875;
RA Lessios H.A., Garrido M.J., Kessing B.D.;
RT "Demographic history of Diadema antillarum, a keystone herbivore on
RT Caribbean reefs.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 268:2347-2353(2001).
DR EMBL; AY012857; AAL33831.2; -.
KW Mitochondrion.
FT NON_TER 1
FT NON_TER 1

```

```
SQ SEQUENCE 10 AA; 1262 MW; COBB101B173B46DD CRC64;

Query Match      28.6%; Score 2; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
Db 9 QP 10

RESULT 75
Q8SHA8 PRELIMINARY; PRT; 10 AA.
AC Q8SHA8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Rhampholeon spectrum.
OS Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Iguania; Acrodonta; Chamaeleonidae;
OC Rhampholeon.
OX NCBI_TaxID=179929;
RN [1]
RP SEQUENCE FROM N.A.
RA Townsend T.M., Larson A.L.;
RT "Molecular Phylogenetics and Mitochondrial Genomic Evolution in the
RT Chamaeleonidae (Reptilia, Squamata).";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF448772; AAL90598.1; -.
KW Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1279 MW; 35BF8E27336409D7 CRC64;

Query Match      28.6%; Score 2; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QP 6
Db 2 QP 3

Search completed: November 25, 2003, 19:34:03
Job time : 14.1453 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:16:09 ; Search time 17.8563 Seconds  
(without alignments)  
62.189 Million cell updates/second

Title: US-09-641-801-24

Perfect score: 7  
Sequence: 1 SWMHOPP 7

Sequence: 1 SWMHQPP 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size :

Total number of hits satisfying chosen parameters: 399878

Minimum	DB	seq	length:	3
Maximum	DB	seq	length:	20

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : A Geneseq 19Jun03:\*

1:	SIDS1/cgcdata/geneseq/geneseq-emb1/AAL1980.DAT.*
2:	SIDS1/cgcdata/geneseq/geneseq-emb1/AAL1981.DAT.*
3:	SIDS1/cgcdata/geneseq/geneseq-emb1/AAL1982.DAT.*
4:	SIDS1/cgcdata/geneseq/geneseq-emb1/AAL1983.DAT.*
5:	SIDS1/cgcdata/geneseq/geneseq-emb1/AAL1984.DAT.*
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7:	SIDS1/cgcdata/geneseq/geneseq-emb1/AAL1986.DAT.*
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19:	SIDS1/cgcdata/geneseq/geneseq-emb1/AAL1998.DAT.*
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23:	SIDS1/cgcdata/geneseq/geneseq-emb1/AAL2002.DAT.*
24:	SIDS1/cgcdata/geneseq/geneseq-emb1/AAL2003.DAT.*
25:	SIDS1/cgcdata/geneseq/geneseq-emb1/AAL2004.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query %			DB	ID	Description
	Score	Match	Length			
1	7	100.0	7	22	AAB72269	Colostrinin derive
2	7	100.0	7	22	AAB72522	Colostrinin pepcid
3	7	100.0	7	22	AAB72554	Colostrinin pepcid
4	7	100.0	7	22	AAB59332	Ewe colostrinin pe
5	7	100.0	7	23	AAE20251	Colostrinin consti
6	7	100.0	7	23	AAE51058	Colostrinin consti
7	7	100.0	7	23	AAO14600	Neural cell regula
8	6	85.7	19	19	AAW40310	Human ITAK protein
9	5	71.4	15	22	AAB72279	Colostrinin derive

83 3 42.9 7 22 AAM44329 H11 binding site c  
84 3 42.9 7 22 AAM45562 H11 binding site c  
85 3 42.9 7 22 AAM45567 H11 binding site c  
86 3 42.9 7 22 AAM45582 H11 binding site c  
87 3 42.9 7 22 AAM45587 H11 binding site c  
88 3 42.9 7 22 AAM45619 H11 binding site c  
89 3 42.9 7 22 AAM45624 H11 binding site c  
90 3 42.9 7 22 AAM45639 H11 binding site c  
91 3 42.9 7 22 AAM45644 H11 binding site c  
92 3 42.9 7 22 AAM45649 H11 binding site c  
93 3 42.9 7 22 AAM45654 H11 binding site c  
94 3 42.9 7 22 AAM45659 H11 binding site c  
95 3 42.9 7 22 AAM45664 H11 binding site c  
96 3 42.9 7 22 AAM45669 H11 binding site c  
97 3 42.9 7 22 AAM45674 H11 binding site c  
98 3 42.9 7 22 AAM45679 H11 binding site c  
99 3 42.9 7 22 AAM45684 H11 binding site c  
100 3 42.9 7 22 AAM45689 H11 binding site c

ALIGNMENTS

RESULT 1  
AAB72269  
ID AAB72269 standard; peptide; 7 AA.  
XX  
AC AAB72269;  
XX  
DT 14-MAY-2001 (first entry)  
XX  
DE Colostrinin derived cytokine inducing peptide SEQ ID 24.  
XX  
KW Colostrinin; immune response; cytokine; blood cell proliferation;  
KW central nervous system disorder; neurological disorder; mental disorder;  
KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;  
KW neurosis; infection.  
XX  
OS Synthetic.  
XX  
FN WO20011937-A2.  
XX  
PD 22-FEB-2001.  
XX  
PF 17-AUG-2000; 2000WO-US22818.  
XX  
PR 17-AUG-1999; 99US-0149311.  
XX  
PA (TEXA ) UNIV TEXAS SYSTEM.  
PA (REGG-) REGEN THERAPEUTICS PLC.  
XX  
PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
XX  
DR WPI; 2001-202804/20.  
XX  
PT Inducing a cytokine and modulating an immune response, useful for  
PT treating central nervous system diseases and bacterial and viral  
PT infections, comprises administering colostrinin as an immunological  
PT regulator -  
XX  
PS Claim 1; Page 34; 50pp; English.  
XX  
CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,  
CC a proline rich polypeptide aggregate contained in colostrum. The  
CC peptides have immune response modulatory activity, and are capable of  
CC inducing cytokines. Colostrinin and its derived peptides are useful for  
CC inducing cytokine production, for modulating an immunological response  
CC and for inducing blood cell proliferation. The peptides are useful in the  
CC treatment of disorders of the central nervous system, neurological  
CC disorders, mental disorders, dementia, neurodegenerative diseases,  
CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic  
CC disorders of the immune system, bacterial and viral infections and  
CC acquired immunological deficiencies.

XX  
SQ Sequence 7 AA;  
Query Match 100.0%; Score 7; DB 22; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SWMHQPP 7  
Db 1 SWMHQPP 7  
RESULT 2  
AAB72522  
ID AAB72522 standard; Peptide; 7 AA.  
XX  
AC AAB72522;  
XX  
DT 09-MAY-2001 (first entry)  
XX  
DE Colostrinin peptide #23.  
XX  
KW Dermatalogical; oxidative stress regulator; colostrinin.  
XX  
OS Unidentified.  
XX  
FN WO200112650-A2.  
XX  
PD 22-FEB-2001.  
XX  
PF 17-AUG-2000; 2000WO-US22665.  
XX  
PR 17-AUG-1999; 99US-0149310.  
XX  
PA (TEXA ) UNIV TEXAS SYSTEM.  
XX  
PI Stanton GJ, Hughes TK, Boldogh I;  
XX  
DR WPI; 2001-218342/22.  
XX  
PT Modulating oxidative stress level in a cell, involves contacting the  
PT cell with an oxidative stress regulator selected from colostrinin, its  
PT constituent peptide, analog or their combinations -  
XX  
PS Claim 6; Page 26; 48pp; English.  
XX  
CC The present invention relates to a method for modulating the oxidative  
CC stress level in a cell or a patient, comprising contacting the cell with,  
CC or administering to the patient, an oxidative stress regulator selected  
CC from colostrinin, or its constituent peptide (e.g. the present peptide),  
CC to change the level of an oxidising species in the cell. The method can  
CC be used to treat oxidative damage to skin, by decreasing or preventing an  
CC increase in the level of damage to a biomolecule of the patient.  
XX  
SQ Sequence 7 AA;  
Query Match 100.0%; Score 7; DB 22; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SWMHQPP 7  
Db 1 SWMHQPP 7  
RESULT 3  
AAB72554  
ID AAB72554 standard; Peptide; 7 AA.  
XX  
AC AAB72554;  
XX  
DT 09-MAY-2001 (first entry)  
XX

DE	Colostrinin peptide #23.
XX	Neuroprotective; neural cell differentiation regulator; colostrinin;
KW	colostrum.
XX	
OS	Unidentified.
XX	
PN	WO200112651-A2.
XX	
PD	22-FEB-2001.
XX	
PF	17-AUG-2000; 2000WO-US22774.
XX	
PP	17-AUG-1999; 99US-0149633.
XX	
PR	(TEXA ) UNIV TEXAS SYSTEM.
XX	
PA	Boldogh I;
XX	
PI	WPI; 2001-226545/23.
XX	
DR	Use of colostrinin, its constituent peptide or analog as a neural cell
XX	regulator, for promoting neural cell differentiation and treating
PT	damaged neural cells in a patient -
PT	
XX	
PS	Claim 6; Page 21; 35pp; English.
XX	
CC	The present invention relates to a method for promoting neural cell
CC	differentiation and treating damaged neural cells, using colostrinin and
CC	colostrinin constituent peptides (e.g. the present peptide) as a neural
CC	cell regulator. Colostrinin is a polypeptide complex found in colostrum.
XX	
SQ	Sequence 7 AA;
Query Match	100.0%; Score 7; DB 22; Length 7;
Best Local Similarity	100.0%; Pred. No. 9.3e+05;
Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 SWMHQPP 7 
Dd	1 SWMHQPP 7
RESULT 4	
AABS9332	
ID	AABS9332 standard; Peptide; 7 AA.
XX	
AC	AAB59332;
XX	
DT	21-MAR-2001 (first entry)
XX	
DE	Ewe colostrinin peptide fragment C-7.
XX	
KW	Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
KW	central nervous system disorder; dietary supplement; beta-amylolyd plaque.
XX	
OS	Ovis sp.
XX	
PN	WO2000075173-A2.
XX	
PD	14-DEC-2000.
XX	
PF	02-JUN-2000; 2000WO-GB02128.
XX	
PR	02-JUN-1999; 99GB-0012852.
XX	
PA	(REGE-) REGEN THERAPEUTICS PLC.
XX	
PI	Georgiades JA;
XX	
DR	WPI; 2001-071058/08.
XX	
PT	Peptides having an N-terminal amino acid sequence isolated from

colostrinin for treating e.g. disorders of the central nervous system and immune system, viral and bacterial infections, and diseases characterized by amyloid plaques -

Claim 7; Page 27; 63pp; English.

The present invention provides the sequences of a number of peptides found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide fragment of colostrum. These peptides can be used in the treatment of central nervous system disorders such as senile dementia, Parkinson's disease, Alzheimer's disease, psychosis and neurosis, immune system disorders such as bacterial and viral infections, to improve the development of a child's immune system, as a dietary supplement, and to promote the dissolution of beta-amyloid plaques.

Sequence 7 AA;

Query Match 100.0%; Score 7; DB 22; Length 7;  
Best Local Similarity 100.0%; Pred. NO. 9.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SWMHQPP 7  
Db 1 SWMHQPP 7

RESULT 5  
AAE20251  
ID AAE20251 standard; peptide; 7 AA.  
XX AC AAE20251;  
XX DT 18-JUN-2002 (first entry)  
XX DE Colostrinin constituent peptide #23.  
XX KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;  
XX KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;  
XX KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;  
XX KW transplantation; implantation; dermatological; vulnery.  
XX OS Unidentified.  
XX FH Key Location/Qualifiers  
FT Modified-site 7 /note= "Optionally C-terminal amide"  
FT XX  
FN WO200213850-A1.  
PD 21-FEB-2002.  
XX  
PF 17-AUG-2000; 2000WO-US22776.  
XX  
PR 17-AUG-2000; 2000WO-US22776.  
XX  
PA (TEXA ) UNIV TEXAS SYSTEM.  
XX  
PI Stanton GJ, Hughes TK, Boldogh I;  
XX  
DR WPI; 2002-269151/31.  
XX  
PT Composition useful for the modulation of blood cell proliferation in a  
PT patient comprises a blood cell regulator selected from colostrinin, its  
PT constituent peptide and/or analog -  
XX  
PS Claim 6; Page 26; 51pp; English.  
XX  
CC The invention relates to a composition which comprises a blood cell  
CC regulator selected from colostrinin, its constituent peptide and/or  
CC analogue. The invention is used for modulating the oxidative stress  
CC level in a cell e.g. mammalian or human cell present in a cell culture,  
CC tissue, organ, or organism; or for treating oxidative damage to the skin  
CC of a patient e.g. animal or human; to modulate oxidative stress during/



CC after a premature birth or normal birth, preventing/delaying aging in a  
 CC patient, enhancing wound healing, and the reduction of side effects of  
 CC cosmetic procedures. The method changes the level of an oxidising species  
 CC in the cell, such as decreases or prevents increase in the level of  
 CC damage to a biomolecule of the patient selected from DNA, protein and/or  
 CC lipid, compared to the same conditions when the oxidative stress  
 CC regulator is not present. The modulation of oxidative stress results in  
 CC enhanced repair, regeneration, and replacement of cells, tissues and  
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
 CC external organs), as well as enhanced preservation of such organs for  
 CC transplantation, implantation, or scientific research. The present  
 CC sequence is a colostrinin constituent peptide.

XX Sequence 7 AA;

Query Match 100.0%; Score 7; DB 23; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SWMHQPP 7  
 |||||  
 Db 1 SWMHQPP 7

# RESULT 6

AAM51058  
 ID AAM51058 standard; Peptide; 7 AA.

XX AAM51058;

DT 30-MAY-2002 (first entry)

XX Colostrinin constituent peptide (casein amino acids 157-163).

DE Colostrinin; colostrum; immunomodulator; cardiovascular;

KW blood cell regulator; cytokine inducer; beta-casein; human.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 7 /note= "Optional C-terminal amidation"

XX WO200213849-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22775.

XX 17-AUG-2000; 2000WO-US22775.

XX (TEXA ) UNIV TEXAS SYSTEM.

PA (REGE-) REGEN THERAPEUTICS PLC.

PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2002-269150/31.

DR Modulation of blood cell proliferation in a patient involves use of  
 PT blood cell regulator selected from colostrinin, its constituent peptide  
 PT and/or analogue -

XX Claim 1; Page 34; 54pp; English.

XX The present sequence is that of a colostrinin constituent peptide  
 CC that is used as an immunological regulator and as a blood cell  
 CC regulator in claimed methods of the invention. It is classified  
 CC as having a beta-casein homologue precursor, and corresponds to  
 CC casein amino acids 157-163. Methods are claimed for: inducing a  
 CC cytokine in a cell by contact with an immunological regulator,  
 CC where the cell is present in a cell culture, a tissue, an organ  
 CC or an organism, and the cell is mammalian, including human;  
 CC modulating an immune response in a cell by contact with the

CC immunological regulator under conditions effective to induce a  
 CC cytokine; modulating an immune response in a patient by administering  
 CC an immunological regulator under conditions effective to induce a  
 CC cytokine, where the immunological regulator is administered topically  
 CC or as part of a dietary supplement, and where the immune response is  
 CC specific or non specific, an interferon response or an antibody  
 CC response; modulating blood cell proliferation by contacting blood  
 CC cells with a blood cell regulator, where the blood cells are present  
 CC in a cell culture or an organism, are mammalian or human, and where  
 CC the blood cells are increased in number or differentiated; and a  
 CC method for modulating blood cell proliferation in a patent. A  
 CC claimed cytokine-inducing composition comprises a pharmaceutical  
 CC carrier and an active agent such as the present peptide.

XX Sequence 7 AA;

Query Match 100.0%; Score 7; DB 23; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SWMHQPP 7  
 |||||  
 Db 1 SWMHQPP 7

# RESULT 7

AAO14600  
 ID AAO14600 standard; peptide; 7 AA.

XX AAO14600;

DT 27-MAY-2002 (first entry)

XX Neural cell regulatory colostrinin peptide 23.

DE Neural cell differentiation; neural cell regulator; colostrinin peptide;

KW neural cell formation; proline-rich polypeptide aggregate; colostrum;

XX neural cell treatment.

XX Unidentified.

XX Key Location/Qualifiers

FT Modified-site 7 /note= "Optional C-terminal amide"

XX WO200213851-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22777.

XX 17-AUG-2000; 2000WO-US22777.

XX (TEXA ) UNIV TEXAS SYSTEM.

PA Boldogh I, Stanton JG, Hughes TK;

XX WPI; 2002-269152/31.

DR Promoting cell differentiation in a patient involves use of blood cell  
 PT regulator selected from colostrinin, its constituent peptide and/or  
 PT analog -

XX Claim 7; Page 21; 37pp; English.

XX The invention comprises a method for promoting cell differentiation (e.g.  
 CC neural cell differentiation). The method involves contacting cells with a  
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the  
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich  
 CC polypeptide aggregate that is present in colostrum. The method of the  
 CC invention is useful for promoting the differentiation of cells and for  
 CC treating damaged neural cells in a patient. The present amino acid  
 CC sequence represents a specifically claimed colostrinin peptide used in

CC the method of the invention.  
 XX Sequence 7 AA;  
 SQ

Query Match 100.0%; Score 7; DB 23; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SWMHQPP 7  
 |||||  
 Db 1 SWMHQPP 7

RESULT 8  
 AAW40310  
 ID AAW40310 standard; Protein; 19 AA.  
 XX  
 AC AAW40310;  
 XX  
 DT 23-JUN-1998 (first entry)  
 XX  
 DE Human ITAK protein peptide substrate.  
 XX  
 KW Interleukin-1/tumour necrosis factor activated kinase; ITAK; inhibitor;  
 KW cytokine mediated inflammation; antagonist; disorder; therapy.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9747750-A1.  
 XX  
 PD 18-DEC-1997.  
 XX  
 PF 09-JUN-1997; 97WO-US08516.  
 XX  
 PR 10-JUN-1996; 96US-0633414.  
 XX  
 PA (IMMV ) IMMUNEX CORP.  
 XX  
 PI Anderson DM, Bird TA, Sims JE, Virca G;  
 XX  
 DR WPI; 1998-052314/05.  
 XX  
 PT Nucleic acid encoding interleukin-1/tumour necrosis factor activated  
 PT kinase - used to identify specific antagonists for treatment of  
 PT cytokine-mediated inflammation  
 XX  
 PS Claim 20; Page 33; 80pp; English.  
 XX  
 CC This sequence represents a peptide substrate used to assay a novel  
 CC interleukin-1/tumour necrosis factor alpha activated kinase (ITAK).  
 CC Antagonists of ITAK are used to treat IL-1 or TNF alpha-mediated  
 CC inflammatory disorders e.g. rheumatoid arthritis, inflammatory bowel  
 CC disease, type I diabetes, psoriasis, Alzheimer's disease, reperfusion  
 CC injury, malignancy, transplant rejection, neuropathy associated with  
 CC human immunodeficiency virus etc. Cells containing ITAK can be used to  
 CC raise antibodies for assay of ITAK or to inhibit IL-1 and TNF alpha  
 CC activity. Gene products that associate with ITAK are potential inhibitors  
 CC and can be used to detect ITAK genes. Antisense sequences inhibit  
 CC expression of ITAK. Inhibition of ITAK selectively blocks cell responses  
 CC to IL-1 and TNF alpha, but not responses to other cytokines.  
 XX  
 SQ Sequence 19 AA;  
 XX

Query Match 85.7%; Score 6; DB 19; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 0.39;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SWMHQP 6  
 |||||  
 Db 12 SWMHQP 17

RESULT 9

AAB72279  
 ID AAB72279 standard; peptide; 15 AA.  
 XX  
 AC AAB72279;  
 XX  
 DT 14-MAY-2001 (first entry)  
 XX  
 DE Colostrinin derived cytokine inducing peptide SEQ ID 34.  
 XX  
 KW Colostrinin; immune response; cytokine; blood cell proliferation;  
 KW central nervous system disorder; neurological disorder; mental disorder;  
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;  
 KW neurosis; infection.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200111937-A2.  
 XX  
 PD 22-FEB-2001.  
 XX  
 PF 17-AUG-2000; 2000WO-US22818.  
 XX  
 PR 17-AUG-1999; 99US-0149311.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 PA (REGE-) REGEN THERAPEUTICS PLC.  
 XX  
 PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
 XX  
 DR WPI; 2001-202804/20.  
 XX  
 PT Inducing a cytokine and modulating an immune response, useful for  
 PT treating central nervous system diseases and bacterial and viral  
 PT infections, comprises administering colostrinin as an immunological  
 PT regulator -  
 XX  
 PS Claim 1; Page 34; 50pp; English.  
 XX  
 CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,  
 CC a proline rich polypeptide aggregate contained in colostrum. The  
 CC peptides have immune response modulatory activity, and are capable of  
 CC inducing cytokines. Colostrinin and its derived peptides are useful for  
 CC inducing cytokine production, for modulating an immunological response  
 CC and for inducing blood cell proliferation. The peptides are useful in the  
 CC treatment of disorders of the central nervous system, neurological  
 CC disorders, mental disorders, dementia, neurodegenerative diseases,  
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic  
 CC disorders of the immune system, bacterial and viral infections and  
 CC acquired immunological deficiencies.  
 XX  
 SQ Sequence 15 AA;  
 XX

Query Match 71.4%; Score 5; DB 22; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.9;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHQPP 7  
 |||||  
 Db 1 MHQPP 5

RESULT 10  
 AAB72531  
 ID AAB72531 standard; Peptide; 15 AA.  
 XX  
 AC AAB72531;  
 XX  
 DT 09-MAY-2001 (first entry)  
 XX  
 DE Colostrinin peptide #32.  
 XX  
 KW Dermatalogical; oxidative stress regulator; colostrinin.  
 XX

```

OS Unidentified.
XX WO200112650-A2.
XX
XX 22-FEB-2001.
XX
XX 17-AUG-2000; 2000WO-US22665.
XX
XX 17-AUG-1999; 99US-0149310.
XX
XX (TEXA ) UNIV TEXAS SYSTEM.
XX
XX Stanton GJ, Hughes TK, Boldogh I;
XX
XX WPI; 2001-218342/22.
XX
XX Modulating oxidative stress level in a cell, involves contacting the
XX cell with an oxidative stress regulator selected from colostrinin, its
XX constituent peptide, analog or their combinations -
XX
XX Claim 6; Page 26; 48pp; English.
XX
XX The present invention relates to a method for modulating the oxidative
XX stress level in a cell or a patient, comprising contacting the cell with,
XX or administering to the patient, an oxidative stress regulator selected
XX from colostrinin, or its constituent peptide (e.g. the present peptide),
XX to change the level of an oxidising species in the cell. The method can
XX be used to treat oxidative damage to skin, by decreasing or preventing an
XX increase in the level of damage to a biomolecule of the patient.
XX
XX Sequence 15 AA;
XX
XX Query Match 71.4%; Score 5; DB 22; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 5.9;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 3 MHQPP 7
XX Db 1 MHQPP 5
XX
XX RESULT 11
XX AAB72563
XX ID AAB72563 standard; Peptide; 15 AA.
XX
XX AC AAB72563;
XX
XX DT 09-MAY-2001 (first entry)
XX
XX DE Colostrinin peptide #32.
XX
XX KW Neuroprotective; neural cell differentiation regulator; colostrinin;
XX colostrum.
XX
XX OS Unidentified.
XX
XX PN WO200112651-A2.
XX
XX PD 22-FEB-2001.
XX
XX PF 17-AUG-2000; 2000WO-US22774.
XX
XX PR 17-AUG-1999; 99US-0149633.
XX
XX PA (TEXA ) UNIV TEXAS SYSTEM.
XX
XX PI Boldogh I;
XX
XX DR WPI; 2001-226545/23.
XX
XX PT Use of colostrinin, its constituent peptide or analog as a neural cell
XX regulator, for promoting neural cell differentiation and treating
XX damaged neural cells in a patient -
XX
XX Claim 6; Page 22; 35pp; English.
XX
XX The present invention relates to a method for promoting neural cell
XX differentiation and treating damaged neural cells, using colostrinin and
XX colostrinin constituent peptides (e.g. the present peptide) as a neural
XX cell regulator. Colostrinin is a polypeptide complex found in colostrum.
XX
XX Sequence 15 AA;
XX
XX Query Match 71.4%; Score 5; DB 22; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 5.9;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 3 MHQPP 7
XX Db 1 MHQPP 5
XX
XX RESULT 12
XX AAB59334
XX ID AAB59334 standard; Peptide; 15 AA.
XX
XX AC AAB59334;
XX
XX DT 21-MAR-2001 (first entry)
XX
XX DE Ewe colostrinin peptide fragment C-9.
XX
XX KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
XX central nervous system disorder; dietary supplement; beta-amyloid plaque.
XX
XX OS Ovis sp.
XX
XX PN WO200075173-A2.
XX
XX PD 14-DEC-2000.
XX
XX PF 02-JUN-2000; 2000WO-GB02128.
XX
XX PR 02-JUN-1999; 99GB-0012852.
XX
XX PA (REGG-) REGEN THERAPEUTICS PLC.
XX
XX PI Georgiades JA;
XX
XX DR WPI; 2001-071058/08.
XX
XX DE Peptides having an N-terminal amino acid sequence isolated from
XX colostrinin for treating e.g. disorders of the central nervous system
XX and immune system, viral and bacterial infections, and diseases
XX characterized by amyloid plaques -
XX
XX PS Claim 7; Page 27; 63pp; English.
XX
XX CC The present invention provides the sequences of a number of peptides
XX found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
XX fragment of colostrum. These peptides can be used in the treatment of
XX central nervous system disorders such as senile dementia, Parkinson's
XX disease, Alzheimer's disease, psychosis and neurosis, immune system
XX disorders such as bacterial and viral infections, to improve the
XX development of a child's immune system, as a dietary supplement, and to
XX promote the dissolution of beta-amyloid plaques.
XX
XX Sequence 15 AA;
XX
XX Query Match 71.4%; Score 5; DB 22; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 5.9;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 3 MHQPP 7
XX Db 1 MHQPP 5

```

## RESULT 13

AAE20261  
ID AAE20261 standard; peptide; 15 AA.

AAE20261;  
AC

XX 18-JUN-2002 (first entry)

XX Colostrinin constituent peptide #32.

XX Blood cell regulator; colostrinin; constituent peptide; oxidative stress;  
KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;  
KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;  
KW transplantation; implantation; dermatological; vulnery.

XX Unidentified.

XX Key Location/Qualifiers  
FH Modified-site 15  
FT /note= "Optionally C-terminal amide"

XX WO200213850-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22776.

XX 17-AUG-2000; 2000WO-US22776.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX Stanton GJ, Hughes TK, Boldogh I;

XX WPI; 2002-269151/31.

XX Composition useful for the modulation of blood cell proliferation in a  
PT patient comprises a blood cell regulator selected from colostrinin, its  
PT constituent peptide and/or analog -

XX Claim 6; Page 26; 5pp; English.

XX The invention relates to a composition which comprises a blood cell  
CC regulator selected from colostrinin, its constituent peptide and/or  
CC analogue. The invention is used for modulating the oxidative stress  
CC level in a cell e.g. mammalian or human cell present in a cell culture,  
CC tissue, organ, or organism; or for treating oxidative damage to the skin  
CC of a patient e.g. animal or human; to modulate oxidative stress during/  
CC after a premature birth or normal birth, preventing/delaying aging in a  
CC patient, enhancing wound healing, and the reduction of side effects of  
CC cosmetic procedures. The method changes the level of an oxidizing species  
CC in the cell, such as decreases or prevents increase in the level of  
CC damage to a biomolecule of the patient selected from DNA, protein and/or  
CC lipid, compared to the same conditions when the oxidative stress  
CC regulator is not present. The modulation of oxidative stress results in  
CC enhanced repair, regeneration, and replacement of cells, tissues and  
CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
CC external organs), as well as enhanced preservation of such organs for  
CC transplantation, implantation, or scientific research. The present  
CC sequence is a colostrinin constituent peptide.

XX Sequence 15 AA;

Query Match 71.4%; Score 5; DB 23; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.9;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHQPP 7

DB 1 MHQPP 5

## RESULT 14

AAW51066

XX ID AAW51066 standard; Peptide; 15 AA.

XX AAW51066;

XX 30-MAY-2002 (first entry)

XX Colostrinin constituent peptide (casein amino acids 159-173).

XX Colostrinin; colostrum; immunomodulator; cardiovascular;

XX Blood cell regulator; cytokine inducer; beta-casein; human.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 15  
FT /note= "optional C-terminal amidation"

XX WO200213849-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22775.

XX 17-AUG-2000; 2000WO-US22775.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX (REGB-) REGEN THERAPEUTICS PLC.

XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2002-269150/31.

XX Modulation of blood cell proliferation in a patient involves use of  
PT blood cell regulator selected from colostrinin, its constituent peptide  
PT and/or analogue -

XX Claim 1; Page 34; 54pp; English.

XX The present sequence is that of a colostrinin constituent peptide  
CC that is used as an immunological regulator and as a blood cell  
CC regulator in claimed methods of the invention. It is classified  
CC as having a beta-casein homologue precursor, and corresponds to  
CC casein amino acids 159-173. Methods are claimed for: inducing a  
CC cytokine in a cell by contact with an immunological regulator,  
CC where the cell is present in a cell culture, a tissue, an organ  
CC or an organism, and the cell is mammalian, including human;  
CC modulating an immune response in a cell by contact with the  
CC immunological regulator under conditions effective to induce a  
CC cytokine; modulating an immune response in a patient by administering  
CC an immunological regulator under conditions effective to induce a  
CC cytokine, where the immunological regulator is administered topically  
CC or as part of a dietary supplement, and where the immune response is  
CC specific or non specific, an interferon response or an antibody  
CC response; modulating blood cell proliferation by contacting blood  
CC cells with a blood cell regulator, where the blood cells are present  
CC in a cell culture or an organism, are mammalian or human, and where  
CC the blood cells are increased in number or differentiated; and a  
CC method for modulating blood cell proliferation in a patient. A  
CC claimed cytokine-inducing composition comprises a pharmaceutical  
CC carrier and an active agent such as the present peptide.

XX Sequence 15 AA;

Query Match 71.4%; Score 5; DB 23; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.9;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHQPP 7

DB 1 MHQPP 5

```

RESULT 15
AAO14610
ID AAO14610 standard; peptide; 15 AA.
XX
AC AAO14610;
XX
DT 27-MAY-2002 (first entry)
XX
DE Neural cell regulatory colostrinin peptide 32.
XX
KW Neural cell differentiation; neural cell regulator; colostrinin peptide;
KW neural cell formation; proline-rich polypeptide aggregate; colostrum;
KW neural cell treatment.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Modified-site 15
FT /note= "Optional C-terminal amide"
XX
PN WO200213851-A1.
XX
PD 21-FEB-2002.
XX
PF 17-AUG-2000; 2000WO-US22777.
XX
PR 17-AUG-2000; 2000WO-US22777.
XX
PA (TEXA ) UNIV TEXAS SYSTEM.
XX
PI Boldogh I, Stanton JG, Hughes TK;
XX
DR WPI; 2002-269152/31.
XX
PT Promoting cell differentiation in a patient involves use of blood cell
PT regulator selected from colostrinin, its constituent peptide and/or
PT analog.
XX
PS Claim 7; Page 22; 37pp; English.
XX
CC The invention comprises a method for promoting cell differentiation (e.g.
CC neural cell differentiation). The method involves contacting cells with a
CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
CC cells in morphology to form neural cells. Colostrinin is a proline-rich
CC polypeptide aggregate that is present in colostrum. The method of the
CC invention is useful for promoting the differentiation of cells and for
CC treating damaged neural cells in a patient. The present amino acid
CC sequence represents a specifically claimed colostrinin peptide used in
CC the method of the invention.
XX
SQ Sequence 15 AA;
XX
Query Match 71.4%; Score 5; DB 23; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 MHQPP 7
Db 1 MHQPP 5
XX
RESULT 16
AAG78781
ID AAG78781 standard; peptide; 10 AA.
XX
AC AAG78781;
XX
DT 10-JAN-2002 (first entry)
XX
DE Stachybotrys echinata derived peptide.
XX
KW Isoindole derivative; cardiant; antidiabetic; antimicrobial;
XX
antibiotic; SERCA2 inhibitor; heart insufficiency; circulatory system;
XX diabetes; infection.
XX
OS Stachybotrys echinata.
XX
PN EP1130027-A1.
XX
PD 05-SEP-2001.
XX
PF 29-FEB-2000; 2000EP-0104114.
XX
PR 29-FEB-2000; 2000EP-0104114.
XX
PA (AVET ) AVENTIS PHARMA DEUT GMBH.
XX
PI Vertesy L, Kogler H, Markus A, Schiell M;
XX
DR WPI; 2001-627636/73.
XX
FT New isoindole derivatives prepared by microbial fermentation, useful
FT for the treatment and prevention of heart insufficiency, diabetes
FT mellitus and microbial infection.
XX
PS Claim 6; Page 18; 21pp; German.
XX
CC The present invention relates to isoindole derivatives capable of acting
CC as SERCA2 inhibitors. These can be used in the prevention and treatment
CC of heart insufficiency, weakness in the heart and circulatory system,
CC diabetes and microbial infection. The present sequence is a peptide which
CC may form part of the compound of the invention.
XX
SQ Sequence 10 AA;
XX
Query Match 57.1%; Score 4; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 MHQP 6
Db 1 MHQP 4
XX
RESULT 17
ABG95549
ID ABG95549 standard; Peptide; 11 AA.
XX
AC ABG95549;
XX
DT 15-JAN-2003 (first entry)
XX
DE Human novel secreted protein gene 86 polypeptide #1.
XX
KW Human; secreted protein; autoimmune disease; chemotaxis;
KW rheumatoid arthritis; hyperproliferative disorder; breast neoplasm;
KW liver neoplasm cardiovascular disorder; cardiac arrest; skin aging;
KW cerebrovascular disorder; cerebral ischaemia; angiogenesis; sunburn;
KW nervous system disorders; Alzheimer's disease; infection;
KW ocular disorder; corneal infection; wound healing; tissue regeneration;
KW epithelial cell proliferation; organ transplantation; food additive;
KW preservative; nutritional.
XX
OS Homo sapiens.
XX
PN US6420526-B1.
XX
PD 16-JUL-2002.
XX
PF 08-SEP-1998; 98US-0149476.
XX
PR 07-MAR-1997; 97US-038621P.
XX
PR 07-MAR-1997; 97US-040161P.
XX
PR 07-MAR-1997; 97US-040162P.
XX
PR 07-MAR-1997; 97US-040163P.

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PR 07-MAR-1997; 97US-040333P.
PR 07-MAR-1997; 97US-040334P.
PR 07-MAR-1997; 97US-040336P.
PR 07-MAR-1997; 97US-040626P.
PR 11-APR-1997; 97US-043311P.
PR 11-APR-1997; 97US-043312P.
PR 11-APR-1997; 97US-043313P.
PR 11-APR-1997; 97US-043314P.
PR 11-APR-1997; 97US-043315P.
PR 11-APR-1997; 97US-043568P.
PR 11-APR-1997; 97US-043569P.
PR 11-APR-1997; 97US-043570P.
PR 11-APR-1997; 97US-043578P.
PR 11-APR-1997; 97US-043580P.
PR 11-APR-1997; 97US-043669P.
PR 11-APR-1997; 97US-043670P.
PR 11-APR-1997; 97US-043671P.
PR 11-APR-1997; 97US-043672P.
PR 11-APR-1997; 97US-043674P.
PR 23-MAY-1997; 97US-047492P.
PR 23-MAY-1997; 97US-047500P.
PR 23-MAY-1997; 97US-047501P.
PR 23-MAY-1997; 97US-047502P.
PR 23-MAY-1997; 97US-047503P.
PR 23-MAY-1997; 97US-047581P.
PR 23-MAY-1997; 97US-047582P.
PR 23-MAY-1997; 97US-047583P.
PR 23-MAY-1997; 97US-047584P.
PR 23-MAY-1997; 97US-047585P.
PR 23-MAY-1997; 97US-047586P.
PR 23-MAY-1997; 97US-047587P.
PR 23-MAY-1997; 97US-047588P.
PR 23-MAY-1997; 97US-047589P.
PR 23-MAY-1997; 97US-047590P.
PR 23-MAY-1997; 97US-047592P.
PR 23-MAY-1997; 97US-047593P.
PR 23-MAY-1997; 97US-047594P.
PR 23-MAY-1997; 97US-047595P.
PR 23-MAY-1997; 97US-047596P.
PR 23-MAY-1997; 97US-047597P.
PR 23-MAY-1997; 97US-047598P.
PR 23-MAY-1997; 97US-047599P.
PR 23-MAY-1997; 97US-047600P.
PR 23-MAY-1997; 97US-047601P.
PR 23-MAY-1997; 97US-047612P.
PR 23-MAY-1997; 97US-047613P.
PR 23-MAY-1997; 97US-047614P.
PR 23-MAY-1997; 97US-047615P.
PR 23-MAY-1997; 97US-047617P.
PR 23-MAY-1997; 97US-047618P.
PR 23-MAY-1997; 97US-047632P.
PR 23-MAY-1997; 97US-047633P.
PR 06-JUN-1997; 97US-048964P.
PR 06-JUN-1997; 97US-048974P.
PR 13-JUN-1997; 97US-049610P.
PR 08-JUL-1997; 97US-051926P.
PR 16-JUL-1997; 97US-052874P.
PR 18-AUG-1997; 97US-055724P.
PR 22-AUG-1997; 97US-056630P.
PR 22-AUG-1997; 97US-056631P.
PR 22-AUG-1997; 97US-056632P.
PR 22-AUG-1997; 97US-056633P.
PR 22-AUG-1997; 97US-056637P.
PR 22-AUG-1997; 97US-056662P.
PR 22-AUG-1997; 97US-056664P.
PR 22-AUG-1997; 97US-056845P.
PR 22-AUG-1997; 97US-056862P.
PR 22-AUG-1997; 97US-056864P.
PR 22-AUG-1997; 97US-056872P.
PR 22-AUG-1997; 97US-056874P.
PR 22-AUG-1997; 97US-056875P.
PR 22-AUG-1997; 97US-056876P.
PR 22-AUG-1997; 97US-056877P.

PR 22-AUG-1997; 97US-056878P.
PR 22-AUG-1997; 97US-056879P.
PR 22-AUG-1997; 97US-056880P.
PR 22-AUG-1997; 97US-056881P.
PR 22-AUG-1997; 97US-056882P.
PR 22-AUG-1997; 97US-056884P.
PR 22-AUG-1997; 97US-056886P.
PR 22-AUG-1997; 97US-056887P.
PR 22-AUG-1997; 97US-056888P.
PR 22-AUG-1997; 97US-056889P.
PR 22-AUG-1997; 97US-056892P.
PR 22-AUG-1997; 97US-056893P.
PR 22-AUG-1997; 97US-056894P.
PR 22-AUG-1997; 97US-056903P.
PR 22-AUG-1997; 97US-056908P.
PR 22-AUG-1997; 97US-056909P.
PR 22-AUG-1997; 97US-056910P.
PR 22-AUG-1997; 97US-056911P.
PR 22-AUG-1997; 97US-057761P.
PR 05-SEP-1997; 97US-057850P.
PR 05-SEP-1997; 97US-057859P.
PR 12-SEP-1997; 97US-058785P.
PR 02-OCT-1997; 97US-061060P.
PR 06-MAR-1998; 98WO-US04493.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Rosen CA, Fischer CL, Soppet DP, Carter KC, Bedharik DR;
PI Endress GA, Yu G, Ni J, Feng P, Young PS, Greene JM, Ferris AM;
PI Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
PI Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
XX
XX MPI; 2002-634796/68.
DR
XX
XX New isolated human secreted protein for diagnosing, preventing,
PT treating or ameliorating medical conditions and used as a food additive
PT or preservative -
XX
XX
XX Disclosure; Column 78; 129pp; English.
XX
XX The invention relates to an isolated protein that is one of 186 human
CC secreted proteins, given in the specification, encoded by one of
CC 309 cDNA sequences also given in the specification. The protein is used
CC in a pharmaceutical composition used to prevent, treat or ameliorate a
CC medical condition in e.g. humans, mice, rabbits, goats, horses, cats,
CC dogs, chickens or sheep. Disorders which are diagnosed or treated include
CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
CC angiogenesis, nervous system disorders e.g. Alzheimer's disease,
CC infections caused by bacteria, viruses and fungi and ocular disorders
CC e.g. corneal infection. The polypeptides can also be used to aid wound
CC healing and epithelial cell proliferation, to prevent skin aging due to
CC sunburn, to maintain organs before transplantation, for supporting cell
CC culture of primary tissues, to regenerate tissues and in chemotaxis. The
CC polypeptides can also be used as a food additive or preservative to
CC increase or decrease storage capabilities, fat content, lipid, protein,
CC carbohydrate, vitamins, minerals, cofactors and other nutritional
CC components. The present sequence represents one of the novel human
CC secreted proteins of the invention.
XX
XX Sequence 11 AA;
Query Match 57.1%; Score 4; DB 23; Length 11;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 HQPP 7
Db 1 HQPP 4

```

RESULT 18



CC secreted protein of the invention.

XX Sequence 11 AA;

SQ

Query Match 57.1%; Score 4; DB 24; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 85;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHQP 6  
 |||||  
 Db 1 MHQP 4

RESULT 20

ABP99483

ID ABP99483 standard; Protein; 11 AA.

XX

AC ABP99483;

XX

DT 26-MAR-2003 (first entry)

XX

DE Human secreted protein SEQ ID NO 427.

XX

XX Human; secreted protein; nootropic; neuroprotective; cytostatic;  
 virucide; dermatological; immunosuppressive; antiinflammatory; anti-HIV;  
 KW vulnery; antibacterial; antiparkinsonian; antiskickling; antianaemic;  
 KW antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective;  
 KW antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant;  
 KW antifungal; antiparasitic; cardiant; immune disorder; infection; vaccine;  
 KW cardiovascular disorder; neurological disease; nephrotropic;  
 KW gene therapy.

XX

OS Homo sapiens.

XX

PN WO20027186-A2.

XX

PD 03-OCT-2002.

XX

PF 26-MAR-2002; 2002WO-US09188.

XX

PR 27-MAR-2001; 2001US-278650P.

PR 12-SEP-2001; 2001US-0950082.

PR 12-SEP-2001; 2001US-0950082.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Rosen CA, Ruben SM;

XX

XX WPI; 2003-040563/03.

DR N-PSDB; ABZ66904.

XX

XX New human secreted proteins encoded by genes contained in cDNA clones  
 (e.g. HGCAC19), useful for preventing, treating or diagnosing e.g.  
 PT AIDS, multiple sclerosis, herpes virus, leukemia, tick-borne  
 PT encephalitis or West Nile fever -

XX

PS Claim 1; Page 1393; 2423pp; English.

XX

XX The invention relates to novel human genes (ABZ66891-ABZ68209) and the  
 CC encoded secreted proteins (ABP99470-ABP99872) useful for preventing,  
 CC treating or ameliorating medical conditions e.g. by protein or gene  
 CC therapy. The genes are isolated from a range of human tissues disclosed  
 CC in the specification. The nucleic acids, proteins, antibodies and  
 CC (ant)agonists are useful in the diagnosis, treatment and prevention of:  
 CC (a) cancer, e.g. breast and ovarian cancer and other cancers of the  
 CC adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver,  
 CC lung or urogenital; (b) immune disorders e.g. Addison's disease,  
 CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,  
 CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid  
 CC arthritis and ulcerative colitis; (c) cardiovascular disorders such as  
 CC myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g.  
 CC cerebral anoxia and epilepsy; and (f) infectious diseases such as viral,  
 CC bacterial, fungal and parasitic infections.

XX

XX Sequence 12 AA;

SQ

Query Match 57.1%; Score 4; DB 21; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 91;

XX

ABZ28056

ID AAB28056 standard; peptide; 12 AA.

XX

AC AAB28056;

XX

DT 02-FEB-2001 (first entry)

XX

DE Human secreted protein SEQ ID NO: 104.

XX

XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;  
 KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;  
 KW vulnery; anticonvulsant; antibacterial; antifungal; antiparasitic;  
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;  
 KW neurological disease; infection; human; secreted protein.

XX

OS Homo sapiens.

XX

PN WO200055177-A2.

XX

PD 21-SEP-2000.

XX

PF 09-MAR-2000; 2000WO-US06058.

XX

PR 12-MAR-1999; 99US-0124145.

PR 03-DEC-1999; 99US-0168654.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Rosen CA, Ruben SM, Komatsoulis G;

XX

XX WPI; 2000-638177/61.

DR N-PSDB; AAC59152.

XX

XX Novel nucleic acids encoding 49 human secreted proteins useful for  
 PT treating cancers, hyperproliferative disorders, inflammatory disorders,  
 PT neurological disorders and cardiovascular disorders -

XX

PS Claim 11; Page 363; 389pp; English.

XX

XX Sequences AAB28012-B28060 represent the amino acid sequences of 49  
 CC human secreted proteins encoded by the genes AAC59108-C59156. The genes  
 CC and proteins are useful for preventing, ameliorating or treating medical  
 CC conditions, e.g. by protein or gene therapy. The genes are isolated from  
 CC a range of human tissues disclosed in the specification. The nucleic  
 CC acids, proteins, antibodies and (ant)agonists are useful in the  
 CC diagnosis, treatment and prevention of: (a) cancer, e.g. breast and  
 CC ovarian cancer, and other cancers of the adrenal gland, bone, bone  
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;  
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune  
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,  
 CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative  
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;  
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and  
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal  
 CC and parasitic infections.

XX

XX Sequence 12 AA;

SQ

Query Match 57.1%; Score 4; DB 21; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 91;



Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHQP 6  
 Db 1 MHQP 4

RESULT 22  
 AAY92771  
 ID AAY92771 standard; peptide; 14 AA.  
 XX  
 AC AAY92771;  
 XX  
 DT 29-AUG-2000 (first entry)  
 XX  
 DE Oligopeptide mimotope C19 of surface LOS of serogroup B meningococcus.  
 XX  
 KW Heptapeptide; epitope; mimotope; surface lipo-oligosaccharide; LOS;  
 KW meningitis; anti-bacterial; anti-inflammatory; vaccine.  
 XX  
 OS Neisseria meningitidis.  
 XX  
 FH Key Location/Qualifiers  
 FT Disulfide-bond 2..10  
 XX  
 PN WO200025814-A2.  
 XX  
 PD 11-MAY-2000.  
 XX  
 PF 27-OCT-1999; 99WO-GB03559.  
 XX  
 PR 30-OCT-1998; 98GB-0023835.  
 XX  
 PA (UNLO) UNIV COLLEGE LONDON.  
 PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.  
 XX  
 PI Charalambous BM, Feavers IM;  
 XX  
 DR WPI; 2000-365403/31.  
 XX  
 PT Use of a mimotope of a surface lipo-oligosaccharide of a serogroup B  
 PT meningococcus for a vaccine against serogroup B meningococci  
 XX  
 PS Example 2; Page 19; 39pp; English.  
 XX  
 CC Minotopes of a surface lipo-oligosaccharide (LOS) of a serogroup B  
 CC meningococcus comprise an oligopeptide which is structurally more  
 CC constrained than an unsubstituted linear form of the oligopeptide. The  
 CC oligopeptide is cyclic and contains a heptapeptide, such as the generic  
 CC sequence of AAY92767. The minotopes are useful in vaccines against  
 CC serogroup B meningococci, especially Neisseria meningitidis, which  
 CC causes meningitis. The LOS is a surface glycolipid that forms a major  
 CC outer membrane component and possesses a terminal galactose acceptor  
 CC sites for sialic acid. Sialylation of the LOS in immunotype B  
 CC meningococci may enhance the ability of the organism to evade the human  
 CC immune response. Therefore alternative target antigens on the surface of  
 CC serogroup B meningococci are important.  
 XX  
 SQ Sequence 14 AA;  
 Query Match 57.1%; Score 4; DB 21; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SWMH 4  
 Db 3 SWMH 6

RESULT 23  
 AAU88216  
 ID AAU88216 standard; Peptide; 17 AA.  
 XX

AC AAU88216;  
 XX  
 DT 18-JUN-2002 (first entry)  
 XX  
 DE Insulin/insulin-like growth factor receptor-binding peptide #180.  
 XX  
 KW Cytostatic; antidiabetic; neuroprotective; cerebroprotective;  
 KW ophthalmological; insulin; receptor; gene therapy; diabetes;  
 KW insulin-like growth factor-1; IGF-1; tumour; prostate; breast;  
 KW diabetic retinopathy; neurological diseases; stroke;  
 KW diabetic neuropathy.  
 XX  
 OS Synthetic.  
 OS  
 PN WO200172771-A2.  
 XX  
 PD 04-OCT-2001.  
 XX  
 PF 29-MAR-2000; 2000WO-US08528.  
 XX  
 PR 29-MAR-2000; 2000WO-US08528.  
 XX  
 PA (DGIB-) DGI BIOTECHNOLOGIES LLC.  
 PA (NOVO) NOVO NORDISK AS.  
 XX  
 PI Beasley J, Blume AJ, Schaeffer L, Pillutla R, Brandt J;  
 PI Brissette R, Spetzler J, Cheng W, Ostergaard S, Mandeckl WS;  
 PI Hansen PH, Ravera M, Hsiao K;  
 XX  
 DR WPI; 2002-025774/03.  
 XX  
 PT Modulating insulin activity in mammalian cells, for treating e.g.  
 PT diabetes and tumours, comprises using peptides that bind to insulin or  
 PT insulin-like growth factor receptors  
 XX  
 PS Disclosure; Page 44; 390pp; English.  
 XX  
 CC The invention relates to a method of modulating insulin activity in  
 CC mammalian cells by administering a peptide that binds the insulin  
 CC receptor (IR). A composition containing a peptide, optionally expressed  
 CC from gene therapy vectors, that binds to Site 1 of IR and an insulin  
 CC agonist are useful for treating diabetes. Also, peptides that are  
 CC antagonists of the insulin-like growth factor-1 (IGF-1) receptor are  
 CC useful for treating insulin-like growth factor (IGF)-sensitive tumours  
 CC (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1  
 CC receptor agonists are useful for treating neurological diseases,  
 CC including stroke and diabetic neuropathy. The peptides are also useful in  
 CC screening for compounds that bind to IR or IGF-1 receptor, potential  
 CC therapeutics and research reagents. AAU8034-AAU90957 represent IR  
 CC and/or IGF-1 receptor-binding peptides and related amino acid sequences  
 CC of the invention.  
 XX  
 SQ Sequence 17 AA;  
 Query Match 57.1%; Score 4; DB 23; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHQP 6  
 Db 12 MHQP 15

RESULT 24  
 AAU90013  
 ID AAU90013 standard; Peptide; 17 AA.  
 XX  
 AC AAU90013;  
 XX  
 DT 18-JUN-2002 (first entry)  
 XX  
 DE Insulin/insulin-like growth factor receptor-binding peptide #1969.  
 XX



XX Pentapeptide paralogue for use as chromatographic affinity ligand.  
 DE HPLC.  
 XX Synthetic.  
 KW WO9106356-A.  
 XX  
 PD 16-MAY-1991.  
 XX  
 XX 31-OCT-1990; 90WO-EP06333.  
 PF  
 XX 31-OCT-1989; 89US-0429721.  
 PR  
 XX (TERR-) TERRAPIN TECHN INC.  
 FA  
 XX Kauvar LM;  
 XX PI  
 XX WPI; 1991-163985/22.  
 DR  
 XX Identifying paralog with specific affinity for analyte - using  
 PT candidate paralogs with systematically varied values of at least  
 PT 2 parameters.  
 XX  
 PS Claim 41; Fig 8; 95pp; English.  
 XX  
 CC Peptide is one of a panel, each of which have systemically varied  
 CC values of at least two parameters. A test protein is matched against  
 CC the panel, and the paralogues with highest binding affinity are  
 CC selected. Selected paralogues are bound to a matrix which is  
 CC incorporated into the HPLC gel and used as affinity ligands.  
 CC Technique is useful in chromatographic separation, purification  
 CC and binding assay.  
 XX  
 XX Sequence 5 AA;  
 SQ  
 Query Match 42.9%; Score 3; DB 12; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2 WMH 4  
 Db 1 WMH 3  
 RESULT 27  
 AAR27038  
 ID AAR27038 standard; peptide; 5 AA.  
 XX  
 AC AAR27038;  
 XX  
 XX 25-MAR-2003 (updated)  
 DT 01-MAR-1993 (first entry)  
 XX  
 XX Consensus heavy chain CDR1 used in humanised Mab.  
 DE  
 XX Monoclonal antibody; complementarity determining region; framework;  
 KW antigens; tumour; melanoma; carcinoma; glioma.  
 KW  
 XX Non human.  
 OS  
 XX WO9215683-A1.  
 PN  
 XX 17-SEP-1992.  
 PD  
 XX 04-MAR-1992; 92WO-EP00480.  
 PF  
 XX 06-MAR-1991; 91EP-0103389.  
 PR  
 XX (MERE ) MERCK PATENT GMBH.  
 PA  
 XX Bendig WM, Kettleborough CA, Saldanha J;  
 PI

XX WPI; 1992-331729/40.  
 DR  
 XX Human monoclonal antibodies binding to human receptors - for  
 PT treatment and diagnosis of tumours, e.g. melanoma and carcinoma  
 XX  
 XX Claim 4; Page 62; 89pp; English.  
 PS  
 XX The CDR1 sequence was that of a consensus sequence of CDR1 deduced  
 CC from antigen binding sites of non-human origin. The sequence is  
 CC from the heavy chain hypervariable region. The sequence may be used  
 CC to produce humanised monoclonal antibodies comprising CDRs of non  
 CC human origin and frameworks of variable and constant regions of  
 CC human heavy and light chains. The humanised antibodies or their  
 CC chimeric variants may be used as therapeutic or diagnostic agents in  
 CC order to combat e.g. glioma, melanoma or carcinoma.  
 CC See also AAR27299-300 and AAR27037-51.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 XX Sequence 5 AA;  
 SQ  
 Query Match 42.9%; Score 3; DB 13; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2 WMH 4  
 Db 3 WMH 5  
 RESULT 28  
 AAR51549  
 ID AAR51549 standard; peptide; 5 AA.  
 XX  
 AC AAR51549;  
 XX  
 XX 25-MAR-2003 (updated)  
 DT 19-OCT-1994 (first entry)  
 XX  
 XX Mimotope peptide #43 from panel of maximally diverse mimotopes.  
 DE  
 XX mimotope panel; rational drug design; candidate drug;  
 KW screening assay; hydrophobicity; antibody repertoire.  
 KW  
 XX Synthetic.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 PH Modified-site 1 /note= "acetylated"  
 FT  
 XX US5300425-A.  
 PN  
 XX 05-APR-1994.  
 XX  
 XX 06-DEC-1989; 89US-0447009.  
 PF  
 XX 13-OCT-1987; 87US-0108130.  
 PR  
 XX 11-OCT-1988; 88US-0255906.  
 PR  
 XX 06-DEC-1989; 89US-0447009.  
 XX  
 XX (TERR-) TERRAPIN TECHNOLOGIES INC.  
 PA  
 XX Kauvar LM;  
 XX PI  
 XX WPI; 1994-109390/13.  
 DR  
 XX Screening of candidate drugs for binding to receptor - by  
 PT comparing inverse image antibody profile of drug with  
 PT mimotope-binding profile of receptor  
 XX  
 XX Example 3; Fig 3; 29pp; English.  
 PS  
 XX A panel of 88 pentapeptides was designed on the basis of decreasing  
 CC

CC hydrophobicity and periodic variation of hydrophobic moment. The  
 CC peptides were labelled with iodine-125 and tested with individual  
 CC members of a basal antibody repertoire. (Spleen cells were  
 CC harvested from mice and used to provide a panel of  
 CC antibody-secreting hybridoma cells as a subset of the complete  
 CC B-cell repertoire). Nearly uniform binding to all antibody members  
 CC of the repertoire was observed. The test was then repeated with the  
 CC addition of a defined amount of analyte to the mixture. A small  
 CC number of wells showed greatly decreased labelling and these  
 CC antibodies represented the successful result of an initial screen  
 CC for those which preferentially bind analyte.  
 CC (Updated on 25-MAR-2003 to correct PF field.)  
 XX  
 SQ Sequence 5 AA;

Query Match 42.9%; Score 3; DB 15; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 WMH 4  
 ||||  
 Db 1 WMH 3

RESULT 29  
 AAR69917  
 ID AAR69917 standard; peptide; 5 AA.  
 XX  
 AC AAR69917;  
 XX

25-MAR-2003 (updated)  
 18-OCT-1995 (first entry)

DE Pentameric mimotope 43 used to obtain highly specific antibodies.

XX mimotope; antibody; production; high specificity; detection;  
 KW immunoassay; high performance liquid chromatography.  
 XX  
 XX Synthetic.

Key Location/Qualifiers  
 Modified-site 1 /note= "Acetyl-Trp"

US5384263-A.

24-JAN-1995.

04-JUN-1993; 93US-0072190.

11-OCT-1988; 88US-0255906.

13-OCT-1987; 87US-0108130.

04-JUN-1993; 93US-0072190.

(TERR-) TERRAPIN TECHNOLOGIES INC.

Kauvar LM;

WPI; 1995-105497/14.

Producing antibodies with high specificity and affinity for an  
 analyte - by immunisation with selected mimotope, also analyte  
 detection kits, useful for immunoassay of materials usually  
 analysed by HPLC

Example 3; Fig 3; 25pp; English.

CC AAR69875-969 are pentameric mimotopes designed on the basis of  
 CC decreasing hydrophobicity and periodic variation of hydrophobic  
 CC moment. All the pentapeptides are acetylated at the N-terminus except  
 CC E12 (for FITC) (sic). E12 is not identified in the specification.  
 CC The mimotopes are used in the method of the invention to obtain  
 CC antibodies specifically and strongly reactive with a desired

CC analyte. The mimotope is obtd. by reacting a panel of starting  
 CC antibodies (Abs) representative of the resting B cell repertoire of a  
 CC mammal with an analyte (so as to identify analyte-reacting Abs) and  
 CC then reacting each of a panel of candidate mimotopes representative  
 CC of a random set of 3D contours with the analyte-reacting Abs. A  
 CC subject is immunised with one or more mimotopes identified and the  
 CC product Abs are recovered from the serum of the subject.  
 CC (Updated on 25-MAR-2003 to correct PF field.)  
 XX  
 SQ Sequence 5 AA;

Query Match 42.9%; Score 3; DB 16; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 WMH 4  
 ||||  
 Db 1 WMH 3

RESULT 30  
 AAR74929  
 ID AAR74929 standard; peptide; 5 AA.  
 XX  
 AC AAR74929;  
 XX

19-JAN-1996 (first entry)

DE H-CDR-1 of anti-idiotypic antibody against human anticancer antibody.

XX Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin;  
 KW complementarity determining region.  
 XX  
 XX Mus sp.

JP07101999-A.

18-APR-1995.

06-OCT-1993; 93JP-0272950.

06-OCT-1993; 93JP-0272950.

(HAGI/) HAGIWARA Y.

WPI; 1995-182987/24.

Novel anti-idiotypic antibody against an human anticancer monoclonal  
 antibody - and DNA sequences encoding the antibody, useful in  
 pharmacology, medicine and biochemical fields.

Claim 1; Page 2; 28pp; Japanese.

CC A new anti-idiotypic antibody against a human anticancer monoclonal  
 CC antibody is claimed. This antibody contains in its heavy chain 3  
 CC complementarity determining regions CDR1 (AAR74929-R74931), CDR2  
 CC (AAR74932-R74935) and CDR3 (AAR74936-R74939), this is also true of the  
 CC light chain which has its own CDR1 (AAR74944-R74946 and AAR85774), CDR2  
 CC (AAR74947-R74949) and CDR3 (AAR74950-R74954). The antibody and DNA  
 CC encoding it are useful in pharmacological, medical and biochemical  
 CC fields.  
 XX  
 SQ Sequence 5 AA;

Query Match 42.9%; Score 3; DB 16; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 WMH 4  
 ||||  
 Db 3 WMH 5

```

RESULT 31
AAW98663
ID AAW98663 standard; peptide; 5 AA.
XX
XX
AC AAR98663;
XX
XX 25-MAR-2003 (updated)
DT 11-MAR-1997 (first entry)
XX
XX Peptide 43 from 88 member diverse mimotope panel.
XX
XX Panel; mimotope; decreasing hydrophobicity; periodic variation;
KW hydrophobic moment; antibody; repertoire; identification; drug;
KW candidate; receptor; binding; ligand; rational; design; selection;
KW treatment; tumour; production; immunological reagent; analyte;
KW detection; trace contaminant; mimotope.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 1
FT /note= "acylated"
XX
XX US5541070-A.
XX
XX 30-JUL-1996.
XX
XX 08-SEP-1993; 93US-0118133.
XX
XX 06-DEC-1989; 89US-0447009.
XX
XX 13-OCT-1987; 87US-0108130.
XX
XX 11-OCT-1988; 88US-0255906.
XX
XX 08-SEP-1993; 93US-0118133.
XX
XX (KAUV/) KAUVAR L M.
XX
XX Kauvar LM;
XX
XX WPI; 1996-361955/36.
XX
XX Identifying candidate drugs that bind a specific receptor by
PT competitive reaction with panel of mimotope(s) - useful in rational
PT drug design
XX
XX Example 3; Fig 3; 27pp; English.
XX
XX The present peptide is a member of a panel of 88 pentapeptide
CC mimotopes designed on the basis of decreasing hydrophobicity, and
CC periodic variation of hydrophobic moment. The panel was synthesised
CC using the method of Geyzen, H. M., et al, Proc. Natl. Acad. Sci.
CC USA (1984), which uses lots of 96 pins; the remaining 8
CC polyethylene pins being controls. The mimotopes were then mixed,
CC 125-I labelled and tested with individual members of a basal
CC antibody (Ab) repertoire. Nearly uniform binding to all members was
CC found. The test was then repeated with the addition of a defined
CC amt. of analyte. A small number showed greatly increased labelling,
CC these Ab representing the successful result of an initial screen
CC for those that pref. bind analyte.
CC The above is an example of a claimed method for identifying members
CC of a panel of candidate drugs, that bind to a receptor having a
CC known ligand. It is useful in rational drug design, e.g. selection
CC of monoclonal Ab for treating individual tumours, and for the prodn.
CC of immunological reagents for any analyte, including those not
CC normally detectable by immunoassay, e.g trace contaminants in soil,
CC air or water.
CC (Updated on 25-MAR-2003 to correct PF field.)
XX
XX Sequence 5 AA;
SQ
Query Match 42.9%; Score 3; DB 17; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 32
AAW39866
ID AAW39866 standard; peptide; 5 AA.
XX
XX AC AAW39866;
XX
XX 16-JUN-1998 (first entry)
DT Heavy chain CDR1 of catalytic antibody 8G4E.
XX
XX Variable domain; lambda light chain; catalytic antibody; degradation;
KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
KW overdose; addiction.
XX
XX Mus sp.
XX
XX OS
XX WO9749800-A1.
XX
XX 31-DEC-1997.
XX
XX 25-JUN-1997; 97WO-US10965.
XX
XX 25-JUN-1996; 96US-0672345.
XX
XX (UYCO ) UNIV COLUMBIA NEW YORK.
XX
XX Landry DW;
XX
XX WPI; 1998-077166/07.
XX
XX New catalytic antibodies able to decompose cocaine, single-chain
PT analogues - used to treat cocaine overdose and addiction, required
PT in far smaller doses than antibodies that antagonise cocaine by
PT simply binding
XX
XX Claim 19; Page 94; 147pp; English.
XX
XX AAW39866-68 represent the sequences of the heavy chain complementarity
CC determining regions (CDRs) of the catalytic antibody 8G4E, which is able
CC to degrade cocaine. A series of cocaine transition state analogues
CC (TSAs) were prepared and used to immunise mice for production of
CC hybridomas. Catalytic antibodies were identified by their capacity to
CC release 3H-benzoic acid from 3H-phenyl cocaine. The 8G4E antibody was
CC identified using TSA3, and has a per minute Kcat of 0.12. The antibodies
CC reduce the concentration of cocaine in a subject, and are used
CC particularly for the treatment of an overdose. They are also used for
CC treating addiction (by reducing the in vivo concentration that can be
CC achieved).
XX
XX Sequence 5 AA;
SQ
Query Match 42.9%; Score 3; DB 19; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4
DB 1 WMH 3

RESULT 33
AAW44181
ID AAW44181 standard; peptide; 5 AA.
XX
XX AC AAW44181;
XX
XX 16-JUN-1998 (first entry)
DT

```

XX DE Monoclonal antibody 12H5 heavy chain CDR SEQ ID NO:25.  
 XX KW Monoclonal antibody; type II phospholipase A2; inhibition; cisplatin;  
 KW amelioration; kidney disorder; nephrotoxicity; anticancer.  
 XX OS Unidentified.  
 XX OS WO9749427-A1.  
 XX PN 31-DEC-1997.  
 XX PD 27-JUN-1997; 97WO-JP02241.  
 XX PF 19-SEP-1996; 96JP-0247635.  
 XX PR 27-JUN-1996; 96JP-0167286.  
 XX PA (YAMA ) YAMANOUCHI PHARM CO LTD.  
 XX PI Hayashi K, Kawauchi Y, Masuho Y, Takasaki J;  
 XX WI; 1998-076914/07.  
 XX DR Amelioration of kidney disorders caused by cisplatin administration  
 XX PT - by treatment with an antibody inhibiting type II phospholipase A2  
 XX PT activity  
 XX PS Disclosure; Page 50; 74pp; Japanese.  
 XX CC The present sequence represents a complementary determining region  
 CC (CDR) from monoclonal antibody 12H5 heavy chain against type II  
 CC phospholipase A2, from the present invention. The present invention  
 CC describes a novel method for the amelioration of kidney disorders  
 CC (such as acute renal failure) associated with the administration of  
 CC cisplatin for the treatment of cancer. The method comprises treatment  
 CC with a monoclonal antibody which inhibits the activity of type II  
 CC phospholipase A2 (particularly of type II phospholipase A2 of human  
 CC origin), or with a protein or peptide possessing the same inhibitory  
 CC activity and containing a part of the antibody sequence. Preferably the  
 CC antibody also inhibits the activity of ape and/or mouse type II  
 CC phospholipase A2, and has the ability to release type II phospholipase  
 CC A2 bound to a cell membrane. Three specific monoclonal antibodies  
 CC having these properties which can be used are 12H5, 10.1 and 1.4.  
 CC derived from hybridomas FERM BP-5300, FERM BP-5298 and FERM BP-5297  
 CC respectively. The method can be used for suppressing the nephrotoxicity  
 CC which is a characteristic feature of cisplatin administration, and  
 CC therefore allowing more efficient use of this drug as an anticancer  
 CC agent, e.g. by allowing an increased dosage to be used.  
 XX CC  
 XX SQ Sequence 5 AA;  
 Query Match 42.9%; Score 3; DB 19; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 WMH 4  
 Db 3 WMH 5  
 RESULT 34  
 AAY48891  
 ID AAY48891 standard; Peptide; 5 AA.  
 XX AC AAY48891;  
 XX DT 20-MAR-2003 (updated)  
 DT 10-DEC-1999 (first entry)  
 XX DE Membrane dipeptidase-binding prostate homing peptide #7.  
 XX KW Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP;  
 KW prostate; ovary; lymph node; adrenal gland; liver; gut; tumour;

KW membrane dipeptidase.  
 XX OS Synthetic.  
 XX OS Homo sapiens.  
 XX FN WO9946284-A2.  
 XX PD 16-SEP-1999.  
 XX PF 10-MAR-1999; 99WO-US05284.  
 XX PR 13-MAR-1998; 98US-0042107.  
 XX PR 26-FEB-1999; 99US-0258754.  
 XX PA (BURN-) BURNHAM INST.  
 XX PI Rajotte D, Pasqualini R, Ruoslahti EI;  
 XX WI; 1999-571717/48.  
 XX DR New peptides which selectively home to organs or tissues, used for,  
 XX PT e.g. identifying target ligands and for therapy of pathological  
 XX PT conditions -  
 XX PS Example 6; Page 151; 193pp; English.  
 XX CC The present invention describes peptides that selectively home to a  
 CC tissue or organ. The peptides can be used for identifying an organ  
 CC or tissue, for identifying a target molecule expressed by an organ or  
 CC tissue or for treating an organ or tissue pathology, where the organ or  
 CC tissue is selected from prostate, lung, skin, retina, pancreas, gut,  
 CC ovary, adrenal gland, liver, and lymph node. The peptide bind to the  
 CC membrane dipeptidase (MDP). AAY48618 to AAY49066 represent sequences  
 CC which are used in the exemplification of the present invention.  
 CC (Updated on 20-MAR-2003 to correct PR field.)  
 XX CC  
 XX SQ Sequence 5 AA;  
 Query Match 42.9%; Score 3; DB 20; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 HQP 6  
 Db 2 HQP 4  
 RESULT 35  
 AAB21923  
 ID AAB21923 standard; Peptide; 5 AA.  
 XX AC AAB21923;  
 XX DT 22-MAR-2001 (first entry)  
 XX DE Human prostate-homing peptide #16.  
 XX KW Cytostatic; homing pro-apoptotic conjugate; tumour; antimicrobial;  
 KW breast; prostate; melanoma; cancer; Kaposi's sarcoma; human.  
 XX OS Homo sapiens.  
 XX FN WO200042973-A2.  
 XX PD 27-JUL-2000.  
 XX PF 21-JAN-2000; 2000WO-US01602.  
 XX PR 22-JAN-1999; 99US-0235902.  
 XX PA (BURN-) BURNHAM INST.  
 XX PI Ellerby HM, Bredesen DE, Pasqualini R, Ruoslahti EI;

XX WPI; 2000-499174/44.  
 DR Homing pro-apoptotic conjugate comprising a tumor homing molecule that  
 PT selectively homes to a mammalian cell type or tissue linked to an  
 PT antimicrobial peptide, useful for the treatment of prostate cancer -  
 XX Example 9; Page 99; 118pp; English.  
 XX The present invention relates to homing pro-apoptotic conjugates,  
 CC comprising of a tumour homing molecule that selectively homes to a  
 CC mammalian cell type or tissue, linked to an antimicrobial peptide. The  
 CC homing pro-apoptotic conjugates are selectively internalised by the  
 CC mammalian cell type or tissue and exhibits high toxicity, especially to  
 CC angiogenic vasculature. The antimicrobial peptide has low mammalian cell  
 CC toxicity when not linked to the tumor homing molecule. The conjugates are  
 CC useful for the treatment of cancer e.g. Kaposi's sarcoma, breast and  
 CC prostate cancer or melanoma. The present sequence is a homing peptide  
 CC isolated in the present invention, which can be conjugated to an  
 CC antimicrobial peptide to make the homing pro-apoptotic conjugates of the  
 CC present invention.  
 XX Sequence 5 AA;  
 SQ Query Match 42.9%; Score 3; DB 21; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 HQP 6  
 ||||  
 Db 2 HQP 4  
 RESULT 36  
 AAB19754  
 ID AAB19754 standard; Peptide; 5 AA.  
 AC AAB19754;  
 XX 19-FEB-2001 (first entry)  
 DT Erythropoietin receptor agonist Mab 3G9 VH region CDR1.  
 DE Erythropoietin receptor; agonist; monoclonal antibody; Mab; mouse;  
 XX heavy chain variable region; antibody engineering; erythropoiesis;  
 KW anaemia; cytopenia; acute renal failure; antianaemic; therapy;  
 KW complementarity determining region; CDR.  
 XX Mus sp.  
 OS WO2000061637-A1.  
 PN 19-OCT-2000.  
 XX 14-APR-2000; 2000WO-US10284.  
 PF 14-APR-1999; 99US-0129263.  
 XX (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA Erickson-Miller CL, Holmes SD, Taylor AH, Young PR;  
 XX WPI; 2000-679469/66.  
 DR Novel erythropoietin receptor agonist antibody useful for enhancing  
 XX erythropoiesis in the treatment of anemia, cytopenia or acute renal  
 PT failure -  
 PT Claim 28; Page 50; 70pp; English.  
 XX The present sequence is that of complementarity determining region  
 CC 1 (CDR1) of the heavy chain variable region (VH) (see AAB19745) of  
 CC 3G9, a murine erythropoietin receptor (EpoR) agonist monoclonal

CC antibody. Claimed EpoR agonist antibodies comprise a VH region  
 CC that includes the 3G9 VH CDRs. These include humanised agonist  
 CC antibodies in which the 3G9 VH CDRs are incorporated into a human  
 CC framework. The EpoR agonist antibodies are used in a claimed  
 CC method for enhancing erythropoiesis, for the treatment of anaemia,  
 CC cytopenia, acute renal failure, and other conditions with depressed  
 CC erythrocyte production. Agonist antibodies of EpoR have the same  
 CC therapeutic utility as the natural ligand, but with the advantages  
 CC of easier purification and longer half-life in vivo.  
 XX Sequence 5 AA;  
 SQ Query Match 42.9%; Score 3; DB 21; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 WMH 4  
 ||||  
 Db 3 WMH 5  
 RESULT 37  
 AAB12174  
 ID AAB12174 standard; peptide; 5 AA.  
 AC AAB12174;  
 XX 10-NOV-2000 (first entry)  
 DT Human CDR1 for IL-2R monoclonal antibody.  
 DE Human; CDR; humanised antibody; complementarity determining region;  
 XX IL-2Ralpha; interleukin-2 receptor; transplant rejection; CD25;  
 KW immunosuppression.  
 XX Homo sapiens.  
 OS WO2000030679-A1.  
 PN 02-JUN-2000.  
 XX 22-NOV-1999; 99WO-EP08988.  
 PF 23-NOV-1998; 98GB-0025632.  
 PR (NOVS ) NOVARTIS AG.  
 PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
 XX Feutren G, Howell RK, Marbach P, Roberts A, Schreier MH, Schulz M;  
 PI WPI; 2000-399934/34.  
 DR Preventing or treating transplant rejection in a recipient comprises  
 XX administering a monoclonal antibody specific for interleukin-2 receptor  
 PT beyond the very early phase following transplantation -  
 PT Disclosure; Page 2; 17pp; English.  
 XX The present sequence is a human complementarity determining region (CDR).  
 CC This sequence was used to generate a humanised antibody specific for the  
 CC alpha subunit of interleukin-2 receptor (IL-2Ralpha). The humanised  
 CC IL-2Ralpha antibody would be useful for preventing or treating transplant  
 CC rejection in a recipient of organ, tissue or modified or unmodified cell  
 CC transplant. The use of a monoclonal antibody specific for IL-2R decreases  
 CC transplant rejection in an immunosuppression-intolerant or non-compliant  
 CC recipient compared with available therapies. Also, undesirable side  
 CC effects associated with current treatments e.g. renal dysfunction,  
 CC hirsutism, gingival hyperplasia and hypertension are avoided.  
 XX Sequence 5 AA;  
 SQ Query Match 42.9%; Score 3; DB 21; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4  
Db 3 WMH 5

RESULT 38  
AA92158  
ID AA92158 standard; Peptide; 5 AA.  
XX AC  
XX AAY92158;  
XX 01-AUG-2000 (first entry)  
XX Murine 15B8 heavy chain variable region CDR 1.  
XX Heavy chain; variable region; complementarity determining region; CDR 1;  
KW anti-Tie2 kinase receptor; monoclonal antibody; 15B8; angiogenetic;  
KW vascular-general; proliferative; antiischemic; cerebroprotective;  
KW cardiant; agonist; antibody inhibition.  
XX  
OS Mus musculus.  
XX  
XX WO200018804-A1.  
XX  
XX 06-APR-2000.  
XX  
XX 28-SEP-1999; 99WO-US22428.  
XX  
XX 28-SEP-1998; 98US-0102098.  
XX  
XX (SMIK ) SMITHKLINE BEECHAM PUC.  
XX (SMIK ) SMITHKLINE BEECHAM PUC.  
XX  
XX Holmes SD, Erickson-miller CL, Winkler JD;  
XX WPI; 2000-293114/25.  
XX  
XX Tie2 receptor agonist antibodies useful for promoting angiogenesis in  
PT patients suffering from strokes and myocardial infarctions  
XX  
XX Claim 12; Page 40; 50pp; English.  
XX  
XX AA92158-60 are heavy chain CDR (complementarity determining regions)  
CC from a novel murine anti-Tie2 kinase receptor agonist monoclonal  
CC antibody 15B8. Tie2 is a single-transmembrane, tyrosine kinase receptor  
CC ('Tie' stands for tyrosine kinase receptor with immunoglobulin and  
CC endothelial growth factor (EGF) homology domain(s)). Anti-Tie2  
CC antibodies may be administered to enhance angiogenesis in mammals  
CC suffering from ischemic disease, myocardial infarction or cerebral stroke  
CC or other vascular diseases such as diabetes. It may also be used to  
CC enhance endothelial cell survival and to promote haematopoietic or  
CC megakaryocyte cell proliferation (claimed).  
XX  
XX Sequence 5 AA;

Query Match 42.9%; Score 3; DB 21; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4  
Db 3 WMH 5

RESULT 39  
AA92158  
ID AA92158 standard; Peptide; 5 AA.  
XX AC  
XX AAY92158;  
XX 19-MAY-2000 (first entry)

XX Chimeric anti-CD25 antibody Ig heavy chain hypervariable region CDR1.  
XX  
XX Chimeric anti-CD25 antibody; CD25 binding molecule; immunoglobulin;  
KW hypervariable region; complementary determining region; CDR1; CDR2; CDR3;  
KW inflammation; rheumatoid arthritis; hyperproliferative skin disease.  
XX  
XX Homo sapiens.  
OS  
XX WO200006604-A2.  
XX  
XX 10-FEB-2000.  
XX  
XX 26-JUL-1999; 99WO-EP05316.  
XX  
XX 27-JUL-1998; 98GB-0016281.  
XX 27-MAY-1999; 99GB-0012460.  
XX (NOVS ) NOVARTIS AG.  
XX (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
PA (UNLO ) UNIV COLLEGE LONDON.  
XX  
XX Amlot PL, Schreier MH;  
PI  
XX WPI; 2000-183090/16.  
XX  
XX Use of CD25 binding molecules in the treatment of rheumatoid arthritis  
PT and inflammatory or hyperproliferative skin diseases -  
XX  
XX Claim 1; Page 11; 14pp; English.  
XX  
XX The present invention describes CD25 binding molecules, which are used  
CC to treat rheumatoid arthritis and inflammatory or hyperproliferative  
CC skin diseases. The CD25 binding molecule comprises at least one  
CC antigen binding site comprising at least one domain which comprises in  
CC sequence, the hypervariable regions CDR1 (having the sequence RYWH),  
CC CDR2 (having the sequence AYPGNSDTSYQKPEG) and CDR3 (having the  
CC sequence DGYVDFP), or their direct equivalents. The CD25 binding  
CC molecules are used in the treatment of rheumatoid arthritis and  
CC inflammatory or hyperproliferative skin diseases, such as psoriasis,  
CC atypical dermatitis, contact dermatitis and further eczematous,  
CC dermatitises, seborrheic dermatitis. Lichen planus, Pemphigus,  
CC bullous Pemphigoid, Epidermolysis bullosa, urticaria, angiodemas,  
CC vasculitides, erythemas, cutaneous eosinophilia, Lupus erythematosus  
CC and acne. A more preferred CD25 binding molecule for use in accordance  
CC with the present invention is selected from a chimeric anti-CD25 antibody  
CC which comprises at least: (i) one immunoglobulin heavy chain, or  
CC fragment, which comprises (i) a variable domain comprising in sequence  
CC the hypervariable regions CDR1, CDR2 and CDR3 (as above) and (ii) the  
CC constant part, or fragment, of a human heavy chain; and (2) one  
CC immunoglobulin light chain, or fragment, which comprises (i) a variable  
CC domain comprising in sequence the hypervariable regions CDR1', CDR2',  
CC and CDR3' (SASSISIMQ, DTSKLAS and HQRSSYT, respectively) and (ii) the  
CC constant part, or fragment, of a human light chain.  
XX  
XX Sequence 5 AA;

Query Match 42.9%; Score 3; DB 21; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4  
Db 3 WMH 5

RESULT 40  
AA014422  
ID AA014422 standard; peptide; 5 AA.  
XX  
XX AA014422;  
XX  
XX 03-MAY-2002 (first entry)



```

XX DE CD25 binding protein domain 1 hypervariable region CDR1.
XX XX
XX KW CD25 binding protein; hypervariable region; CDR1; gastrointestinal tract;
XX KW inflammatory disease; irritable bowel syndrome; IBS; Crohn's disease;
XX KW ulcerative colitis; inflammatory intestinal disease; medicament.
XX OS Unidentified.
XX PN WO200172845-A1.
XX XX
XX PD 04-OCT-2001.
XX XX
XX PF 28-MAR-2001; 2001WO-EP03541.
XX XX
XX PR 30-MAR-2000; 2000GB-0007911.
XX XX
XX PA (NOVS ) NOVARTIS AG.
XX PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX FI Adam H, Faerber L;
XX XX
XX DR WPI; 2001-626258/72.
XX XX
XX PT CD25 binding molecule which comprises antigen binding site comprising
XX PT fully defined CDR1, CDR2, CDR3 hypervariable regions, for treating
XX PT Crohn's disease, ulcerative colitis, irritable bowel syndrome -
XX PS Claim 1; Page 12; 19pp; English.
XX XX
XX CC The invention comprises a CD25 binding protein comprising at least one
XX CC CD25 binding domain containing the hypervariable regions CDR1, CDR2 and
XX CC CDR3. The CD25 binding domain 1 hypervariable regions are shown in
XX CC AA014422 - AA014424, CD25 binding domain 2 hypervariable regions are
XX CC shown in AA014425 - AA014427. The CD25 binding protein is useful for
XX CC treating an inflammatory disease of the gastrointestinal tract, such as:
XX CC irritable bowel syndrome, IBS; Crohn's disease; ulcerative colitis; or
XX CC other inflammatory intestinal disease. The CD25 binding protein is also
XX CC useful in the manufacture of a medicament for the treatment of
XX CC inflammatory disease of the intestinal tract. The present amino acid
XX CC sequence represents the CD25 binding domain 1 hypervariable region CDR1.
XX XX
XX SQ Sequence 5 AA;
XX Query Match 42.9%; Score 3; DB 22; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 WNH 4
XX DB 3 WNH 5
XX
XX RESULT 41
XX AAG63123
XX ID AAG63123 standard; Protein; 5 AA.
XX AC AAG63123;
XX XX
XX DT 01-OCT-2001 (first entry)
XX XX
XX DE Amino acid sequence of a human adenovirus 5 Elb 8.3 kDa protein.
XX XX
XX KW Adenovirus protein; Ad; complementing cell line; Ad vector;
XX KW replication-incompetent Ad vector; El-deleted virus;
XX KW transgene expression; Ad5.
XX OS Human adenovirus type 5.
XX XX
XX PN WO200144280-A2.
XX XX
XX PD 21-JUN-2001.
XX XX
XX PF 07-DEC-2000; 2000WO-US33123.
XX XX
XX PR 14-DEC-1999; 99US-0170550.
XX XX
XX XX 11-APR-2000; 2000US-0196266.
XX PA (GENO-) GENOVO INC.
XX XX
XX PI Himes VB, Rasty S, Peluso RW;
XX XX
XX DR WPI; 2001-475764/51.
XX DR N-PSDB; AAH42482.
XX XX
XX PT New nucleic acids for creating complementing cell lines that enable
XX PT production of high titer adenovirus vectors, comprises a sequence of a
XX PT polynucleotide which is not a naturally-occurring adenoviral nucleotide
XX PT sequence -
XX XX
XX PS Example 1; Page 96; 104pp; English.
XX XX
XX CC The specification describes a nucleic acid molecule, comprising a
XX CC polynucleotide encoding 5 contiguous amino acids of a naturally-occurring
XX CC adenovirus (Ad) polypeptide, where the polynucleotide is not a
XX CC naturally-occurring adenoviral nucleotide sequence and is useful for
XX CC creating complementing cell lines that enable the efficient production
XX CC of high titer Ad vectors. The nucleic acid molecule is useful for
XX CC creating Ad-complementary cell lines which are useful for high yield
XX CC production of recombinant replication-incompetent Ad vectors, in the
XX CC absence of detectable replication competent Ad. The adenoviruses
XX CC free of contamination with RCA are suitable for preclinical and
XX CC clinical use. El-deleted viruses are suitable for applications in which
XX CC transient transgene expression is therapeutic (e.g. p53 gene transfer
XX CC in cancer, beta-interferon gene transfer in cancer, platelet derived
XX CC growth factor (PDGF) gene transfer in wound healing, and vascular
XX CC endothelial growth factor (VEGF) gene transfer in vascular diseases of
XX CC the heart and limbs). The present sequence encodes a human Ad5 Elb 8.3
XX CC kDa protein. It is used to construct an E1 complementation element, for
XX CC use in the course of the invention.
XX XX
XX SQ Sequence 5 AA;
XX Query Match 42.9%; Score 3; DB 22; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 5 QPP 7
XX DB 1 QPP 3
XX
XX RESULT 42
XX AAE06499
XX ID AAE06499 standard; peptide; 5 AA.
XX XX
XX AC AAE06499;
XX XX
XX DT 25-SEP-2001 (first entry)
XX XX
XX DE Mouse prostate homing peptide #16.
XX XX
XX KW Mouse; chimeric prostate-homing pro-apoptotic peptide;
XX KW prostate-homing peptide; antimicrobial peptide; prostate cancer;
XX KW tumour homing molecule; cytostatic.
XX OS Mus sp.
XX XX
XX PN WO200153342-A1.
XX XX
XX PD 26-JUL-2001.
XX XX
XX PF 16-JAN-2001; 2001WO-US01362.
XX XX
XX PR 21-JAN-2000; 2000US-0489582.
XX XX

```



CC therapeutic doses since the mutant immunoglobulin has increased serum  
 CC half-life and persistence. This sequence represents a peptide associated  
 CC with catalytic domains of the immunoglobulin and mutant immunoglobulin  
 CC discussed in the invention.

SQ Sequence 5 AA;

Query Match 42.9%; Score 3; DB 23; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHQ 5  
 |||  
 Db 2 MHQ 4

RESULT 45

ID AAU1183  
 ID AAU1183 standard; Peptide; 5 AA.

XX AAU1183;

XX 25-FEB-2002 (first entry)

DE Mouse antibody Act-1/LDP-02, heavy chain variable region CDR1.

XX Mouse; antibody; Act-1; alpha4beta7 integrin; anti-inflammatory;  
 KW anti-asthmatic; immunosuppressive; heavy chain variable region;  
 KW humanised antibody; LDP-02; leukocyte infiltration; mucosal tissue;  
 KW quiescent inflammatory bowel disease; ulcerative colitis;  
 KW Crohn's disease; ileitis; Coeliac disease; nontropical sprue;  
 KW enteropathy; seronegative arthropathy; collagenous colitis;  
 KW eosinophilic gastroenteritis; pouchitis; ileoanal anastomosis;  
 KW pancreatitis; insulin-dependent diabetes mellitus; mastitis;  
 KW cholecystitis; cholangitis; pericholangitis; chronic bronchitis;  
 KW chronic sinusitis; asthma; graft versus host disease; CDR1;  
 KW complementarity determining region.

XX Mus musculus.

XX WO200178779-A2.

XX 25-OCT-2001.

XX 13-APR-2001; 2001WO-US12234.

XX 14-APR-2000; 2000US-0550082.

XX 27-DEC-2000; 2000US-0748960.

XX (MILL-) MILLENNIUM PHARM INC.

XX (GETH) GENENTECH INC.

XX Brettman LR, Fox JA, Allison DE;

XX WPI; 2002-0552333/07.

XX Treating a human with a disease associated with leukocyte infiltration  
 PT of mucosal tissues, e.g. inflammatory bowel disease, asthma or graft  
 PT versus host disease, by administering an anti-alpha4 beta 7 integrin  
 PT antibody -

XX Claim 8; Fig 5; 81pp; English.

XX The invention relates to treating a human having a disease associated  
 CC with leukocyte infiltration of mucosal tissues, comprising administering  
 CC a humanised immunoglobulin (e.g. the humanised version of mouse  
 CC antibody Act-1, LDP-02) or its antigen-binding fragment, which has  
 CC binding specificity for alpha4beta7 integrin. The immunoglobulin or its  
 CC fragment comprises an antigen binding region of non-human origin and at  
 CC least a portion of an antibody of human origin. Also included is a method  
 CC for inhibiting relapse and/or recurrence of quiescent inflammatory bowel  
 CC disease in a human by administering the humanised immunoglobulin or its  
 CC antigen-binding fragment, which has binding specificity for alpha4beta7

CC integrin. The treatment is used for treating a human having a disease  
 CC associated with leukocyte infiltration of mucosal tissues, e.g.  
 CC inflammatory bowel disease (e.g. ulcerative colitis, Crohn's disease,  
 CC ileitis, Coeliac disease, nontropical sprue, enteropathy associated with  
 CC seronegative arthropathies, microscopic or collagenous colitis,  
 CC eosinophilic gastroenteritis, pouchitis and ileoanal anastomosis),  
 CC pancreatitis, insulin-dependent diabetes mellitus, mastitis,  
 CC cholecystitis, cholangitis, pericholangitis, chronic bronchitis,  
 CC chronic sinusitis, asthma or graft versus host disease. The method is  
 CC also useful for inhibiting relapse and/or recurrence of quiescent  
 CC inflammatory bowel disease in a human, where quiescence has been induced  
 CC by medical or surgical therapy. The present sequence is a mouse  
 CC Act-1/LDP-02 antibody heavy chain variable region complementarity  
 CC determining region as incorporated into the humanised antibody of the  
 CC invention.

SQ Sequence 5 AA;

Query Match 42.9%; Score 3; DB 23; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4  
 |||  
 Db 3 WMH 5

RESULT 46

AB882654

ID AB882654 standard; peptide; 5 AA.

XX AB882654;

XX 19-FEB-2003 (first entry)

DE CDR1 fragment of a chimeric anti-CD25 antibody.

XX CD25; immunosuppressive; hepatotropic; antiasthmatic; dermatological;  
 KW antiarthritic; cytostatic; nephrotropic; neuroprotective; antiulcer;  
 KW antiinflammatory; vasotropic; complementarity determining region;  
 KW steroid; CDR; anti-CD25 antibody.

XX Unidentified.

XX WO200281508-A2.

XX 17-OCT-2002.

XX 05-APR-2002; 2002WO-EP03808.

XX 06-APR-2001; 2001GB-0009816.

XX 06-APR-2001; 2001GB-0008817.

XX 06-APR-2001; 2001GB-0008821.

XX (UYBR-) UNIV BRISTOL.

XX Hearing SD, Dayan CM, Norman MR;

XX WPI; 2003-067514/06.

XX CD25 binding molecules useful for prevention and treatment of  
 PT autoimmune hepatitis, asthma, eczema, vasculitis, temporal arthritis,  
 PT leukemia, multiple sclerosis and Crohn's disease in steroid-resistant  
 PT patients -

XX Claim 1; Page 20; 22pp; English.

XX The invention relates to a CD25 binding molecule (I) comprising at least  
 CC one antigen binding site having at least one domain which comprises in  
 CC sequence, the hypervariable regions CDR1, CDR2 and CDR3 (complementarity  
 CC determining region), for use in prevention or treatment of diseases such  
 CC as autoimmune hepatitis, asthma, eczema, vasculitis, temporal arthritis,  
 CC leukemia, glomerulonephritis, multiple sclerosis and Crohn's disease in a

CC steroid-resistant patient. (I) is useful in the manufacture of a  
 CC medicament for use in the prevention and treatment of autoimmune  
 CC hepatitis, asthma, eczema, vasculitis, temporal arthritis, systemic lupus  
 CC erythematosus, leukemia, glomerulonephritis, multiple sclerosis,  
 CC ulcerative colitis, sarcoid and Crohn's disease in a steroid-sensitive or  
 CC steroid-resistant patient. (I) is coadministered with a further drug  
 CC substance. The use of CD25 binding molecules make the steroid-sensitive  
 CC patients respond quicker and allow a lower dose of steroids to be used,  
 CC thus significantly reducing the side effects of steroid treatments. The  
 CC present sequence represents a hypervariable CDR1 fragment of a chimeric  
 CC anti-CD25 antibody, a CD25 binding molecule.  
 XX  
 SQ Sequence 5 AA;

Query Match 42.9%; Score 3; DB 24; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4  
 ||||  
 Db 3 WMH 5

RESULT 47  
 AAR11738  
 ID AAR11738 standard; Protein; 6 AA.

AC AAR11738;  
 XX  
 XX  
 XX 25-MAR-2003 (updated)  
 DT 02-JUL-1991 (first entry)  
 XX  
 XX Peptide epitope derived from P69 gene.  
 DE  
 XX Yeast; Bordetella pertussis; P69; fusion protein; vaccine;  
 KW whooping cough.  
 KW  
 XX Synthetic.  
 OS  
 XX EP425082-A.  
 PN  
 XX  
 PD 02-MAY-1991.  
 XX  
 XX 03-SEP-1990; 90EP-0309614.  
 PF  
 XX 04-SEP-1989; 89GB-0019940.  
 PR 21-MAY-1990; 90GB-0011358.  
 XX  
 XX (WELL ) WELLCOME FOUND LTD.  
 PA  
 XX Charles IG, Fairweather NF;  
 PI  
 XX WPI; 1991-126587/18.  
 XX  
 XX Polypeptide for vaccine against eg Bordetella pertussis -  
 PT comprises amino acid sequence encoded by P 69 gene of B. pertussis  
 PT CN2992, or another strain of B. pertussis or B. parapertussis.  
 XX  
 XX Claim 6; Page 12; 24pp; English.

XX The peptide is composed of the amino acids encoded by nucleotides  
 CC 1885-1902 of the P.69 gene of Bordetella pertussis CN 2992. It is  
 CC an epitope and can be used to prepare a vaccine against whooping  
 CC cough. The peptide may be synthesised by std. methods or produced  
 CC as a recombinant fusion protein with the N-terminal of the HBV core  
 CC antigen, pref. under control of the GAL7 promoter.  
 CC See also AAR11737 and AAR11739.  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 CC  
 XX  
 SQ Sequence 6 AA;

Query Match 42.9%; Score 3; DB 12; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 QPP 7  
 ||||  
 Db 4 QPP 6

RESULT 48  
 AAR24983  
 ID AAR24983 standard; Protein; 6 AA.

AC AAR24983;  
 XX  
 XX 25-MAR-2003 (updated)  
 DT 04-DEC-1992 (first entry)  
 XX  
 XX Arg-Arg contg. antimicrobial peptide.  
 DE  
 XX Binding assays; acceptor; antibody; diagnosis; therapeutic agents;  
 KW multiple oligomer mixture; antimicrobial.  
 KW  
 XX Synthetic.

OS  
 XX WO9209300-A1.  
 PN  
 XX 11-JUN-1992.  
 PD  
 XX 20-NOV-1991; 91WO-US08694.  
 PF  
 XX 21-NOV-1990; 90US-0617023.  
 PR 16-MAY-1991; 91US-0701658.  
 PR 19-NOV-1991; 91US-0797551.  
 XX

(ITER-) ITEREX PHARM LP.

PI Appel JR, Blondelle S, Cuervo JH, Houghten RA, Pinilla C;  
 XX WPI; 1992-216794/26.  
 DR

XX Synthesis of multiple oligomer mixts., esp. oligopeptide mixts. - by  
 PT coupling solid support particles with monomeric repeating unit  
 PT cpds., used in binding assays for acceptors or antibodies and  
 PT diagnosis

XX Example; Page 142; 198pp; English.

XX The sequence is that of an oligopeptide which forms part of an  
 CC equimolar mixture of monomeric repeating unit oligopeptides. The  
 CC oligomer mixture can be used in binding assays for acceptors or  
 CC antibodies, in diagnosis and for identifying therapeutic agents.  
 CC The peptide inhibits growth of E.coli (IC-50 24ug/ml).  
 CC See also AAR24498-R24510, AAR24960-R25016 and AAR25018-R25035.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 CC (Updated on 25-MAR-2003 to correct PR field.)  
 CC

XX Sequence 6 AA;

Query Match 42.9%; Score 3; DB 13; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4  
 ||||  
 Db 4 WMH 6

RESULT 49  
 AAR62181  
 ID AAR62181 standard; Protein; 6 AA.

AC AAR62181;

XX 25-MAR-2003 (updated)

DT	03-MAY-1995	(first entry)	
XX			
DE	U1 snRNP 70K protein amino acids 156-161, homologous to rubella virus.		
XX			
XX	Small ribonucleoprotein complex; U1 snRNP; 70K protein; epitope;		
KW	autoantibody; immunoinfective cluster virus; nuclear protein antigen;		
KW	systemic rheumatic disorder; Rubella virus; German measles;		
KW	systemic lupus erythematosus; scleroderma.		
OS			
XX	Homo sapiens.		
XX			
XX	WO9420141-A1.		
PN			
XX			
PD	15-SEP-1994.		
XX			
XX	10-MAR-1994; 94WO-US02631.		
PF			
XX			
XX	11-MAR-1993; 93US-0029850.		
PR			
XX			
XX	(UYSC-) UNIV SOUTHERN CALIFORNIA.		
PA			
XX			
XX	Douvas A, Ehresmann G, Takehana Y;		
PI			
XX	WPI; 1994-302689/37.		
DR			
XX			
XX	Methods for treating immunoinfective cluster virus infections -		
PT	utilise antibodies or fragments characteristic of auto antibodies		
PT	produced by patients with rheumatic disorders		
XX			
XX	Disclosure; Page 67; 106pp; English.		
PS			
XX			
CC	A comparison of the U1 snRNP 70K protein sequence with proteins		
CC	from immunoinfective cluster viruses revealed widespread		
CC	homologies. The importance of these homologous motifs is that they		
CC	are epitopes for autoantibodies occurring in high titres in systemic		
CC	rheumatic disorders. Sera from such patients could be used for		
CC	treatment of immunoinfective cluster virus infections.		
CC	(Updated on 25-MAR-2003 to correct PN field.)		
XX			
XX			
SQ	Sequence 6 AA;		
	Query Match 42.9%; Score 3; DB 15; Length 6;		
	Best Local Similarity 100.0%; Pred. No. 9.3e+05;		
	Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	5 QPP 7		
Db	2 QPP 4		
RESULT 50			
AA73901			
ID	AA73901 standard; peptide; 6 AA.		
XX			
AC	AA73901;		
XX			
XX			
DT	25-MAR-2003 (updated)		
DT	05-DEC-1995 (first entry)		
XX			
DE	Neisseria meningitidis opacity related protein POPM3 peptide 1-5.		
XX			
KW	Neisseria meningitidis; opacity related protein POPM3; vaccine;		
KW	meningitis related homologous antigenic sequence; MRHAS; RV-1;		
KW	immunoassay; diagnosis; treatment; prophylactic; bacterial;		
KW	viral; Peptide 1-5.		
XX			
XX	Neisseria meningitidis.		
OS			
XX			
XX	WO9509232-A2.		
PN			
XX			
PD	06-APR-1995.		
XX			
XX	28-SEP-1994; 94WO-CA00516.		
PF			

PA (HOUG-) HOUGHTEN PHARM INC.  
 XX  
 PI Appel JR, Houghten RA, Pinilla C;  
 XX  
 DR WPI; 1996-432985/43.  
 XX  
 XX Identifying oligopeptide ligands for an acceptor - by scanning  
 PT synthetic peptide combinatorial libraries comprising  
 PT self-solubilising, unsupported mixed oligopeptide(s)  
 XX  
 XX Example 5; Column 52; 75pp; English.  
 PS  
 XX The invention relates to a method of identifying oligopeptide ligands to  
 CC a protein by scanning synthetic combinatorial peptide libraries (SCPL).  
 CC The SCPL comprise sets of hexamers which contain either one of 6  
 CC predetermined amino acids at one predetermined position in the hexamer  
 CC and each set may have one predetermined amino acid at 1 of 6  
 CC predetermined pos. in the hexamer. The method is useful for identifying  
 CC biologically active sequences of e.g. pharmaceutical use. The peptides  
 CC esp. inhibit the binding of e.g. an antibody to its antigen, a ligand to  
 CC its receptor, etc.  
 CC met-enkephalin  
 CC The peptides AAW08641-66 and AAW09226-35 are N-terminally acylated and  
 CC C-terminally amidated peptides, isolated from a SCPL, which inhibit the  
 CC Met-enkephalin analogue (D-Ala, MePhe, Gly-O)-enkephalin (DAGO) from  
 CC binding to the mu opioid receptor. This peptide inhibits binding with  
 CC an IC50 of about 21 nM.  
 CC (Updated on 25-MAR-2003 to correct PF field.)  
 XX  
 XX Sequence 6 AA;  
 SQ

Query Match 42.9%; Score 3; DB 17; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 WMH 4  
 DB 4 WMH 6

RESULT 52  
 AAY29633  
 ID AAY29633 standard; peptide; 6 AA.  
 XX  
 AC AAY29633;  
 XX  
 XX 19-OCT-1999 (first entry)  
 DT  
 DE Phosphoenolpyruvate carboxylase peptide #2.  
 XX  
 KW Phosphoenolpyruvate carboxylase; PEPc; organic acid; succinic acid;  
 KW aerobic Coryneform microbe; Brevibacterium flavum MJ-233.  
 XX  
 OS Brevibacterium flavum.  
 XX  
 PN JP11196887-A.  
 XX  
 PD 27-JUL-1999.  
 XX  
 XX 16-JAN-1998; 98JP-0020360.  
 PF  
 XX 16-JAN-1998; 98JP-0020360.  
 XX  
 XX (MITU) MITSUBISHI CHEM CORP.  
 PA  
 XX WPI; 1999-496658/42.  
 DR  
 XX Preparation of organic acid e.g. succinic acid - comprises reacting  
 PT phosphoenol-pyruvate carboxylase gene recombinant microbe  
 PT anaerobically with substrate  
 XX  
 XX Example 1; Page 13; 18pp; Japanese.  
 PS  
 XX

CC The present invention describes the preparation of an organic acid  
 CC comprising reacting an aerobic Coryneform microbe recombined by  
 CC phosphoenolpyruvate carboxylase (PEPC) gene anaerobically with an  
 CC organic raw material in a reaction liquid containing carbonate ion,  
 CC bicarbonate ion or carbon dioxide gas. The method can prepare an  
 CC organic acid such as succinic acid efficiently in a high yield. The  
 CC present sequence represents a peptide from Brevibacterium flavum MJ-233  
 CC PEPc, used in the exemplification of the present invention.  
 XX  
 XX Sequence 6 AA;  
 SQ

Query Match 42.9%; Score 3; DB 20; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SWM 3  
 DB 1 SWM 3

RESULT 53  
 AAY36355  
 ID AAY36355 standard; Protein; 6 AA.  
 XX  
 AC AAY36355;  
 XX  
 DT 17-SEP-1999 (first entry)  
 DT  
 DE Fragment of human secreted protein encoded by gene 3.  
 DE  
 XX Human; secreted protein; cancer; tumour; developmental abnormality;  
 KW foetal deficiency; blood disorder; immune system disorder; inflammation;  
 KW autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;  
 KW schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;  
 KW atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;  
 KW digestive disorder; endocrine disorder; infection; AIDS.  
 XX  
 OS Homo sapiens.  
 OS  
 PN WO9931117-A1.  
 XX  
 XX 24-JUN-1999.  
 PD  
 XX 17-DEC-1998; 98WO-US27059.  
 PF  
 XX 19-DEC-1997; 97US-0068369.  
 XX 18-DEC-1997; 97US-0068006.  
 PR 18-DEC-1997; 97US-0068007.  
 PR 18-DEC-1997; 97US-0068008.  
 PR 18-DEC-1997; 97US-0068053.  
 PR 18-DEC-1997; 97US-0068054.  
 PR 18-DEC-1997; 97US-0068057.  
 PR 18-DEC-1997; 97US-0068064.  
 PR 18-DEC-1997; 97US-0070923.  
 PR 13-DEC-1997; 97US-0068169.  
 PR 19-DEC-1997; 97US-0068365.  
 PR 19-DEC-1997; 97US-0068367.  
 PR 19-DEC-1997; 97US-0068368.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Carter KC, Duan RD, Feng P, Ferrie AM, Florence C;  
 PI Florence K, Greene JM, Janat F, Kyaw H, Moore PA;  
 PI Ni J, Rosen CA, Ruben SM, Shi Y, Soppet DR, Wei Y;  
 PI Yu G;  
 XX  
 DR WPI; 1999-418749/35.  
 XX  
 XX New isolated human genes encoding secreted polypeptides  
 PT  
 XX Disclosure; Page 419; 537pp; English.  
 PS  
 XX AAX97916 to AAX98029 represent 110 isolated human secreted protein

CC genes. AAY36224 to AAY36727 represent the secreted proteins encoded by  
 CC the 110 human genes. The genes and their corresponding secreted  
 CC polypeptides are useful for preventing, treating or ameliorating medical  
 CC conditions, e.g. by protein or gene therapy. Also pathological conditions  
 CC can be diagnosed by determining the amount of the new polypeptides in a  
 CC sample or by determining the presence of mutations in the new genes.  
 CC Specific uses are described for each of the 110 genes, based on which  
 CC tissues they are most highly expressed in, and include developing  
 CC products for the diagnosis or treatment of cancer, tumours, developmental  
 CC abnormalities and foetal deficiencies, blood disorders, diseases of the  
 CC immune system, autoimmune diseases, inflammation, allergies, Alzheimer's  
 CC and cognitive disorders, schizophrenia, arthritis, asthma, psoriasis,  
 CC sepsis, skin disorders, atherosclerosis, diabetes, cardiovascular  
 CC disorders, kidney disorders, digestive/endocrine disorders, infections  
 CC and AIDS. The polypeptides are also useful for identifying their binding  
 CC partners. The sequences given in AAX97907 to AAX97915 and AAY36223 are  
 CC used in the exemplification of the present invention.

XX Sequence 6 AA;  
 Query Match 42.9%; Score 3; DB 20; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQP 6  
 DB 4 HQP 6

RESULT 54  
 AAB28300  
 ID AAB28300 standard; Peptide; 6 AA.

AC AAB28300;  
 XX  
 DT 14-FEB-2001 (first entry)

XX Human secreted peptide #17 encoded by cDNA#23.

DE Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;  
 KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;  
 KW vulnery; anticonvulsant; antibacterial; antifungal; antiparasitic;  
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;  
 KW neurological disease; infection; human; secreted protein.

XX Homo sapiens.  
 OS  
 XX WO200058355-A1.  
 PN  
 XX 05-OCT-2000.

XX 22-MAR-2000; 2000WO-US07527.  
 PF  
 XX 26-MAR-1999; 99US-0126501.  
 PR  
 XX 22-DEC-1999; 99US-0171551.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM, Komatsoulis G;

XX WPI; 2000-602358/57.  
 DR  
 XX N-PSDB; AAC67653.

XX Nucleic acid molecules encoding human secreted proteins, used in  
 PT preventing, treating or ameliorating a disorder, e.g. Alzheimer's and  
 PT Parkinson's diseases and cancers -

XX Claim 11; Page 346; 367pp; English.

XX Sequences AAB28278-B28326 represent the amino acid sequences of 50  
 CC human secreted proteins encoded by the genes AAC67631-C67680. The genes  
 CC and proteins are useful for preventing, ameliorating or treating medical  
 CC conditions, e.g. by protein or gene therapy. The genes are isolated from

CC a range of human tissues disclosed in the specification. The nucleic  
 CC acids, proteins, antibodies and (ant)agonists are useful in the  
 CC diagnosis, treatment and prevention of: (a) cancer, e.g. breast and  
 CC ovarian cancer, and other cancers of the adrenal gland, bone, bone  
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;  
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune  
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,  
 CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative  
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;  
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and  
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal  
 CC and parasitic infections.

XX Sequence 6 AA;

Query Match 42.9%; Score 3; DB 21; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4  
 DB 1 WMH 3

RESULT 55  
 AAB72258  
 ID AAB72258 standard; peptide; 6 AA.

XX AAB72258;

XX 14-MAY-2001 (first entry)

XX Colostrinin derived cytokine inducing peptide SEQ ID 13.

DE Colostrinin; immune response; cytokine; blood cell proliferation;  
 KW central nervous system disorder; neurological disorder; mental disorder;  
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;  
 KW neurosis; infection.

XX Synthetic.

XX WO200111937-A2.

XX 22-FEB-2001.

XX 17-AUG-2000; 2000WO-US22818.

XX 17-AUG-1999; 99US-0149311.

XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA (REGG-) REGEN THERAPEUTICS PLC.

XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2001-202804/20.

XX Inducing a cytokine and modulating an immune response, useful for  
 PT treating central nervous system diseases and bacterial and viral  
 PT infections, comprises administering colostrinin as an immunological  
 PT regulator -

XX Claim 1; Page 34; 50pp; English.

XX Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,  
 CC a proline rich polypeptide aggregate contained in colostrum. The  
 CC peptides have immune response modulatory activity, and are capable of  
 CC inducing cytokines. Colostrinin and its derived peptides are useful for  
 CC inducing cytokine production, for modulating an immunological response  
 CC and for inducing blood cell proliferation. The peptides are useful in the  
 CC treatment of disorders of the central nervous system, neurological  
 CC Alzheimer's disease, mental disorders, dementia, neurodegenerative diseases,  
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic  
 CC disorders of the immune system, bacterial and viral infections and

```

CC acquired immunological deficiencies.
XX
SQ Sequence 6 AA;

Query Match 42.9%; Score 3; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
Db 3 QPP 5

RESULT 56
AAB72511
ID AAB72511 standard; Peptide; 6 AA.
XX
AC AAB72511;
XX
DT 09-MAY-2001 (first entry)
XX
DE Colostrinin peptide #12.
XX
KW Dermatological; oxidative stress regulator; colostrinin.
XX
OS Unidentified.
XX
PN WO200112650-A2.
XX
PD 22-FEB-2001.
XX
PF 17-AUG-2000; 2000WO-US22665.
XX
PR 17-AUG-1999; 99US-0149310.
XX
PI Stanton GJ, Hughes TK, Boldogh I;
XX
DR WPI; 2001-218342/22.
XX
PT Modulating oxidative stress level in a cell, involves contacting the
PT cell with an oxidative stress regulator selected from colostrinin, its
PT constituent peptide, analog or their combinations -
XX
PS Claim 6; Page 25; 48pp; English.
XX
CC The present invention relates to a method for modulating the oxidative
CC stress level in a cell or a patient, comprising contacting the cell with,
CC or administering to the patient, an oxidative stress regulator selected
CC from colostrinin, or its constituent peptide (e.g. the present peptide),
CC to change the level of an oxidising species in the cell. The method can
CC be used to treat oxidative damage to skin, by decreasing or preventing an
CC increase in the level of damage to a biomolecule of the patient.
XX
SQ Sequence 6 AA;

Query Match 42.9%; Score 3; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
Db 3 QPP 5

RESULT 57
AAB72543
ID AAB72543 standard; Peptide; 6 AA.
XX
AC AAB72543;
XX
DT 09-MAY-2001 (first entry)
XX
DE Colostrinin peptide #12.
XX
KW Neuroprotective; neural cell differentiation regulator; colostrinin;
KW colostrinum.
XX
OS Unidentified.
XX
PN WO200112651-A2.
XX
PD 22-FEB-2001.
XX
PF 17-AUG-2000; 2000WO-US22774.
XX
PR 17-AUG-1999; 99US-0149633.
XX
PA (TEXA ) UNIV TEXAS SYSTEM.
XX
PI Boldogh I;
XX
DR WPI; 2001-226545/23.
XX
PT Use of colostrinin, its constituent peptide or analog as a neural cell
PT regulator, for promoting neural cell differentiation and treating
PT damaged neural cells in a patient -
XX
PS Claim 6; Page 21; 35pp; English.
XX
CC The present invention relates to a method for promoting neural cell
CC differentiation and treating damaged neural cells, using colostrinin and
CC colostrinin constituent peptides (e.g. the present peptide) as a neural
CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.
XX
SQ Sequence 6 AA;

Query Match 42.9%; Score 3; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
Db 3 QPP 5

RESULT 58
AAB59319
ID AAB59319 standard; Peptide; 6 AA.
XX
AC AAB59319;
XX
DT 21-MAR-2001 (first entry)
XX
DE Ewe colostrinin peptide fragment B-4.
XX
KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
XX
OS Ovis sp.
XX
PN WO2000075173-A2.
XX
PD 14-DEC-2000.
XX
PF 02-JUN-2000; 2000WO-GH02128.
XX
PR 02-JUN-1999; 99GB-0012852.
XX
PA (REGG-) REGEN THERAPEUTICS PLC.
XX
PI Georgiades JA;
XX
DR WPI; 2001-071058/08.
XX

```



PT Peptides having an N-terminal amino acid sequence isolated from  
 PT colostrinin for treating e.g. disorders of the central nervous system  
 PT and immune system, viral and bacterial infections, and diseases  
 PT characterized by amyloid plaques -

XX Claim 7; Page 27; 63pp; English.

XX The present invention provides the sequences of a number of peptides  
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
 CC fragment of colostrin. These peptides can be used in the treatment of  
 CC central nervous system disorders such as senile dementia, Parkinson's  
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
 CC disorders such as bacterial and viral infections, to improve the  
 CC development of a child's immune system, as a dietary supplement, and to  
 CC promote the dissolution of beta-amyloid plaques.

XX Sequence 6 AA;

Query Match 42.9%; Score 3; DB 22; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7  
 ||||  
 Db 3 QPP 5

RESULT 59

AAB55512

ID AAB55512 standard; Peptide; 6 AA.

AC AAB55512;

XX 07-MAR-2001 (first entry)

XX Human elastase variant segment peptide SEQ ID NO:82.

XX Human; elastase; variant; substrate; mutant; mutagenesis; histidine;  
 KW human neutrophil elastase; H43A; cytostatic; proteolysis; ADEPT;  
 KW antibody-directed enzyme activated prodrug therapy.

XX Homo sapiens.

XX WO200068363-A2.

XX 16-NOV-2000.

XX 04-MAY-2000; 2000WO-US066592.

XX 05-MAY-1999; 99US-0132640.

XX (GETH ) GENENTECH INC.

XX Carter PJ, Dall'Acqua W, Rodrigues M;

XX WPI; 2001-007389/01.

XX Elastase variant (H43A) having altered substrate specificity useful for  
 PT antibody-directed enzyme activated prodrug therapy -

PS Example 4; Fig 3; 79pp; English.

XX The present invention describes a purified elastase variant (I) with  
 CC an amino acid sequence different from that of a precursor elastase,  
 CC the difference comprising a substitution of an active site histidine  
 CC residue corresponding to residue 43 in human neutrophil elastase with  
 CC a different amino acid residue so that (I) has substrate specificity  
 CC substantially different from the precursor elastase. (I) has cytostatic  
 CC activity, and can be used in antibody-directed enzyme activated prodrug  
 CC therapy. The elastase variant can be used to cleave a particular  
 CC substrate, especially those containing histidine residues at the  
 CC substrate site. Site-specific proteolysis is useful in therapeutic  
 CC applications, e.g. for antibody-directed enzyme activated prodrug

CC therapy (ADEPT). AAC88022, AAC88023 and AAB55432 to AAB55526 represent  
 CC sequences used in the exemplification of the present invention.

SQ Sequence 6 AA;

Query Match 42.9%; Score 3; DB 22; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MEHQ 5  
 ||||  
 Db 2 MEHQ 4

RESULT 60

AAE20240

ID AAE20240 standard; peptide; 6 AA.

XX AAE20240;

XX 18-JUN-2002 (first entry)

XX Colostrinin constituent peptide #12.

XX Blood cell regulator; colostrinin; constituent peptide; oxidative stress;  
 KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;  
 KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;  
 KW transplantation; implantation; dermatological; vulnery.

XX Unidentified.

XX Key Location/Qualifiers

FT Modified-site 6

FT /note= "Optionally C-terminal amide"

XX WO200213850-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22776.

XX 17-AUG-2000; 2000WO-US22776.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX Stanton GJ, Hughes TK, Boldogh I;

XX WPI; 2002-269151/31.

XX Composition useful for the modulation of blood cell proliferation in a  
 PT patient comprises a blood cell regulator selected from colostrinin, its  
 PT constituent peptide and/or analog -

PS Claim 6; Page 25; 51pp; English.

XX The invention relates to a composition which comprises a blood cell  
 CC regulator selected from colostrinin, its constituent peptide and/or  
 CC analogue. The invention is used for modulating the oxidative stress  
 CC level in a cell e.g. mammalian or human cell present in a cell culture,  
 CC tissue, organ, or organism; or for treating oxidative damage to the skin  
 CC of a patient e.g. animal or human; to modulate oxidative stress during/  
 CC after a premature birth or normal birth, preventing/delaying aging in a  
 CC patient, enhancing wound healing, and the reduction of side effects of  
 CC cosmetic procedures. The method changes the level of an oxidising species  
 CC in the cell, such as decreases or prevents increase in the level of  
 CC damage to a biomolecule of the patient selected from DNA, protein and/or  
 CC lipid, compared to the same conditions when the oxidative stress  
 CC regulator is not present. The modulation of oxidative stress results in  
 CC enhanced repair, regeneration, and replacement of cells, tissues and  
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
 CC external organs), as well as enhanced preservation of such organs for  
 CC transplantation, implantation, or scientific research. The present  
 CC sequence is a colostrinin constituent peptide.

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XX  Sequence      6 AA;
SQ
Query Match      42.9%; Score 3; DB 23; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  5 QPP 7
Db  3 QPP 5

RESULT 61
AAMS1047
ID  AAMS1047 standard; Peptide; 6 AA.
XX
AC  AAMS1047;
XX
DT  30-MAY-2002 (first entry)
XX
DE  Colostrinin constituent peptide.
XX
KW  Colostrinin; colostrum; immunomodulator; cardiovascular;
KW  blood cell regulator; cytokine inducer; beta-casein; human.
XX
OS  Homo sapiens.
XX
FH  Key      Location/Qualifiers
FT  Modified-site 6 /note= "optional C-terminal amidation"
FT  WO200213849-A1.
PN
PD  21-FEB-2002.
XX
XX  17-AUG-2000; 2000WO-US22775.
XX
XX  17-AUG-2000; 2000WO-US22775.
XX
PA  (TEXA ) UNIV TEXAS SYSTEM.
PA  (REGE-) REGEN THERAPEUTICS PLC.
XX
XX  Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
XX  WPI; 2002-269150/31.
XX
PT  Modulation of blood cell proliferation in a patient involves use of
PT  blood cell regulator selected from colostrinin, its constituent peptide
PT  and/or analogue -
XX
XX  Claim 1; Page 34; 54pp; English.
XX
CC  The present sequence is that of a colostrinin constituent peptide
CC  that is used as an immunological regulator and as a blood cell
CC  regulator in claimed methods of the invention. The peptide is
CC  classified as having a beta-casein homologue precursor. Methods
CC  are claimed for: inducing a cytokine in a cell by contact with an
CC  immunological regulator, where the cell is present in a cell
CC  culture, a tissue, an organ or an organism, and the cell is
CC  mammalian, including human; modulating an immune response in a cell
CC  by contact with the immunological regulator under conditions in a
CC  effective to induce a cytokine; modulating an immune response in a
CC  patient by administering an immunological regulator under conditions
CC  effective to induce a cytokine, where the immunological regulator
CC  is administered topically or as part of a dietary supplement, and
CC  where the immune response is specific or non specific, an interferon
CC  response or an antibody response; modulating blood cell proliferation
CC  by contacting blood cells with a blood cell regulator, where the
CC  blood cells are present in a cell culture or an organism, are
CC  mammalian or human, and where the blood cells are increased in
CC  number or differentiated; and a method for modulating blood cell
CC  proliferation in a patent. A claimed cytokine-inducing composition
CC  comprises a pharmaceutical carrier and an active agent such as the

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CC  present peptide.
XX
SQ  Sequence      6 AA;
Query Match      42.9%; Score 3; DB 23; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  5 QPP 7
Db  3 QPP 5

RESULT 62
AAO14589
ID  AAO14589 standard; peptide; 6 AA.
XX
AC  AAO14589;
XX
DT  27-MAY-2002 (first entry)
XX
DE  Neural cell regulatory colostrinin peptide 12.
XX
KW  Neural cell differentiation; neural cell regulator; colostrinin peptide;
KW  neural cell formation; proline-rich polypeptide aggregate; colostrum;
KW  neural cell treatment.
XX
OS  Unidentified.
XX
FH  Key      Location/Qualifiers
FT  Modified-site 6 /note= "Optional C-terminal amide"
FT  WO200213851-A1.
PN
PD  21-FEB-2002.
XX
XX  17-AUG-2000; 2000WO-US22777.
XX
XX  17-AUG-2000; 2000WO-US22777.
XX
PA  (TEXA ) UNIV TEXAS SYSTEM.
XX
XX  Boldogh I, Stanton JG, Hughes TK;
XX  WPI; 2002-269152/31.
XX
PT  Promoting cell differentiation in a patient involves use of blood cell
PT  regulator selected from colostrinin, its constituent peptide and/or
PT  analog -
XX
XX  Claim 7; Page 21; 37pp; English.
XX
CC  The invention comprises a method for promoting cell differentiation (e.g.
CC  neural cell differentiation). The method involves contacting cells with a
CC  neural cell regulator (i.e. a colostrinin peptide) in order to change the
CC  cells in morphology to form neural cells. Colostrinin is a proline-rich
CC  polypeptide aggregate that is present in colostrum. The method of the
CC  invention is useful for promoting the differentiation of cells and for
CC  treating damaged neural cells in a patient. The present amino acid
CC  sequence represents a specifically claimed colostrinin peptide used in
CC  the method of the invention.
XX
SQ  Sequence      6 AA;
Query Match      42.9%; Score 3; DB 23; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  5 QPP 7
Db  3 QPP 5

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RESULT 63
AAR77269
ID AAR77269 standard; peptide; 7 AA.
XX AC AAR77269;
XX AC AAR77269;
XX AC AAR77269;
DT 06-FEB-1996 (first entry)
DE MRSA-230 tryptic peptide fragment #3.
XX Tryptic peptide; Staphylococcus aureus; methicillin-resistant; antibody;
KW detection; vaccine; slide agglutination assay; lysothaphin digestion.
XX Staphylococcus aureus.
OS WO9516915-A1.
XX WO9516915-A1.
XX 22-JUN-1995.
XX 14-DEC-1994; 94WO-FI00564.
XX 17-DEC-1993; 93US-0169524.
XX (UYHE-) UNIV HELSINKI LICENSING LTD OY.
XX Hilden P, Kuusela P;
XX WPI; 1995-231663/30.
XX Detection of Staphylococcus aureus esp. methicillin-resistant
PT strains - using anti-MRSA-230 antibodies which may be used in
PT vaccine compositions to promote an immune response against S. aureus
XX Example 3; Page 14; 30pp; English.
XX The sequences represented by AAR77267-72 are tryptic peptide fragments
CC of MRSA-230. These fragments could be used to generate a set of probes
CC for MRSA-230. MRSA-230 is a 230kD protein that was isolated from
CC lysothaphin digests of methicillin-resistant Staphylococcus aureus. The
CC S.aureus used test negative in standard S.aureus agglutination assays.
CC Anti-MRSA-230 antibodies can be constructed by immunising rabbits with
CC heat killed S.aureus that are agglutination negative. The S.aureus used
CC to create these antibodies contain the MRSA-230 protein and this protein
CC was the principle target of the antibodies. The antibodies can then be
CC used in a method of detection of methicillin-resistant S.aureus that are
CC not detected in slide agglutination assays. MRSA-230, and its active
CC fragments, can be used in vaccine compositions which promote an immune
CC response to MRSA-230 and S.aureus.
XX SQ Sequence 7 AA;
Query Match 42.9%; Score 3; DB 16; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 QPP 7
Db 1 QPP 3
|||
|||

RESULT 64
AAR73902
ID AAR73902 standard; peptide; 7 AA.
XX AC AAR73902;
XX AC AAR73902;
DT 25-MAR-2003 (updated)
DT 05-DEC-1995 (first entry)
XX Streptococcus pneumoniae surface protein A peptide 423-429.
DE Streptococcus pneumoniae; surface protein A; vaccine;
KW Streptococcus pneumoniae; surface protein A; vaccine;

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KW meningitis related homologous antigenic sequence; MRHAS; RV-1;
KW immunoassay; diagnosis; treatment; prophylactic; bacterial;
XX viral; peptide 423-429.
XX Streptococcus pneumoniae.
XX OS WO9509232-A2.
XX WO9509232-A2.
XX 06-APR-1995.
XX 28-SEP-1994; 94WO-CA00516.
XX 28-SEP-1993; 93US-0127499.
XX (SHAR/) SHARMA L R.
XX (VALS/) VAN ALSTYNE D.
XX Sharma LR, Van Alstyne D;
XX WPI; 1995-147431/19.
XX New peptide(s) and corresp. antibodies for the treatment of
PT meningitis - the peptide(s) corresp. to homologous antigenic
PT sites on bacterial and viral agents and on chemokine(s), used for
PT detecting and preventing meningitis
XX Claim 35; Page 76; 98pp; English.
XX AAR73912 is the Streptococcus pneumoniae surface protein A. It
CC contains the meningitis related antigenic sequences (MRHAS) claimed
CC in AAR73890 and AAR73902, which are recognised by a monoclonal
CC antibody from the hybridoma Rubella virus (RV)-1. The claimed MRHAS
CC peptides may be used in immunoassays to diagnose the presence of
CC bacterial and/or viral meningitis agents in a sample, or in
CC prophylactic and therapeutic meningitis treatments. The peptides may
CC also be used as vaccines against meningitis.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 7 AA;
Query Match 42.9%; Score 3; DB 16; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 QPP 7
Db 3 QPP 5
|||
|||

RESULT 65
AAR73883
ID AAR73883 standard; peptide; 7 AA.
XX AC AAR73883;
XX AC AAR73883;
DT 25-MAR-2003 (updated)
DT 05-DEC-1995 (first entry)
XX Rubella virus glycosylated membrane-associated protein E2 313-319.
XX Rubella virus glycosylated membrane associated protein E2; vaccine;
KW Rubella virus; glycosylated membrane associated protein E2; vaccine;
KW meningitis related homologous antigenic sequence; MRHAS;
XX RV-1; immunoassay; diagnosis; treatment; prophylactic; bacterial;
XX viral; peptide 313-319; Therien strain.
XX Rubella virus.
XX OS WO9509232-A2.
XX WO9509232-A2.
XX 06-APR-1995.
XX 28-SEP-1994; 94WO-CA00516.
XX

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PR 28-SEP-1993; 93US-0127499.
PA (SHAR/) SHARMA L R.
PA (VALS/) VAN ALSTYNE D.
XX
PI Sharma LR, Van Alstyne D;
XX
DR WPI; 1995-147431/19.
XX
XX New peptide(s) and corresp. antibodies for the treatment of
PT meningitis - the peptide(s) corresp. to homologous antigenic
PT sites on bacterial and viral agents and on chemokine(s), used for
PT detecting and preventing meningitis
XX
XX Claim 35; Page 75; 98pp; English.
XX
CC AAR73917 is the Rubella virus Therein strain glycosylated membrane
CC associated protein E2. It contains the meningitis related antigenic
CC sequences (MRHAS) claimed in AAR73883-R73885 and AAR73897, which are
CC recognised by a monoclonal antibody from the hybridoma Rubella
CC virus (RV)-1. The claimed MRHAS peptides may be used in
CC immunoassays to diagnose the presence of bacterial and/or viral
CC meningitis agents in a sample, or in prophylactic and therapeutic
CC against meningitis. The peptides may also be used as vaccines
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 7 AA;
XX
Query Match 42.9%; Score 3; DB 16; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 QPP 7
DB |||
3 QPP 5
RESULT 66
AAR73897
ID AAR73897 standard; peptide; 7 AA.
XX
AC AAR73897;
XX
XX 25-MAR-2003 (updated)
DT 05-DEC-1995 (first entry)
XX
DE Rubella virus glycosylated membrane-associated protein E2 313-319.
XX
XX Rubella virus; glycosylated membrane associated protein E2; vaccine;
KW meningitis related homologous antigenic sequence; MRHAS;
KW RV-1; immunoassay; diagnosis; treatment; prophylactic; bacterial;
KW viral; peptide 313-319; Therien strain.
XX
OS Rubella virus.
XX
XX WO9509232-A2.
XX
PD 06-APR-1995.
XX
XX 28-SEP-1994; 94WO-CA00516.
XX
XX 28-SEP-1993; 93US-0127499.
XX
XX (SHAR/) SHARMA L R.
XX (VALS/) VAN ALSTYNE D.
XX
XX Sharma LR, Van Alstyne D;
XX
XX WPI; 1995-147431/19.
XX
XX New peptide(s) and corresp. antibodies for the treatment of
PT meningitis - the peptide(s) corresp. to homologous antigenic
PT sites on bacterial and viral agents and on chemokine(s), used for
PT detecting and preventing meningitis
XX
XX Claim 35; Page 75; 98pp; English.
XX
CC AAR73916 is the Rubella virus strain M33 core structural glycoprotein.
CC It contains the meningitis related antigenic sequences (MRHAS)
CC claimed in AAR73879-R73882, which are recognised by a monoclonal
CC antibody from the hybridoma Rubella virus (RV)-1. The claimed MRHAS
CC peptides may be used in immunoassays to diagnose the presence of
CC bacterial and/or viral meningitis agents in a sample, or in

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PT sites on bacterial and viral agents and on chemokine(s), used for
PT detecting and preventing meningitis
XX
XX Claim 35; Page 75; 98pp; English.
XX
CC AAR73915 is the Rubella virus Therien strain glycosylated membrane
CC associated protein E2. It contains the meningitis related antigenic
CC sequences (MRHAS) claimed in AAR73883-R73885 and AAR73897, which are
CC recognised by a monoclonal antibody from the hybridoma Rubella
CC virus (RV)-1. The claimed MRHAS peptides may be used in
CC immunoassays to diagnose the presence of bacterial and/or viral
CC meningitis agents in a sample, or in prophylactic and therapeutic
CC against meningitis. The peptides may also be used as vaccines
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 7 AA;
XX
Query Match 42.9%; Score 3; DB 16; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 QPP 7
DB |||
3 QPP 5
RESULT 67
AAR73879
ID AAR73879 standard; peptide; 7 AA.
XX
AC AAR73879;
XX
XX 25-MAR-2003 (updated)
DT 05-DEC-1995 (first entry)
XX
DE Rubella virus strain M33 core structural peptide MRHAS 102-108.
XX
XX Rubella virus; strain M33; core structural glycoprotein; vaccine;
KW meningitis related homologous antigenic sequence; MRHAS; RV-1;
KW immunoassay; diagnosis; treatment; prophylactic; bacterial;
KW viral; peptide 102-108.
XX
OS Rubella virus.
XX
XX WO9509232-A2.
XX
PD 06-APR-1995.
XX
XX 28-SEP-1994; 94WO-CA00516.
XX
XX 28-SEP-1993; 93US-0127499.
XX
XX (SHAR/) SHARMA L R.
XX (VALS/) VAN ALSTYNE D.
XX
XX Sharma LR, Van Alstyne D;
XX
XX WPI; 1995-147431/19.
XX
XX New peptide(s) and corresp. antibodies for the treatment of
PT meningitis - the peptide(s) corresp. to homologous antigenic
PT sites on bacterial and viral agents and on chemokine(s), used for
PT detecting and preventing meningitis
XX
XX Claim 35; Page 75; 98pp; English.
XX
CC AAR73916 is the Rubella virus strain M33 core structural glycoprotein.
CC It contains the meningitis related antigenic sequences (MRHAS)
CC claimed in AAR73879-R73882, which are recognised by a monoclonal
CC antibody from the hybridoma Rubella virus (RV)-1. The claimed MRHAS
CC peptides may be used in immunoassays to diagnose the presence of
CC bacterial and/or viral meningitis agents in a sample, or in

```

CC prophylactic and therapeutic meningitis treatments. The peptides  
 CC may also be used as vaccines against meningitis.  
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 7 AA;

SQ Query Match 42.9%; Score 3; DB 16; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7  
 |||

Db 3 QPP 5

RESULT 68

AAAY20876  
 ID AAY20876 standard; Protein; 7 AA.

AC AAY20876;

XX 22-JUL-1999 (first entry)

DE Human presenilin I mutant protein fragment 22.

XX Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;  
 KW frameshift mutation; age-related disease; neurodegenerative disorder;  
 KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;  
 KW Huntington's disease; multiple sclerosis; alcoholic liver disease;  
 KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;  
 KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;  
 KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;  
 KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;  
 KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;  
 KW high mobility group protein-C; neuroendocrine specific protein A.

XX Synthetic.

OS Homo sapiens.

XX WO9845322-A2.

XX 15-OCT-1998.

XX 02-APR-1998; 98WO-IB00705.

XX 10-APR-1997; 97US-0043163.

XX (UYUT-) RIJKSUNIV UTRECHT.

PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.

PA (UYRO-) UNIV ROTTERDAM ERASMUS.

XX Burbach JPH, Grosveld FG, Van Leeuwen FW;

XX WPI; 1998-609901/51.

DR N-PSDB; AAX75761.

XX Diagnosing disease by detecting frameshift mutations in RNA or

PT corresponding protein mutations - used to diagnose cancer and

PT neurological diseases, particularly Alzheimer's disease, and also

PT for treatment and prevention with specific ribozymes or wild-type

PT RNA

XX Disclosure; Figure 10; 258pp; English.

XX This invention describes a novel method for the diagnosis of a disease  
 CC caused by, or associated with, an RNA molecule that has a frameshift  
 CC mutation. The method is used to diagnose age-related diseases, especially  
 CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's  
 CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,  
 CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II  
 CC and many others listed) or susceptibility to these disorders. The method  
 CC allows a definitive diagnosis of Alzheimer's disease in living patients,  
 CC at an early stage. It is based on the observation that disease may be

CC caused by mutations in RNA rather than DNA. The invention describes the  
 CC use of neuronal system RNA molecules, specifically proteins including  
 CC beta-amyloid precursor protein (beta-APP), the microtubule associated  
 CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule  
 CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,  
 CC neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic  
 CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma  
 CC 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group  
 CC protein-C (HMGP-C) and neuroendocrine specific protein A.

SQ Sequence 7 AA;

Query Match 42.9%; Score 3; DB 19; Length 7;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7  
 |||

Db 2 QPP 4

RESULT 69

AAW61049

ID AAW61049 standard; peptide; 7 AA.

AC AAW61049;

XX 25-SEP-1998 (first entry)

DE Peptide from mouse IgG1 that is important for FcRn binding.

KW Immunoglobulin G; IgG; FcRn binding; half-life; increase; decrease;

KW treatment; idiopathic thrombocytopenic purpura; ITP;

KW Kawasaki disease; AIDS; Guillain-Barre syndrome; dermatomyositis.

XX Synthetic.

OS Mus sp.

XX WO9823289-A1.

XX 04-JUN-1998.

XX 26-NOV-1997; 97WO-US21437.

XX 27-NOV-1996; 96US-0031607.

PA (GEHO) GEN HOSPITAL CORP.

PA (UYBR-) UNIV BRANDEIS.

PI Israel EJ, Simister NE;

XX WPI; 1998-322461/28.

XX New antibody having altered Fc receptor binding site - allows

PT increased or decreased half-lives and clearance rates, useful for,

PT e.g. tumour imaging or treatment of AIDS

XX Example 2; Fig 2A; 32pp; English.

XX AAW61048-57 represent partial amino acid sequence of different  
 CC immunoglobulin G (IgG) molecules. These peptides have been identified  
 CC as being important for FcRn binding. The specification describes a  
 CC non-naturally occurring IgG having an altered amino acid sequence  
 CC compared to native IgG, which binds to FcRn with increased or  
 CC decreased affinity. FcRn is a receptor found on the intestinal surface  
 CC of the neonate and is responsible passage of maternal milk IgG from the  
 CC intestinal lumen to the systemic circulation via the intestinal  
 CC epithelial cells. FcRn is also used to prevent clearance of circulating  
 CC IgG from the circulation. Altering the binding site on an IgG for FcRn  
 CC allows greater or lower affinity for the FcRn receptor, which  
 CC subsequently increases or decreases the half-life of circulating IgG,  
 CC respectively. IgG's with an increased half-life can be used to treat  
 CC immune conditions or diseases such as idiopathic thrombocytopenic

CC purpura (ITP), Kawasaki disease, AIDS, Guillain-Barre syndrome and  
 CC dermatomyositis.  
 XX  
 SQ Sequence 7 AA;

Query Match 42.9%; Score 3; DB 19; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHQ 5  
 ||||  
 Db 2 MHQ 4

RESULT 70  
 AAY16906  
 ID AAY16906 standard; peptide; 7 AA.  
 XX  
 AC AAY16906;  
 XX  
 DT 20-JUL-1999 (first entry)  
 XX  
 DE Heat shock protein (hsp) binding peptide.  
 XX  
 KW Conjugate peptide; heat shock protein; hsp; phage display library; virus;  
 KW surface protein; tethering peptide; chaperone process; cytokine; cancer;  
 KW neoplastic disease; infectious disease; bacterium; immune system; fungus;  
 KW acquired immune deficiency; autoimmune disease.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9922761-A1.  
 XX  
 PD 14-MAY-1999.  
 XX  
 PF 22-OCT-1998; 98WO-US22335.  
 XX  
 PR 31-OCT-1997; 97US-0961707.  
 XX  
 PA (SLOK ) SLOAN KETTERING INST CANCER RES.  
 XX  
 PI Hartl U, Hoe MH, Houghton A, Mayhew M, Moroi Y;  
 PI Querfelli O, Rothman JE;  
 XX  
 DR WPI; 1999-313177/26.  
 XX  
 PT Identifying peptides which bind heat shock proteins  
 XX  
 PS Examples; Page 20; 155pp; English.  
 XX  
 CC The invention relates to conjugate peptides engineered to noncovalently  
 CC bind to heat shock proteins (hsp). A method of identifying a hsp binding  
 CC peptide comprises (a) contacting a phage display library having  
 CC bacteriophage expressing, in a surface protein, inserted peptides with a  
 CC hsp target, and bound to a benzquinone anisamycin antibiotic (BAA), in a  
 CC physiologic binding buffer; (b) isolating a phage binding to the hsp  
 CC target; and (c) identifying the inserted peptide expressed. The peptides  
 CC which bind to a hsp can be used as tethering peptides for a hsp which may  
 CC serve as an accessory in a chaperone process and/or may comprise a  
 CC cytokine. They can also be coupled to antigens to induce an immune  
 CC response. Such compositions can be used for treating neoplastic disease,  
 CC e.g. cancers, infectious diseases, e.g. diseases caused by a bacterium,  
 CC virus, protozoan, mycoplasma, fungus, yeast, parasite or prion, or a  
 CC disease of the immune system, e.g. acquired immune deficiencies or  
 CC autoimmune diseases.  
 XX  
 SQ Sequence 7 AA;

Query Match 42.9%; Score 3; DB 20; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQP 6

Db ||||  
 1 HQP 3

RESULT 71  
 AAB16495  
 ID AAB16495 standard; Peptide; 7 AA.  
 XX  
 AC AAB16495;  
 XX  
 DT 27-OCT-2000 (first entry)  
 XX  
 DE Linear peptide that binds to angiostatin SEQ ID # 86.  
 XX  
 KW Angiogenesis-inhibiting protein receptor; angiogenesis; angiostatin;  
 KW endostatin; plasminogen; laminin; treatment; wound healing; solid tumour;  
 KW psoriasis; scleroderma; myocardial angiogenesis; Crohn's disease;  
 KW cerebral collateral; arteriovenous malformation; rubecosis; cancer;  
 KW diabetic retinopathy; arthritis; wound healing; peptic ulcer;  
 KW Helicobacter related disease; fracture; cat scratch fever.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200032631-A2.  
 XX  
 PD 08-JUN-2000.  
 XX  
 PF 06-DEC-1999; 99WO-US28897.  
 XX  
 PR 04-DEC-1998; 98US-0206059.  
 XX  
 PA (ENTR-) ENTREMED INC.  
 XX  
 PI MacDonald NJ, Sim KL;  
 XX  
 DR WPI; 2000-412290/35.  
 XX  
 PT New angiogenesis-inhibiting protein receptors, useful in methods for  
 PT treating diseases and processes that are mediated by angiogenesis, such  
 PT as solid tumours, psoriasis, scleroderma and myocardial angiogenesis -  
 XX  
 PS Claim 1; Page 50; 100pp; English.  
 XX  
 CC This invention relates to angiogenesis-inhibiting protein receptors, and  
 CC the DNA sequences encoding them. Angiogenesis is the generation of new  
 CC blood vessels into a tissue, and normally occurs in wound healing,  
 CC foetal and embryonal development and the formation of the corpus luteum,  
 CC endometrium and placenta. Angiostatin is a protein (see AAB16450 and  
 CC AAA68202) involved in angiogenesis, and has an amino acid sequence  
 CC similar to that of a plasminogen fragment (see murine plasminogen  
 CC AAB16490). Angiostatin has the ability to inhibit angiogenesis.  
 CC Endostatin is also an angiogenesis inhibiting protein (see AAB16451 and  
 CC AAA68203). Sequences AAA68242 and AAB16522 represent coding and protein  
 CC sequences of human laminin. Laminin is an angiostatin binding protein, of  
 CC and some of the peptides of the invention share homology with regions of  
 CC laminin. Peptides AAB16452-B16521 (excluding AAB16490) are the  
 CC angiogenesis-inhibiting protein receptor fragments of the invention. The  
 CC peptides bind either angiostatin or endostatin and can be used in methods  
 CC for treating diseases and processes that are mediated by angiogenesis,  
 CC such as solid tumours, psoriasis, scleroderma, myocardial angiogenesis,  
 CC Crohn's disease, cerebral collaterals, arteriovenous malformations,  
 CC rubecosis, diabetic retinopathy, arthritis, wound healing, peptic ulcers,  
 CC Helicobacter related diseases, fractures, placenta and cat scratch  
 CC fever. They are useful for the detection and prognosis of cancer. DNA  
 CC sequences A628204-A628241 encode the peptides of the invention.  
 XX  
 SQ Sequence 7 AA;

Query Match 42.9%; Score 3; DB 21; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7

Db  
|||  
2 QPP 4

RESULT 72  
AAB17249  
ID AAB17249 standard; Peptide; 7 AA.  
XX  
AC AAB17249;  
XX  
DT 31-OCT-2000 (first entry)  
XX  
DE SH3 antagonist peptide sequence SEQ ID NO:305.  
XX  
KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;  
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;  
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;  
KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;  
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;  
KW vascular endothelial growth factor; matrix metalloproteinase;  
KW asthma; thrombosis; pharmaceutical.  
XX  
OS Synthetic.  
XX  
PN WO200024782-A2.  
XX  
PD 04-MAY-2000.  
XX  
PF 25-OCT-1999; 99WO-US25044.  
XX  
PR 23-OCT-1998; 98US-0105371.  
PR 22-OCT-1999; 99US-0428082.  
XX  
PA (AMGE-) AMGEN INC.  
XX  
PI Feige U, Liu C, Cheetham J, Boone TC;  
XX  
DR WPI; 2000-350702/30.  
XX  
PT Novel composition of matter comprising an Fc domain and  
PT pharmacologically active peptides, useful for treating cancer and  
PT autoimmune diseases -  
XX  
PS Claim 39; Page 302; 608pp; English.  
XX  
CC The present invention describes composition of matter (I) comprising an  
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:  
CC (X1)a-P1-(X2)b, where: P1 = an Fc domain; X1 and X2 = are each  
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,  
CC -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4  
CC where P1, P2, P3, and P4 = are each independently sequences of  
CC pharmacologically active peptides; L1, L2, L3, and L4 = are each  
CC independently linkers; and a, b, c, d, e, and f = are each independently  
CC 0 or 1, provided that at least 1 of a and b is 1. The composition can  
CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive  
CC activities. DNAs, vectors and host cells from the present invention can  
CC be used for producing pharmaceutical compositions. The compositions are  
CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.  
CC The use of an Fc domain (rather than a Fab domain) can provide a longer  
CC half-life or incorporate functions such as Fc receptor binding, protein  
CC A binding, complement fixation, and possibly placental transfer. AAB69443  
CC to AAB69526 and AAB16955 to AAB18003 represent nucleotide and amino acid  
CC sequences used in the exemplification of the present invention.  
XX  
SQ Sequence 7 AA;

Query Match 42.9%; Score 3; DB 21; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 QPP 7  
|||  
Db 3 QPP 5

RESULT 73  
AAY92768  
ID AAY92768 standard; peptide; 7 AA.  
XX  
AC AAY92768;  
XX  
DT 29-AUG-2000 (first entry)  
XX  
DE Heptapeptide mimotope of surface LOS of serogroup B meningococcus.  
XX  
KW Heptapeptide; epitope; mimotope; surface lipo-oligosaccharide; LOS;  
KW meningitis; anti-bacterial; anti-inflammatory; vaccine.  
XX  
OS Neisseria meningitidis.  
XX  
PN WO200025814-A2.  
XX  
PD 11-MAY-2000.  
XX  
PF 27-OCT-1999; 99WO-GB03559.  
XX  
PR 30-OCT-1998; 98GB-0023835.  
XX  
PA (UNLO ) UNIV COLLEGE LONDON.  
PA (NABI-) NAT INST BIOLOGICAL STANDARDS & CO.  
XX  
PI Charalambous BM, Feavers IM;  
XX  
DR WPI; 2000-365403/31.  
XX  
PT Use of a mimotope of a surface lipooligosaccharide of a serogroup B  
PT meningococcus for a vaccine against serogroup B meningococci  
XX  
PS Claim 13; Page 26; 39pp; English.  
XX  
CC This is a preferred heptapeptide epitope mimotope of a surface  
CC lipooligosaccharide (LOS) of a serogroup B meningococcus. The mimotopes  
CC are useful in vaccines against serogroup B meningococci, especially  
CC Neisseria meningitidis, which causes meningitis. The LOS is a surface  
CC glycolipid that forms a major outer membrane component and possesses a  
CC terminal galactose acceptor sites for sialic acid. Sialylation of the LOS  
CC in immunotype B meningococci may enhance the ability of the organism to  
CC evade the human immune response. Therefore alternative target antigens on  
CC the surface of serogroup B meningococci are important.  
XX  
SQ Sequence 7 AA;  
Query Match 42.9%; Score 3; DB 21; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 QPP 6  
|||  
Db 4 QPP 6  
RESULT 74  
AAU72048  
ID AAU72048 standard; Peptide; 7 AA.  
XX  
AC AAU72048;  
XX  
DT 26-FEB-2002 (first entry)  
XX  
DE Melanoma antigen, javelin peptide #34.  
XX  
KW Melanoma antigen; MART-1; MAGE-1; gp100; cytostatic; immune response;  
KW immunotherapeutic; heat shock protein; tyrosinase; BAGE; NYEs01; GM2;  
KW tyrosinase related protein 1; tyrosinase related protein 2; vaccine;  
KW javelin molecule; melanoma antigen recognised by T cells-1; human.  
XX

OS Bacteriophage M13.  
 XX WO200178655-A2.  
 XX  
 XX 25-OCT-2001.  
 XX  
 XX 17-APR-2001; 2001WO-US12449.  
 XX  
 XX 17-APR-2000; 2000US-197462P.  
 XX  
 XX (HOUGH/) HOUGHTON A.  
 XX (LIVI/) LIVINGSTON P.  
 XX (ALAW/) AL-AWQATI Q.  
 XX (MAYH/) MAYHEW M.  
 XX (HOEM/) HOE M.  
 XX  
 XX Houghton A, Livingston P, Al-awqati Q, Mayhew M, Hoe M;  
 XX WPI; 2001-663092/76.  
 XX  
 XX Anti cancer vaccine for the treatment of melanoma comprises a heat  
 XX shock protein and a melanoma antigen i.e. tyrosinase -  
 XX  
 XX Disclosure; Page 16; 150pp; English.  
 XX  
 XX The invention relates to a method of induction of an immune response,  
 XX comprising administration of an immunotherapeutic composition, comprising  
 XX a heat shock protein, and a melanoma antigen, where the melanoma  
 XX antigen is selected from tyrosinase, tyrosinase related protein 1,  
 XX tyrosinase related protein 2, gp 100, MAGE antigens, BAGE antigens,  
 XX NYEs01, MART antigens, GM2, antigenic portions and combinations of these.  
 XX The melanoma antigen is covalently bound to a javelin molecule, where the  
 XX melanoma antigen bound to the javelin molecule is non-covalently bound to  
 XX the heat shock protein. The composition is useful for inducing an immune  
 XX response for the treatment of melanoma. AAU71980-AAU72481 represent  
 XX melanoma antigen peptides of the invention.  
 XX  
 XX Sequence 7 AA;  
 XX  
 XX Query Match 42.9%; Score 3; DB 22; Length 7;  
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX Qy 4 HQP 6  
 XX Db 1 HQP 3  
 XX  
 XX RESULT 75  
 XX AAU43873  
 XX ID AAU43873 standard; Peptide; 7 AA.  
 XX AC AAU43873;  
 XX  
 XX 25-OCT-2001 (first entry)  
 XX  
 XX H11 binding site consensus conforming peptide (CCP) #144.  
 XX  
 XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;  
 XX immunogenically cross-reactive; cancer; immunogenic cancer cell;  
 XX cytostatic; vaccine; tumour-specific immunogenic response inducer;  
 XX astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;  
 XX ependymoma; medulloblastoma; primitive neural ectodermal tumour.  
 XX  
 XX Homo sapiens.  
 XX Synthetic.  
 XX  
 XX CA2290722-A1.  
 XX  
 XX 08-JUN-2001.  
 XX  
 XX 08-DEC-1999; 99CA-2290722.

PR 08-DEC-1999; 99CA-2290722.  
 XX (NOVO-) NOVOPHARM BIOTECH INC.  
 XX  
 XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;  
 XX Entwistle JM, MacDonald GC;  
 XX WPI; 2001-425937/46.  
 XX  
 XX Composition useful for treating and diagnosing cancer, comprises stress  
 XX protein-peptide complexes associated with tumor, and isolated  
 XX antigen-binding fragments of an antibody that binds specifically to the  
 XX complex -  
 XX  
 XX Example 4; Page 101; 154pp; English.  
 XX  
 XX The present invention describes a composition (I) comprising stress  
 XX protein-peptide complexes (SPPC) associated with tumours that is  
 XX specifically immunogenically cross-reactive with cell surface-associated  
 XX SPPCs specific to target cancer (TC). Also described is an isolated  
 XX antigen-binding fragment of an antibody that binds specifically to SPPCs  
 XX or a population of different SPPCs consisting of immunogenic cancer cell  
 XX surface-associated SPPC of TC. (I) has cytostatic activity and can be  
 XX used in vaccine production and as a tumour-specific immunogenic response  
 XX inducer. (I) is useful for treating 71 types of cancers or tumours in a  
 XX subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,  
 XX oligodendroglioma, ependymoma, medulloblastoma, and primitive neural  
 XX ectodermal tumour (PNET). (I) is useful as cancer immunogen including  
 XX vaccines. (I) is useful for diagnostic and palliative use, for detecting  
 XX or imaging cancer cells, and to monitor the course of amelioration of  
 XX malignancy in an individual. AAU43707 to AAU47109 represent peptides  
 XX which are used in the exemplification of the present invention.  
 XX  
 XX Sequence 7 AA;  
 XX  
 XX Query Match 42.9%; Score 3; DB 22; Length 7;  
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX Qy 5 QPP 7  
 XX Db 5 QPP 7  
 XX  
 XX Search completed: November 25, 2003, 19:27:12  
 XX Job time : 19.8663 secs



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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:25:48 ; Search time 11.2326 Seconds  
(without alignments)  
114.943 Million cell updates/sec

Title: US-09-641-801-24

Perfect score: 7

Sequence: 1 SWNHQP 7

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Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 184443283 residues

Word size : 0

Total number of hits satisfying chosen parameters: 139996

Minimum DB seq length: 3

Maximum DB seq length: 20

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Database : Published Applications AA:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	7	15	US-10-281-652-24
2	7	100.0	10	15	US-10-185-815-89
3	6	85.7	19	12	US-10-372-736-3
4	5	71.4	15	15	US-10-281-652-34
5	4	57.1	10	9	US-09-794-346-1
6	4	57.1	11	11	US-09-809-391-689
7	4	57.1	11	12	US-09-882-171-689
8	4	57.1	17	12	US-09-962-756-1752
9	4	57.1	20	12	US-10-195-730-261
10	4	57.1	20	12	US-09-933-767-773
11	4	57.1	20	15	US-10-023-282-773
12	3	42.9	5	9	US-09-748-960-12
13	3	42.9	5	9	US-09-765-086-223
14	3	42.9	5	9	US-09-933-497B-26
15	3	42.9	5	10	US-09-770-002-1
					Sequence 24, Appl
					Sequence 89, Appl
					Sequence 3, Appl
					Sequence 34, Appl
					Sequence 1, Appl
					Sequence 689, App
					Sequence 12, App
					Sequence 1751, App
					Sequence 262, App
					Sequence 773, App
					Sequence 773, App
					Sequence 12, Appl
					Sequence 12, Appl
					Sequence 223, App
					Sequence 26, Appl
					Sequence 1, Appl

5 11 US-09-940-727B-70 Sequence 70, Appl  
6 15 US-10-097-065-334 Sequence 334, Appl  
6 15 US-10-227-353-7 Sequence 7, Appl  
6 15 US-10-281-652-13 Sequence 13, Appl  
7 9 US-09-873-676-86 Sequence 86, Appl  
7 11 US-09-821-687-7 Sequence 7, Appl  
7 11 US-09-954-385-347 Sequence 347, Appl  
7 12 US-10-052-578-176 Sequence 176, Appl  
7 12 US-09-990-832C-10 Sequence 10, Appl  
7 12 US-10-053-520-176 Sequence 176, Appl  
7 12 US-10-286-457-92 Sequence 92, Appl  
7 12 US-10-038-899-4 Sequence 4, Appl  
7 12 US-10-220-033-21 Sequence 21, Appl  
7 12 US-10-053-498B-176 Sequence 176, Appl  
7 15 US-10-015-979-84 Sequence 84, Appl  
7 15 US-10-281-652-1 Sequence 1, Appl  
8 7 US-08-344-824-263 Sequence 263, Appl  
8 10 US-09-765-614B-6 Sequence 6, Appl  
8 10 US-09-925-715-2 Sequence 2, Appl  
8 10 US-09-791-378-285 Sequence 285, Appl  
8 10 US-09-883-825-35 Sequence 35, Appl  
8 11 US-09-999-724-58 Sequence 124, Appl  
8 12 US-10-365-908-98 Sequence 58, Appl  
8 12 US-09-829-382-11 Sequence 98, Appl  
8 12 US-10-038-899-3 Sequence 11, Appl  
8 12 US-10-357-929A-21 Sequence 3, Appl  
8 15 US-10-158-596A-105 Sequence 21, Appl  
8 15 US-10-017-193-4 Sequence 105, Appl  
8 15 US-10-254-446A-232 Sequence 4, Appl  
9 9 US-09-748-960-11 Sequence 232, Appl  
9 10 US-09-780-053-165 Sequence 11, Appl  
9 10 US-09-780-053-456 Sequence 165, Appl  
9 10 US-09-780-053-517 Sequence 456, Appl  
9 10 US-09-780-053-620 Sequence 517, Appl  
9 10 US-09-862-179A-11 Sequence 620, Appl  
9 10 US-09-862-179A-18 Sequence 11, Appl  
9 10 US-09-017-743C-69 Sequence 18, Appl  
9 11 US-09-938-864-108 Sequence 69, Appl  
9 11 US-09-938-864-143 Sequence 108, Appl  
9 11 US-09-938-864-148 Sequence 143, Appl  
9 11 US-09-938-864-180 Sequence 148, Appl  
9 11 US-09-938-864-243 Sequence 180, Appl  
9 11 US-09-938-864-281 Sequence 243, Appl  
9 11 US-09-791-477-108 Sequence 281, Appl  
9 11 US-09-791-477-143 Sequence 108, Appl  
9 11 US-09-791-477-148 Sequence 143, Appl  
9 11 US-09-791-477-180 Sequence 148, Appl  
9 11 US-09-791-477-243 Sequence 180, Appl  
9 11 US-09-791-477-281 Sequence 243, Appl  
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9 11 US-09-785-019-243 Sequence 180, Appl  
9 11 US-09-785-019-281 Sequence 243, Appl  
9 12 US-09-932-165-66 Sequence 281, Appl  
9 12 US-09-932-165-669 Sequence 669, Appl  
9 12 US-09-932-165-1013 Sequence 1013, Appl  
9 12 US-09-932-165-1212 Sequence 1212, Appl  
9 12 US-09-932-165-1222 Sequence 1222, Appl  
9 12 US-10-153-883B-47 Sequence 47, Appl  
9 12 US-10-155-833B-50 Sequence 50, Appl  
9 12 US-10-271-617-11 Sequence 11, Appl  
9 12 US-10-022-066-34 Sequence 34, Appl  
9 12 US-10-022-066-488 Sequence 488, Appl  
9 12 US-10-365-908-80 Sequence 80, Appl  
9 12 US-10-038-899-2 Sequence 2, Appl  
9 12 US-10-119-536A-11 Sequence 11, Appl  
9 12 US-10-195-835-108 Sequence 108, Appl  
9 12 US-10-195-835-143 Sequence 143, Appl  
9 12 US-10-195-835-180 Sequence 148, Appl  
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90 3 42.9 9 12 US-10-195-835-281 Sequence 281, App  
91 3 42.9 9 12 US-10-286-333-108 Sequence 108, App  
92 3 42.9 9 12 US-10-286-333-143 Sequence 143, App  
93 3 42.9 9 12 US-10-286-333-148 Sequence 148, App  
94 3 42.9 9 12 US-10-286-333-180 Sequence 180, App  
95 3 42.9 9 12 US-10-286-333-243 Sequence 243, App  
96 3 42.9 9 12 US-10-286-333-281 Sequence 281, App  
97 3 42.9 9 15 US-10-125-635A-108 Sequence 108, App  
98 3 42.9 9 15 US-10-125-635A-143 Sequence 143, App  
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100 3 42.9 9 15 US-10-125-635A-180 Sequence 180, App

## ALIGNMENTS

RESULT 1  
US-10-281-652-24  
; Sequence 24, Application US/10281652  
; Publication No. US20030091606A1  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/10/281,652  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US/09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 24  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-10-281-652-24

Query Match 100.0%; Score 7; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SWMHQPP 7  
Db 1 SWMHQPP 7

RESULT 2  
US-10-185-815-89  
; Sequence 89, Application US/10185815  
; Publication No. US20030096354A1  
; GENERAL INFORMATION:  
; APPLICANT: Elan Corporation, plc  
; APPLICANT: O'Mahony, Daniel  
; APPLICANT: Lambkin, Imelda  
; APPLICANT: Higgins, Lisa  
; TITLE OF INVENTION: Peyer's Patch And/or M-Cell Targeting Ligands  
; FILE REFERENCE: E1067-20093  
; CURRENT APPLICATION NUMBER: US/10/185,815  
; CURRENT FILING DATE: 2002-10-09  
; PRIOR APPLICATION NUMBER: 60/302,591  
; PRIOR FILING DATE: 2001-07-02  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 89  
; LENGTH: 10

; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Segment of CAPHI beta casein precursor  
US-10-185-815-89

Query Match 100.0%; Score 7; DB 15; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.038;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SWMHQPP 7  
Db 1 SWMHQPP 7

RESULT 3  
US-10-372-736-3  
; Sequence 3, Application US/10372736  
; Publication No. US20030166223A1  
; GENERAL INFORMATION:  
; APPLICANT: Sims, John E.  
; APPLICANT: Virca, G. Duke  
; APPLICANT: Bird, Timothy A.  
; APPLICANT: Anderson, Dirk M.  
; TITLE OF INVENTION: Polypeptides Having Kinase Activity  
; FILE REFERENCE: 2005-B  
; CURRENT APPLICATION NUMBER: US/10/372,736  
; CURRENT FILING DATE: 2003-02-21  
; PRIOR APPLICATION NUMBER: 08/870,529  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/059,979  
; PRIOR FILING DATE: 1996-06-10  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-10-372-736-3

Query Match 85.7%; Score 6; DB 12; Length 19;  
Best Local Similarity 100.0%; Pred. No. 0.87;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SWMHQPP 6  
Db 12 SWMHQPP 17

RESULT 4  
US-10-281-652-34  
; Sequence 34, Application US/10281652  
; Publication No. US20030091606A1  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/10/281,652  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US/09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 34  
; LENGTH: 15

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-34
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Best Local Similarity 100.0%; Pred.No.11;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 MHQPP 7
Db      1 MHQPP 5

RESULT 5
US-09-794-346-1
; Sequence 1, Application US/09794346
; Patent No. US20010031857A1
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharma Deutschland GmbH
; TITLE OF INVENTION: Memo Peptides, Process for Their Preparation and Use Thereof
; FILE REFERENCE: 02481.1728
; CURRENT APPLICATION NUMBER: US/09/794,346
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: EP 00104114.4
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: PCT/EP 01/01661
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Description of Artificial Sequence: Memmoniaella echinata, FH 227
US-09-794-346-1
Query Match      57.1%; Score 4; DB 9; Length 10;
Best Local Similarity 100.0%; Pred.No.1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 MHQP 6
Db      1 MHQP 4

RESULT 6
US-09-809-391-689
; Sequence 689, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 689
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-809-391-689
Query Match      57.1%; Score 4; DB 11; Length 11;
Best Local Similarity 100.0%; Pred.No.1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 HOPP 7
Db      1 HOPP 4

RESULT 7
US-09-882-171-689
; Sequence 689, Application US/09882171
; Publication No. US20030175858A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/882,171
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
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; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/043,580  
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; PRIOR APPLICATION NUMBER: 60/056,631  
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; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/048,964  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/057,650  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: 60/056,884  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/057,669  
; PRIOR FILING DATE: 1997-09-05

Query Match 57.1%; Score 4; DB 12; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQPP 7

Db 1 HQPP 4

RESULT 8

US-09-962-756-1752  
; Sequence 1752, Application US/09962756  
; Publication No. US20030195147A1  
; GENERAL INFORMATION:  
; APPLICANT: PILLIUTLA, RENUKA  
; APPLICANT: BRISSETTE, RENEE  
; APPLICANT: BLUME, ARTHUR J.  
; APPLICANT: SCHAFER, LAUGE  
; APPLICANT: BRANDT, JAKOB  
; APPLICANT: GOLDSTEIN, NEIL I.  
; APPLICANT: SPETZLER, JANE  
; APPLICANT: OSTERGAARD, SOREN  
; APPLICANT: HANSEN, PER HERTZ  
; TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS  
; FILE REFERENCE: 1878-4051US1  
; CURRENT APPLICATION NUMBER: US/09/962,756  
; CURRENT FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: 09/538,038  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: 09/146,127  
; PRIOR FILING DATE: 1998-09-02  
; NUMBER OF SEQ ID NOS: 2227  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1752  
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; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide  
; OTHER INFORMATION: peptide  
US-09-962-756-1752

Query Match 57.1%; Score 4; DB 12; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 3 MHQP 6  
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Db 12 MHQP 15

RESULT 9  
US-10-195-730-261  
; Sequence 261, Application US/10195730  
; Publication No. US20030144492A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et. al  
; TITLE OF INVENTION: 101 Human Secreted Proteins  
; FILE REFERENCE: P2017P1  
; CURRENT APPLICATION NUMBER: US/10/195,730  
; CURRENT FILING DATE: 2002-07-16  
; PRIOR APPLICATION NUMBER: US/09/281,976  
; PRIOR FILING DATE: 1999-03-31  
; PRIOR APPLICATION NUMBER: 60/060,837  
; PRIOR FILING DATE: 1997-10-02  
; PRIOR APPLICATION NUMBER: 60/060,862  
; PRIOR FILING DATE: 1997-10-02  
; NUMBER OF SEQ ID NOS: 390  
; SOFTWARE: PatentIn Ver. 2.0  
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; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-195-730-261

Query Match 57.1%; Score 4; DB 12; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 4 HQPP 7  
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Db 11 HQPP 14

RESULT 10  
US-09-933-767-773  
; Sequence 773, Application US/09933767  
; Publication No. US20030181692A1  
; GENERAL INFORMATION:  
; APPLICANT: Ni et. al.  
; TITLE OF INVENTION: 207 Human Secreted Proteins  
; FILE REFERENCE: P2007P2  
; CURRENT APPLICATION NUMBER: US/09/933,767  
; CURRENT FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: PCT/US01/05614  
; PRIOR FILING DATE: 2001-02-21  
; PRIOR APPLICATION NUMBER: 60/184,836  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/193,170  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: 09/205,258  
; PRIOR FILING DATE: 1998-12-04  
; PRIOR APPLICATION NUMBER: PCT/US98/11422  
; PRIOR FILING DATE: 1998-06-04  
; PRIOR APPLICATION NUMBER: 60/048,885  
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; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,893  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,900  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,901  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,892  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,915  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/049,019  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,970  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,972  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,916  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/049,373  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,875  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/049,374  
; PRIOR FILING DATE: 1997-06-06

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; PRIOR APPLICATION NUMBER: 60/048,917
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,949
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,974
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,883
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,897
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,898
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,962
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,963
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,877
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,878
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,054
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,064
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,053
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/070,923
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/085,925
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,921
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,923
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,922
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/092,921
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/094,657
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1245
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 773
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-933-767-773

Query Match      57.1%; Score 4; DB 12; Length 20;
Best Local Similarity 100.0%; Pred.No.1.9e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 HOPP 7
Db      1 HOPP 4

RESULT 11
US-10-023-282-773
; Sequence 773, Application US/10023282
; Publication No. US20030092893A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
```

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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 773
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-023-282-773

Query Match          57.1%; Score 4; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQPP 7
Db 1 HQPP 4

RESULT 12
US-09-748-960-12
; Sequence 12, Application US/09748960
; Patent No. US20010046496A1
; GENERAL INFORMATION:
; APPLICANT: Brettman, Lee R.
; APPLICANT: Fox, Judith A.
; TITLE OF INVENTION: Method of Administering an Antibody
; FILE REFERENCE: 1855-2007-001
; CURRENT APPLICATION NUMBER: US/09/748,960
; CURRENT FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: US/09/550,082
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)...(5)
; OTHER INFORMATION: CDR1 of the heavy chain of antibodies Act-1 and
; OTHER INFORMATION: LDP-02
US-09-748-960-12

Query Match          42.9%; Score 3; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 WMH 4
Db 3 WMH 5

RESULT 13
US-09-765-086-223
; Sequence 223, Application US/09765086
; Patent No. US20010046498A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Wadih, Arap
; APPLICANT: Bredeesen, Dale E.

; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 773
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-023-282-773

Query Match          57.1%; Score 4; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQPP 7
Db 1 HQPP 4

RESULT 12
US-09-748-960-12
; Sequence 12, Application US/09748960
; Patent No. US20010046496A1
; GENERAL INFORMATION:
; APPLICANT: Brettman, Lee R.
; APPLICANT: Fox, Judith A.
; TITLE OF INVENTION: Method of Administering an Antibody
; FILE REFERENCE: 1855-2007-001
; CURRENT APPLICATION NUMBER: US/09/748,960
; CURRENT FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: US/09/550,082
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)...(5)
; OTHER INFORMATION: CDR1 of the heavy chain of antibodies Act-1 and
; OTHER INFORMATION: LDP-02
US-09-748-960-12

Query Match          42.9%; Score 3; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 WMH 4
Db 3 WMH 5

RESULT 13
US-09-765-086-223
; Sequence 223, Application US/09765086
; Patent No. US20010046498A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Wadih, Arap
; APPLICANT: Bredeesen, Dale E.

; APPLICANT: Ellerby, H. Michael
; TITLE OF INVENTION: Chimeric Prostate-Homing Peptides With
; TITLE OF INVENTION: Pro-Apoptotic Activity
; FILE REFERENCE: P-LJ 3844
; CURRENT APPLICATION NUMBER: US/09/765,086
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 09/489,582
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 235
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 223
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-765-086-223

Query Match          42.9%; Score 3; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQP 6
Db 2 HQP 4

RESULT 14
US-09-933-497B-26
; Sequence 26, Application US/09933497B
; Patent No. US20020098193A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Elizabeth S.
; TITLE OF INVENTION: IMMUNOGLOBIN-LIKE DOMAINS WITH INCREASED HALF LIVES
; FILE REFERENCE: UTSD:483
; CURRENT APPLICATION NUMBER: US/09/933,497B
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 60/013,563
; PRIOR FILING DATE: 1996-03-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptides
US-09-933-497B-26

Query Match          42.9%; Score 3; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MHQ 5
Db 2 MHQ 4

RESULT 15
US-09-770-002-1
; Sequence 1, Application US/09770002
; Patent No. US20020110558A1
; GENERAL INFORMATION:
; APPLICANT: Peter Lloyd Amlot
; APPLICANT: Max H. Schreier
; APPLICANT: Karin Schreier
; TITLE OF INVENTION: Use of CD25 binding molecules in the
; TITLE OF INVENTION: treatment of rheumatoid arthritis or skin diseases.
; FILE REFERENCE: 4-30583A/30967C1
; CURRENT APPLICATION NUMBER: US/09/770,002
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/EP99/05316
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; PRIOR FILING DATE: 1999-07-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 5
; TYPE: PRT
; ORGANISM: mus musculus
; FEATURE:
US-09-770-002-1

Query Match
Best Local Similarity 42.9%; Score 3; DB 10; Length 5;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4
Db 3 WMH 5

RESULT 16
US-09-940-727B-70
; Sequence 70, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 70
; LENGTH: 5
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-70

Query Match
Best Local Similarity 42.9%; Score 3; DB 11; Length 5;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4
Db 3 WMH 5

RESULT 17
US-10-097-065-334
; Sequence 334, Application US/10097065
; Publication No. US2003005236A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Paul A. et al.
; TITLE OF INVENTION: 110 Human Secreted Proteins
; FILE REFERENCE: P2021P1
; CURRENT APPLICATION NUMBER: US/10/097,065
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: PCT/US98/27059
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: 60/070,923
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,007
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,057
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,006
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,369

; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,367
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,169
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,053
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,064
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,054
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,008
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,365
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 334
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-097-065-334

Query Match
Best Local Similarity 42.9%; Score 3; DB 15; Length 6;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQP 6
Db 4 HQP 6

RESULT 18
US-10-227-353-7
; Sequence 7, Application US/10227353
; Publication No. US20030087383A1
; GENERAL INFORMATION:
; APPLICANT: CLARE, JEFFREY J.
; ROMANOS, MICHAEL A.
; TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN YEAST
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Millen, White, Zelano & Branigan, P.C.
; STREET: 2200 Clarendon Blvd., Suite 1400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/227,353
; FILING DATE: 26-Aug-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,269C
; FILING DATE: 02-Jun-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lebovitz, Richard M.
; REGISTRATION NUMBER: 37,067
; REFERENCE/DOCKET NUMBER: Popov-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 243-6333
; TELEFAX: (703) 243-6410
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid

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;  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-10-227-353-7  
  
Query Match 42.9%; Score 3; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 5 QPP 7  
Db 4 QPP 6  
|||  
|||  
  
RESULT 19  
US-10-281-652-13  
; Sequence 13, Application US/10281652  
; Publication No. US20030091606A1  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/10/281,652  
; PRIOR FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US/09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-10-281-652-13  
  
Query Match 42.9%; Score 3; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 5 QPP 7  
Db 3 QPP 5  
|||  
|||  
  
RESULT 20  
US-09-873-676-86  
; Sequence 86, Application US/09873676  
; Patent No. US2002007289A1  
; GENERAL INFORMATION:  
; APPLICANT: MacDonald, Nicholas J.  
; APPLICANT: Sim, Kim L.  
; TITLE OF INVENTION: Angiotensin and Endostatin Binding Proteins and Methods of Use  
; FILE REFERENCE: 05213-0378 (43170-259333)  
; CURRENT APPLICATION NUMBER: US/09/873,676  
; CURRENT FILING DATE: 2001-06-04  
; PRIOR APPLICATION NUMBER: US 60/209,065  
; PRIOR FILING DATE: 2000-06-02  
; PRIOR APPLICATION NUMBER: US 60/289,387  
; PRIOR FILING DATE: 2001-05-08  
; NUMBER OF SEQ ID NOS: 123  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 86  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

;  
; OTHER INFORMATION: Synthetic Peptide  
US-09-873-676-86  
  
Query Match 42.9%; Score 3; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 5 QPP 7  
Db 2 QPP 4  
|||  
|||  
  
RESULT 21  
US-09-821-687-7  
; Sequence 7, Application US/09821687  
; Patent No. US20020106724A1  
; GENERAL INFORMATION:  
; APPLICANT: MIKOSHIBA, KATSUHIKO  
; APPLICANT: MIZUTANI, AKIHIRO  
; TITLE OF INVENTION: RNA-BINDING PROTEIN  
; FILE REFERENCE: 081356/0162  
; CURRENT APPLICATION NUMBER: US/09/821,687  
; CURRENT FILING DATE: 2001-07-03  
; PRIOR APPLICATION NUMBER: JP 2000-299812  
; PRIOR FILING DATE: 2000-09-29  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-821-687-7  
  
Query Match 42.9%; Score 3; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 4 QPP 6  
Db 2 QPP 4  
|||  
|||  
  
RESULT 22  
US-09-954-385-347  
; Sequence 347, Application US/09954385  
; Publication No. US20030100467A1  
; GENERAL INFORMATION:  
; APPLICANT: Ahle, Wolfgang  
; APPLICANT: Baldwin, Toby L.  
; APPLICANT: Van Gastel, Franciscus J.C.  
; APPLICANT: Janssen, Giselle G.  
; APPLICANT: Murray, Christopher J.  
; APPLICANT: Wang, Huaming  
; APPLICANT: Winetzkv, Deborah S.  
; TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide  
; TITLE OF INVENTION: Complexes  
; FILE REFERENCE: GC690  
; CURRENT APPLICATION NUMBER: US/09/954,385  
; CURRENT FILING DATE: 2001-09-12  
; NUMBER OF SEQ ID NOS: 433  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 347  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: binding peptide  
US-09-954-385-347  
  
Query Match 42.9%; Score 3; DB 11; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7  
|||  
Db 2 QPP 4

RESULT 23  
US-10-052-578-176  
; Sequence 176, Application US/10052578  
; Publication No. US20030134787A1  
; GENERAL INFORMATION:  
; APPLICANT: Sloan-Kettering Institute for Cancer Research  
; APPLICANT: Rothman, James E.  
; APPLICANT: Mayhew, Mark  
; APPLICANT: Hoe, Mee H.  
; APPLICANT: Houghton, Alan  
; APPLICANT: Hartl, Ulrich  
; APPLICANT: Querfelli, Ouathek  
; APPLICANT: Moroi, Yoichi  
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES  
; FILE REFERENCE: 11746/46003  
; CURRENT APPLICATION NUMBER: US/10/052,578  
; CURRENT FILING DATE: 2002-01-17  
; PRIOR APPLICATION NUMBER: 08/961,707  
; PRIOR FILING DATE: 1997-10-31  
; NUMBER OF SEQ ID NOS: 321  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 176  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: peptide in ml3 coliphage  
US-10-052-578-176

Query Match 42.9%; Score 3; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05; 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQP 6  
|||  
Db 1 HQP 3

RESULT 24  
US-09-990-832C-10  
; Sequence 10, Application US/09990832C  
; Publication No. US20030149235A1  
; GENERAL INFORMATION:  
; APPLICANT: University Court of the University of Glasgow  
; FILE REFERENCE: PC/MC/JM/P1910US  
; CURRENT APPLICATION NUMBER: US/09/990,832C  
; CURRENT FILING DATE: 2003-01-27  
; NUMBER OF SEQ ID NOS: 127  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Targeting peptide sequence  
US-09-990-832C-10

Query Match 42.9%; Score 3; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05; 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7  
|||  
Db 4 QPP 6

RESULT 25

US-10-053-520-176  
; Sequence 176, Application US/10053520  
; Publication No. US20030166530A1  
; GENERAL INFORMATION:  
; APPLICANT: Sloan-Kettering Institute for Cancer Research  
; APPLICANT: Rothman, James E.  
; APPLICANT: Mayhew, Mark  
; APPLICANT: Hoe, Mee H.  
; APPLICANT: Houghton, Alan  
; APPLICANT: Hartl, Ulrich  
; APPLICANT: Querfelli, Ouathek  
; APPLICANT: Moroi, Yoichi  
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES  
; FILE REFERENCE: 11746/46004  
; CURRENT APPLICATION NUMBER: US/10/053,520  
; CURRENT FILING DATE: 2002-10-01  
; PRIOR APPLICATION NUMBER: 08/961,707  
; PRIOR FILING DATE: 1997-10-31  
; NUMBER OF SEQ ID NOS: 321  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 176  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: peptide in ml3 coliphage  
US-10-053-520-176

Query Match 42.9%; Score 3; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05; 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQP 6  
|||  
Db 1 HQP 3

RESULT 26  
US-10-286-457-92  
; Sequence 92, Application US/10286457  
; Publication No. US20030166004A1  
; GENERAL INFORMATION:  
; APPLICANT: JENO GYURIS et al.  
; TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY  
; FILE REFERENCE: GPCI-POI-178  
; CURRENT APPLICATION NUMBER: US/10/286,457  
; CURRENT FILING DATE: 2002-11-01  
; PRIOR APPLICATION NUMBER: 60/334822  
; PRIOR FILING DATE: 2001-11-01  
; NUMBER OF SEQ ID NOS: 684  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 92  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: artificial sequence isolated from random peptide libraries, b  
; OTHER INFORMATION: ability to selectively bind to endothelial cells  
US-10-286-457-92

Query Match 42.9%; Score 3; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05; 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7  
|||  
Db 1 QPP 3

RESULT 27  
US-10-038-899-4  
; Sequence 4, Application US/10038899  
; Publication No. US20030186406A1

GENERAL INFORMATION:  
APPLICANT: KIKUCHI, KOKICHI  
SAITO, NORIYUKI  
SAHARA, HIROMITSU  
YASOJIMA, TAKAHIRO  
WADA, YOSHIMASA  
SUZUKI, MANABU  
HAMURO, JUNJI  
TITLE OF INVENTION: PEPTIDE CAPABLE OF INDUCING IMMUNE  
RESPONSE TO HUMAN GASTRIC CANCER AND AGENT FOR PREVENTING  
OR TREATING HUMAN GASTRIC CANCER, CONTAINING THE PEPTIDE  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
P.C.  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/038,899  
FILING DATE: 08-Jan-2002  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/723,116  
FILING DATE: 30-SEP-1996  
APPLICATION NUMBER: JP 253491/1995  
FILING DATE: 29-SEP-1995  
APPLICATION NUMBER: JP 217140/1996  
FILING DATE: 19-AUG-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 10-821-0X  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: HUMAN  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-10-038-899-4  
Query Match 42.9%; Score 3; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SWM 3  
Db 2 SWM 4  
RESULT 28  
US-10-220-033-21  
Sequence 21, Application US/10220033  
Publication No. US20030186906A1  
GENERAL INFORMATION:  
APPLICANT: Schlengersiepen, Karl-Hermann  
TITLE OF INVENTION: Mixture comprising an inhibitor or suppressor of a gene  
and a molecule binding to an expression product of that

; TITLE OF INVENTION: gene  
; FILE REFERENCE: P88119US0  
; CURRENT APPLICATION NUMBER: US/10/220,033  
; CURRENT FILING DATE: 2003-03-17  
; PRIOR APPLICATION NUMBER: PCT/EP01/02694  
; PRIOR FILING DATE: 2001-03-10  
; PRIOR APPLICATION NUMBER: EP00105190.3  
; PRIOR FILING DATE: 2000-03-11  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: peptide  
; OTHER INFORMATION: obtained by screening randomly synthesized  
; OTHER INFORMATION: peptides  
; US-10-220-033-21  
Query Match 42.9%; Score 3; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 5 QPP 7  
Db 1 QPP 3  
RESULT 29  
US-10-053-498B-176  
Sequence 176, Application US/10053498B  
Publication No. US20030194409A1  
GENERAL INFORMATION:  
APPLICANT: Sloan-Kettering Institute for Cancer Research  
APPLICANT: Rothman, James E.  
APPLICANT: Mayhew, Mark  
APPLICANT: Hoe, Mee H.  
APPLICANT: Houghton, Alan  
APPLICANT: Hartl, Ulrich  
APPLICANT: Querfelli, Ouathek  
APPLICANT: Moroi, Yoichi  
TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES  
FILE REFERENCE: 11746/46002  
CURRENT APPLICATION NUMBER: US/10/053,498B  
CURRENT FILING DATE: 2002-01-17  
PRIOR APPLICATION NUMBER: 08/961,707  
PRIOR FILING DATE: 1997-10-31  
NUMBER OF SEQ ID NOS: 321  
SOFTWARE: WordPerfect 8.0 for Windows  
SEQ ID NO 176  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: peptide in ml3 coliphage  
US-10-053-498B-176  
Query Match 42.9%; Score 3; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 4 HQP 6  
Db 1 HQP 3  
RESULT 30  
US-10-015-979-84  
Sequence 84, Application US/10015979  
Publication No. US20030036050A1  
GENERAL INFORMATION:  
APPLICANT: Quax, Wilhelmus J.

```
; APPLICANT: Verhaert, Raymond M.D.
; APPLICANT: Beekwilder, Martinus J.
; APPLICANT: Aehle, Wolfgang
; TITLE OF INVENTION: Enzyme Selection
; FILE REFERENCE: 2183-5207US
; CURRENT APPLICATION NUMBER: US/10/015,979
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: PCT/NL00/00399
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/138,443
; PRIOR FILING DATE: 1999-06-10
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 84
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CB4 mutant isolated by selected
; OTHER INFORMATION: tion
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(7)
; OTHER INFORMATION:
US-10-015-979-84

Query Match 42.9%; Score 3; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4
Db 5 WMH 7

RESULT 31
US-10-281-652-1
; Sequence 1, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-1

Query Match 42.9%; Score 3; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
Db 2 QPP 4

RESULT 32
```

```
US-08-344-824-263
; Sequence 263, Application US/08344824
; Publication No. US20030152560A1
; GENERAL INFORMATION:
; APPLICANT: SETTE, Alessandro
; APPLICANT: SIDNEY, John
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
; NUMBER OF SEQUENCES: 399
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Street Tower, 20th
; STREET: Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,824
; FILING DATE: 23-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,634
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-80-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 263:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-344-824-263

Query Match 42.9%; Score 3; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
Db 4 QPP 6

RESULT 33
US-09-765-614B-6
; Sequence 6, Application US/09765614B
; Patent No. US20020102215A1
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to
; TITLE OF INVENTION: diagnostic/therapeutic
; TITLE OF INVENTION: agents
; FILE REFERENCE: REF/Klaveness/054
; CURRENT APPLICATION NUMBER: US/09/765,614B
; CURRENT FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
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```
; OTHER INFORMATION: Sequence:Fibronectin
; OTHER INFORMATION: Peptide
US-09-765-614B-6

Query Match          42.9%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred.No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
Db 2 QPP 4

RESULT 34
US-09-925-715-2
; Sequence 2, Application US/09925715
; Patent No. US20020102217A1
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic
; TITLE OF INVENTION: agents
; FILE REFERENCE: REF/Klaveness/206
; CURRENT APPLICATION NUMBER: US/09/925,715
; CURRENT FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 2
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Fibronectin
; OTHER INFORMATION: peptide
US-09-925-715-2

Query Match          42.9%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred.No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
Db 2 QPP 4

RESULT 35
US-09-791-378-285
; Sequence 285, Application US/09791378
; Patent No. US20020142303A1
; GENERAL INFORMATION:
; APPLICANT: Parekh, Rajesh
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: SCHIZOPHRENIA
; FILE REFERENCE: 9195-061-999
; CURRENT APPLICATION NUMBER: US/09/791,378
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/750,395
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 677
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 285
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-378-285

Query Match          42.9%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred.No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
Db 1 QPP 3
```

```
RESULT 36
US-09-883-825-35
; Sequence 35, Application US/09883825
; Patent No. US20020151024A1
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; Bentley, Kelley
; Charbonneau, Harry
; Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; Bicknell
; STREET: Two First National Plaza, 20 South Clark
; Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/883,825
; FILING DATE: 18-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/123,783
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/297,494
; APPLICATION NUMBER: <Unknown>
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20020151024A1and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-09-883-825-35

Query Match          42.9%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred.No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 WMH 4
Db 4 WMH 6

RESULT 37
US-09-826-290-124
; Sequence 124, Application US/09826290
; Patent No. US20020164668A1
; GENERAL INFORMATION:
; APPLICANT: Durham, L.Kathryn
; APPLICANT: Friedman, David L.
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; APPLICANT: Kimmel, Lida H.
```

```

; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Potter, David M.
; APPLICANT: Rohlf, Christian
; APPLICANT: Silber, B. Michael
; APPLICANT: Stiger, Thomas R.
; APPLICANT: Sunderland, P. Trey
; APPLICANT: Townsend, Robert Reid
; APPLICANT: White, Frost
; APPLICANT: Williams, Stephen A.
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
; TITLE OF INVENTION: Uses Therefor, Including Diagnosis and Treatment of
; TITLE OF INVENTION: Alzheimer's Disease
; FILE REFERENCE: 2572-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/826,290
; PRIOR FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/194,504
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/253,647
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 492
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124
; LENGTH: 8
; TYPE: PRT
; ORGANISM: homo sapien
US-09-826-290-124

Query Match          42.9%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
Db 2 QPP 4

RESULT 38
US-09-999-724-58
; Sequence 58, Application US/09999724
; Publication No. US20030022355A1
; GENERAL INFORMATION:
; APPLICANT: WICKHAM, THOMAS J.
; APPLICANT: KOVESDI, IMRE
; APPLICANT: BROUGH, DOUGLAS E.
; TITLE OF INVENTION: VECTORS AND METHODS FOR GENE TRANSFER
; FILE REFERENCE: 212960
; CURRENT APPLICATION NUMBER: US/09/999,724
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 09/101,751
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: WO 96US19150
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 08/700,846
; PRIOR FILING DATE: 1996-08-21
; PRIOR APPLICATION NUMBER: US 08/701,124
; PRIOR FILING DATE: 1996-08-21
; PRIOR APPLICATION NUMBER: US 08/563,368
; PRIOR FILING DATE: 1995-11-28
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 58
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-999-724-58

Query Match          42.9%; Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
```

```

Db 2 QPP 4

RESULT 39
US-10-365-908-98
; Sequence 98, Application US/10365908
; Publication No. US20030170268A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/365,908
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 98
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-365-908-98

Query Match          42.9%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
Db 2 QPP 4

RESULT 40
US-09-829-382-11
; Sequence 11, Application US/09829382
; Publication No. US20030175293A1
; GENERAL INFORMATION:
; APPLICANT: Masure, H. Robert
; APPLICANT: Rosenow, Carsten I.
; APPLICANT: Tuomanen, Theresa M.
; APPLICANT: Wizemann, Elaine
; TITLE OF INVENTION: CHOLINE BINDING PROTEINS FOR
; TITLE OF INVENTION: ANTI-PNEUMOCOCCAL VACCINES
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/829,382
; FILING DATE: 09-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/847,065
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
```

```
;
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-158 ..
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-829-382-11

Query Match 42.9%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
Db 2 QPP 4

RESULT 41
US-10-038-899-3
; Sequence 3, Application US/10038899
; Publication No. US20030186406A1
; GENERAL INFORMATION:
; APPLICANT: KIKUCHI, KOKICHI
; SAITO, NORIYUKI
; SAHARA, HIROMITSU
; YASOJIMA, TAKAHIRO
; WADA, YOSHIMASA
; SUZUKI, MANABU
; HAMURO, JUNJI
; TITLE OF INVENTION: PEPTIDE CAPABLE OF INDUCING IMMUNE
; RESPONSE TO HUMAN GASTRIC CANCER AND AGENT FOR PREVENTING
; OR TREATING HUMAN GASTRIC CANCER, CONTAINING THE PEPTIDE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/038,899
; FILING DATE: 08-Jan-2002
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/723,116
; FILING DATE: 30-SEP-1996
; APPLICATION NUMBER: JP 253491/1995
; FILING DATE: 29-SEP-1995
; APPLICATION NUMBER: JP 217140/1996
; FILING DATE: 19-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-821-0X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
```

```
;
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: HUMAN
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-038-899-3

Query Match 42.9%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SWM 3
Db 2 SWM 4

RESULT 42
US-10-357-929A-21
; Sequence 21, Application US/10357929A
; Publication No. US20030216322A1
; GENERAL INFORMATION:
; APPLICANT: Tatiana I. Samoylova
; APPLICANT: Valery A. Petrenko
; APPLICANT: Nancy R. Cox
; APPLICANT: Nancy E. Morrison
; APPLICANT: Henry J. Baker
; APPLICANT: Ludmila P. Globa
; TITLE OF INVENTION: Peptides for Recognition and Targeting
; FILE OF INVENTION: of Glial Cell Tumors
; FILE REFERENCE: 35721/259047
; CURRENT APPLICATION NUMBER: US/10/357,929A
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 10/357,929
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 60/354,188
; PRIOR FILING DATE: 2002-02-04
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-357-929A-21

Query Match 42.9%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQP 6
Db 6 HQP 8

RESULT 43
US-10-158-596A-105
; Sequence 105, Application US/10158596A
; Publication No. US20030068900A1
; GENERAL INFORMATION:
; APPLICANT: Belcher, Angela
; APPLICANT: Flynn, Christine
; TITLE OF INVENTION: BIOLOGICAL CONTROL OF NANOPARTICLE NUCLEATION, SHAPE AND CRYST
; FILE REFERENCE: 119927-1052
; CURRENT APPLICATION NUMBER: US/10/158,596A
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/296,013
; PRIOR FILING DATE: 2001-06-05
```

; NUMBER OF SEQ ID NOS: 110  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 105  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: peptide retrieved from phage biopanning  
US-10-158-596A-105

Query Match 42.9%; Score 3; DB 15; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHQ 5  
|||  
Db 4 MHQ 6

## RESULT 44

US-10-017-193-4  
; Sequence 4, Application US/10017193  
; Publication No. US20030113478A1  
; GENERAL INFORMATION:  
; APPLICANT: Dang, Mai Huong  
; APPLICANT: Chiu, Phillip  
; TITLE OF INVENTION: Surface Coating Method and Coated Device  
; FILE REFERENCE: 52200-8010  
; CURRENT APPLICATION NUMBER: US/10/017,193  
; CURRENT FILING DATE: 2001-12-12  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: attachment peptide from fibronectin  
US-10-017-193-4

Query Match 42.9%; Score 3; DB 15; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7  
|||  
Db 2 QPP 4

## RESULT 45

US-10-254-446A-232  
; Sequence 232, Application US/10254446A  
; Publication No. US20030113714A1  
; GENERAL INFORMATION:  
; APPLICANT: Belcher, Angela M  
; APPLICANT: Smalley, Richard E.  
; APPLICANT: Lee, Seung-Wuk  
; TITLE OF INVENTION: BIOLOGICAL CONTROL OF NANOPARTICLES  
; FILE REFERENCE: 11927-1066  
; CURRENT APPLICATION NUMBER: US/10/254,446A  
; CURRENT FILING DATE: 2003-02-19  
; PRIOR APPLICATION NUMBER: 60/325,664  
; PRIOR FILING DATE: 2001-09-28  
; NUMBER OF SEQ ID NOS: 245  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 232  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: peptide with peptide binding sequence retrieved from phage biopanning  
US-10-254-446A-232

Query Match 42.9%; Score 3; DB 15; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHQ 5  
|||  
Db 4 MHQ 6

## RESULT 46

US-09-748-960-11  
; Sequence 11, Application US/09748960  
; Patent No. US20010046496A1  
; GENERAL INFORMATION:  
; APPLICANT: Fox, Judith A.  
; APPLICANT: Allison, David Edward  
; TITLE OF INVENTION: Method of Administering an Antibody  
; FILE REFERENCE: 1855.2007-001  
; CURRENT APPLICATION NUMBER: US/09/748,960  
; CURRENT FILING DATE: 2000-12-27  
; PRIOR APPLICATION NUMBER: US 09/550,082  
; PRIOR FILING DATE: 2000-04-14  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (1)...(9)  
; OTHER INFORMATION: CDR3 of the light chain of antibodies Act-1 and  
; OTHER INFORMATION: LDP-02  
US-09-748-960-11

Query Match 42.9%; Score 3; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HOP 6  
|||  
Db 5 HOP 7

## RESULT 47

US-09-780-053-165  
; Sequence 165, Application US/09780053  
; Patent No. US20020102640A1  
; GENERAL INFORMATION:  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Mary Faris  
; APPLICANT: Elana Levin  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN  
; FILE REFERENCE: 129 5USU1  
; CURRENT APPLICATION NUMBER: US/09/780,053  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/181,261  
; PRIOR FILING DATE: 2000-02-09  
; NUMBER OF SEQ ID NOS: 716  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 165  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-09-780-053-165



Query Match 42.9%; Score 3; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7  
|||  
Db 5 QPP 7

RESULT 48  
US-09-780-053-456  
; Sequence 456, Application US/09780053  
; Patent No. US20020102640A1  
; GENERAL INFORMATION:  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Mary Paris  
; APPLICANT: Elana Levin  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN  
; FILE REFERENCE: 129.5USU1  
; CURRENT APPLICATION NUMBER: US/09/780,053  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR FILING DATE: 2000-02-09  
; NUMBER OF SEQ ID NOS: 716  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 456  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-09-780-053-456

Query Match 42.9%; Score 3; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7  
|||  
Db 4 QPP 6

RESULT 49  
US-09-780-053-517  
; Sequence 517, Application US/09780053  
; Patent No. US20020102640A1  
; GENERAL INFORMATION:  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Mary Paris  
; APPLICANT: Elana Levin  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN  
; FILE REFERENCE: 129.5USU1  
; CURRENT APPLICATION NUMBER: US/09/780,053  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR FILING DATE: 2000-02-09  
; NUMBER OF SEQ ID NOS: 716  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 517  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-09-780-053-517

Query Match 42.9%; Score 3; DB 10; Length 9;

Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7  
|||  
Db 4 QPP 6

RESULT 50  
US-09-780-053-620  
; Sequence 620, Application US/09780053  
; Patent No. US20020102640A1  
; GENERAL INFORMATION:  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Mary Paris  
; APPLICANT: Elana Levin  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN  
; FILE REFERENCE: 129.5USU1  
; CURRENT APPLICATION NUMBER: US/09/780,053  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR FILING DATE: 2000-02-09  
; NUMBER OF SEQ ID NOS: 716  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 620  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-09-780-053-620

Query Match 42.9%; Score 3; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7  
|||  
Db 4 QPP 6

RESULT 51  
US-09-862-179A-11  
; Sequence 11, Application US/09862179A  
; Patent No. US20020147306A1  
; GENERAL INFORMATION:  
; APPLICANT: Pawson, Anthony  
; TITLE OF INVENTION: PEPTIDES THAT MODULATE THE INTERACTION OF B CLASS EPHRINS  
; FILE REFERENCE: MTSI-P01-009  
; CURRENT APPLICATION NUMBER: US/09/862,179A  
; CURRENT FILING DATE: 2001-05-21  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 11  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: PDZ inhibitory peptide  
US-09-862-179A-11

Query Match 42.9%; Score 3; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQP 6  
|||  
Db 2 HQP 4

```
RESULT 52
US-09-862-179A-18
; Sequence 18, Application US/09862179A
; Patent No. US20020147306A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Danny
; APPLICANT: Pawson, Anthony
; TITLE OF INVENTION: PEPTIDES THAT MODULATE THE INTERACTION OF B CLASS EPHRINS
; TITLE OF INVENTION: AND PDZ DOMAINS
; FILE REFERENCE: MTSI-P01-009
; CURRENT APPLICATION NUMBER: US/09/862,179A
; CURRENT FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Negative control peptide
US-09-862-179A-18

Query Match          42.9%; Score 3; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 HOP 6
Db      2 HOP 4

RESULT 53
US-09-017-743C-69
; Sequence 69, Application US/09017743C
; Patent No. US20020177694A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
;           Sidnev, John
;           Southwood, Scott
; TITLE OF INVENTION: HLA Binding Peptides and Their
;           Uses
; NUMBER OF SEQUENCES: 146
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/017,743C
; FILING DATE: 03-Feb-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/590,298
; FILING DATE: 23-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Parent, Annette S.
; REGISTRATION NUMBER: 42,058
; REFERENCE/DOCKET NUMBER: 018623-008050US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 69:

US-09-017-743C-69

Query Match          42.9%; Score 3; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 QPP 7
Db      3 QPP 5

RESULT 54
US-09-938-864-108
; Sequence 108, Application US/09938864
; Publication No. US20030072767A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
;           McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C5
; CURRENT APPLICATION NUMBER: US/09/938,864
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 108
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-938-864-108

Query Match          42.9%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 MHQ 5
Db      4 MHQ 6

RESULT 55
US-09-938-864-143
; Sequence 143, Application US/09938864
; Publication No. US20030072767A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
;           McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C5
; CURRENT APPLICATION NUMBER: US/09/938,864
```

```
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 143
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-938-864-143
```

```
Query Match 42.9%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 3 MHQ 5
Db 1 MHQ 3
```

#### RESULT 56

```
US-09-938-864-148
; Sequence 148, Application US/09938864
; Publication No. US20030072767A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C5
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 148
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-938-864-148
```

```
Query Match 42.9%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 3 MHQ 5
Db 2 MHQ 4
```

#### RESULT 57

```
US-09-938-864-180
; Sequence 180, Application US/09938864
; Publication No. US20030072767A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C5
```

```
; CURRENT APPLICATION NUMBER: US/09/938,864
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 180
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-938-864-180
```

```
Query Match 42.9%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 3 MHQ 5
Db 5 MHQ 7
```

#### RESULT 58

```
US-09-938-864-243
; Sequence 243, Application US/09938864
; Publication No. US20030072767A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C5
; CURRENT APPLICATION NUMBER: US/09/938,864
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 243
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-938-864-243
```

```
Query Match 42.9%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 3 MHQ 5
Db 6 MHQ 8
```

#### RESULT 59

```
US-09-938-864-281
; Sequence 281, Application US/09938864
; Publication No. US20030072767A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C5
```

```
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C5
```

```
; FILE REFERENCE: 210121.465C5
; CURRENT APPLICATION NUMBER: US/09/938,864
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 281
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-938-864-281

Query Match          42.9%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 MHQ 5
      |||
Db      1 MHQ 3

RESULT 60
US-09-791-477-108
; Sequence 108, Application US/09791477
; Publication No. US20030082194A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
; TITLE OF INVENTION: AND THERAPY OF MALIGNANT MESOTHELIOMA
; FILE REFERENCE: 2077.000200
; CURRENT APPLICATION NUMBER: US/09/791,477
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/184,070
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 108
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-477-108

Query Match          42.9%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 MHQ 5
      |||
Db      4 MHQ 6

RESULT 61
US-09-791-477-143
; Sequence 143, Application US/09791477
; Publication No. US20030082194A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
; TITLE OF INVENTION: AND THERAPY OF MALIGNANT MESOTHELIOMA
; FILE REFERENCE: 2077.000200
; CURRENT APPLICATION NUMBER: US/09/791,477
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/184,070
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 143
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-477-143

Query Match          42.9%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 MHQ 5
      |||
Db      4 MHQ 6

RESULT 62
US-09-791-477-148
; Sequence 148, Application US/09791477
; Publication No. US20030082194A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
; TITLE OF INVENTION: AND THERAPY OF MALIGNANT MESOTHELIOMA
; FILE REFERENCE: 2077.000200
; CURRENT APPLICATION NUMBER: US/09/791,477
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/184,070
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 148
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-477-148

Query Match          42.9%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 MHQ 5
      |||
Db      2 MHQ 4

RESULT 63
US-09-791-477-180
; Sequence 180, Application US/09791477
; Publication No. US20030082194A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
; TITLE OF INVENTION: AND THERAPY OF MALIGNANT MESOTHELIOMA
; FILE REFERENCE: 2077.000200
; CURRENT APPLICATION NUMBER: US/09/791,477
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/184,070
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 180
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-477-180

Query Match          42.9%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 MHQ 5
      |||
Db      5 MHQ 7

RESULT 64
US-09-791-477-243
```

```

; Sequence 243, Application US/09791477
; Publication No. US20030082194A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
; TITLE OF INVENTION: AND THERAPY OF MALIGNANT MESOTHELIOMA
; FILE REFERENCE: 2077.000200
; CURRENT APPLICATION NUMBER: US/09/791,477
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/184,070
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 243
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-477-243

```

```

Query Match 42.9%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 3 MHQ 5
Db 6 MHQ 8

```

```

RESULT 65
US-09-791-477-281
; Sequence 281, Application US/09791477
; Publication No. US20030082194A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
; TITLE OF INVENTION: AND THERAPY OF MALIGNANT MESOTHELIOMA
; FILE REFERENCE: 2077.000200
; CURRENT APPLICATION NUMBER: US/09/791,477
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/184,070
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 281
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-791-477-281

```

```

Query Match 42.9%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 3 MHQ 5
Db 1 MHQ 3

```

```

RESULT 66
US-09-785-019-108
; Sequence 108, Application US/09785019
; Publication No. US20030082196A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1

```

```

; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C4
; CURRENT APPLICATION NUMBER: US/09/785,019
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 108
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-785-019-108

```

```

Query Match 42.9%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 3 MHQ 5
Db 4 MHQ 6

```

```

RESULT 67
US-09-785-019-143
; Sequence 143, Application US/09785019
; Publication No. US20030082196A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C4
; CURRENT APPLICATION NUMBER: US/09/785,019
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 143
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-785-019-143

```

```

Query Match 42.9%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 3 MHQ 5
Db 1 MHQ 3

```

```

RESULT 68
US-09-785-019-148
; Sequence 148, Application US/09785019
; Publication No. US20030082196A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C4
; CURRENT APPLICATION NUMBER: US/09/785,019
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 376

```

```
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 148
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-785-019-148

Query Match          42.9%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 MHQ 5
Db      2 MHQ 4

RESULT 69
US-09-785-019-180
; Sequence 180, Application US/09785019
; Publication No. US20030082196A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Sleath, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C4
; CURRENT APPLICATION NUMBER: US/09/785,019
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 180
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-785-019-180

Query Match          42.9%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 MHQ 5
Db      5 MHQ 7

RESULT 70
US-09-785-019-243
; Sequence 243, Application US/09785019
; Publication No. US20030082196A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Sleath, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C4
; CURRENT APPLICATION NUMBER: US/09/785,019
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 243
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien

US-09-785-019-243
; Sequence 66, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: PARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AVA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatP2E11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

```
;
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-66

Query Match      42.9%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 QPP 7
      |||
Db      3 QPP 5

RESULT 73
US-09-932-165-669
; Sequence 669, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatrF2e11 USEFUL IN TREATMENT AND
; FILE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR FILING DATE: 2000-08-17
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 669
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-669

Query Match      42.9%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 QPP 7
      |||
Db      3 QPP 5

RESULT 74
US-09-932-165-1013
; Sequence 1013, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatrF2e11 USEFUL IN TREATMENT AND
; FILE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
```

```
;
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1013
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-1013
```

```
Query Match      42.9%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      5 QPP 7
      |||
Db      5 QPP 7
```

```
RESULT 75
US-09-932-165-1212
; Sequence 1212, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatrF2e11 USEFUL IN TREATMENT AND
; FILE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1212
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-1212
```

```
Query Match      42.9%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      5 QPP 7
      |||
Db      1 QPP 3
```

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Search completed: November 25, 2003, 20:37:01
Job time : 12.2326 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:16:22 ; Search time 5.65698 Seconds  
(without alignments)  
52.356 Million cell updates/sec

Title: US-09-641-801-24

Perfect score: 7

Sequence: 1 SWHQPP 7

Scoring table: OIIGO

Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.ppep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	4	US-09-641-803-24
2	6	85.7	19	3	US-08-870-529-3
3	6	85.7	19	4	US-09-544-794-3
4	5	71.4	15	4	US-09-641-803-34
5	4	57.1	11	4	US-09-149-476-689
6	4	57.1	20	4	US-09-205-258-773
7	3	42.9	4	3	US-08-810-720-12
8	3	42.9	5	1	US-08-014-979-52
9	3	42.9	5	1	US-07-946-421-4
10	3	42.9	5	1	US-08-318-970B-1
11	3	42.9	5	2	US-08-672-345C-70
12	3	42.9	5	3	US-08-774-354B-2
13	3	42.9	5	3	US-09-258-754-278
14	3	42.9	5	3	US-09-042-107-278
15	3	42.9	5	3	US-08-811-463-26
16	3	42.9	5	3	US-08-214-095D-70
17	3	42.9	5	4	US-09-406-532-5
18	3	42.9	5	4	US-08-479-089A-7
19	3	42.9	5	4	US-09-082-358B-31
20	3	42.9	5	4	US-07-669-545B-7
21	3	42.9	5	6	5217869-43
22	3	42.9	5	6	5464756-28
23	3	42.9	6	1	US-08-253-854-40
24	3	42.9	6	1	US-08-127-499A-22
25	3	42.9	6	1	US-08-482-847-22
26	3	42.9	6	1	US-08-237-716-7
27	3	42.9	6	1	US-08-704-170-89

28	3	42.9	6	3	US-08-460-269C-7	Sequence 7, Appli
29	3	42.9	6	4	US-09-641-803-13	Sequence 13, Appli
30	3	42.9	6	5	PCT-US94-03631-89	Sequence 89, Appli
31	3	42.9	7	1	US-08-169-524-3	Sequence 3, Appli
32	3	42.9	7	1	US-08-081-539-113	Sequence 113, App
33	3	42.9	7	1	US-08-127-499A-3	Sequence 3, Appli
34	3	42.9	7	1	US-08-127-499A-7	Sequence 7, Appli
35	3	42.9	7	1	US-08-127-499A-10	Sequence 10, Appli
36	3	42.9	7	1	US-08-127-499A-25	Sequence 25, Appli
37	3	42.9	7	1	US-08-466-647-113	Sequence 113, App
38	3	42.9	7	1	US-08-482-847-3	Sequence 3, Appli
39	3	42.9	7	1	US-08-482-847-7	Sequence 7, Appli
40	3	42.9	7	1	US-08-482-847-10	Sequence 10, Appli
41	3	42.9	7	1	US-08-482-847-25	Sequence 25, Appli
42	3	42.9	7	2	US-08-723-116-4	Sequence 4, Appli
43	3	42.9	7	3	US-08-774-354B-4	Sequence 4, Appli
44	3	42.9	7	4	US-09-103-808-4	Sequence 4, Appli
45	3	42.9	7	4	US-09-641-803-1	Sequence 1, Appli
46	3	42.9	8	1	US-07-872-644-35	Sequence 35, Appli
47	3	42.9	8	1	US-08-291-349A-5	Sequence 5, Appli
48	3	42.9	8	1	US-08-297-494-35	Sequence 35, Appli
49	3	42.9	8	1	US-07-990-296-3	Sequence 3, Appli
50	3	42.9	8	1	US-08-297-510-35	Sequence 35, Appli
51	3	42.9	8	1	US-08-479-532-35	Sequence 35, Appli
52	3	42.9	8	1	US-08-455-526-35	Sequence 35, Appli
53	3	42.9	8	1	US-08-455-525-35	Sequence 35, Appli
54	3	42.9	8	2	US-08-723-116-3	Sequence 3, Appli
55	3	42.9	8	2	US-08-480-133A-3	Sequence 3, Appli
56	3	42.9	8	2	US-08-699-965-2	Sequence 2, Appli
57	3	42.9	8	2	US-08-435-149-6	Sequence 6, Appli
58	3	42.9	8	2	US-09-025-706-10	Sequence 10, Appli
59	3	42.9	8	3	US-08-394-748A-13	Sequence 13, Appli
60	3	42.9	8	3	US-09-139-491-35	Sequence 35, Appli
61	3	42.9	8	3	US-08-774-354B-5	Sequence 5, Appli
62	3	42.9	8	3	US-08-916-913A-3	Sequence 3, Appli
63	3	42.9	8	3	US-09-025-622-10	Sequence 10, Appli
64	3	42.9	8	3	US-08-847-665-11	Sequence 11, Appli
65	3	42.9	8	3	US-08-960-054A-6	Sequence 6, Appli
66	3	42.9	8	3	US-08-958-993A-6	Sequence 6, Appli
67	3	42.9	8	4	US-08-959-206A-2	Sequence 2, Appli
68	3	42.9	8	4	US-09-103-808-3	Sequence 3, Appli
69	3	42.9	8	4	US-09-101-751A-58	Sequence 58, Appli
70	3	42.9	8	4	US-09-591-564-3	Sequence 3, Appli
71	3	42.9	8	5	PCT-US92-03222-35	Sequence 35, Appli
72	3	42.9	8	5	PCT-US93-11781-3	Sequence 3, Appli
73	3	42.9	8	5	PCT-US95-02478-13	Sequence 13, Appli
74	3	42.9	9	1	US-08-139-054-7	Sequence 7, Appli
75	3	42.9	9	2	US-08-723-116-2	Sequence 2, Appli
76	3	42.9	9	2	US-08-370-509-10	Sequence 10, Appli
77	3	42.9	9	2	US-08-765-179B-17	Sequence 17, Appli
78	3	42.9	9	3	US-08-159-339A-250	Sequence 250, App
79	3	42.9	9	3	US-08-664-962B-15	Sequence 15, Appli
80	3	42.9	9	3	US-09-311-743-15	Sequence 15, Appli
81	3	42.9	9	4	US-09-103-808-2	Sequence 2, Appli
82	3	42.9	9	4	US-09-163-748C-11	Sequence 11, Appli
83	3	42.9	9	4	US-09-341-982-26	Sequence 26, Appli
84	3	42.9	10	1	US-08-190-788A-31	Sequence 31, Appli
85	3	42.9	10	1	US-08-383-474B-36	Sequence 36, Appli
86	3	42.9	10	1	US-08-465-391A-31	Sequence 31, Appli
87	3	42.9	10	2	US-08-472-659-9	Sequence 9, Appli
88	3	42.9	10	2	US-08-723-116-1	Sequence 1, Appli
89	3	42.9	10	2	US-08-464-538B-31	Sequence 31, Appli
90	3	42.9	10	2	US-08-474-661-9	Sequence 9, Appli
91	3	42.9	10	2	US-08-556-597-131	Sequence 131, App
92	3	42.9	10	2	US-08-556-597-159	Sequence 159, App
93	3	42.9	10	2	US-08-463-076B-75	Sequence 75, Appli
94	3	42.9	10	2	US-08-611-977-9	Sequence 9, Appli
95	3	42.9	10	3	US-08-348-518C-26	Sequence 26, Appli
96	3	42.9	10	3	US-08-476-509B-26	Sequence 26, Appli
97	3	42.9	10	3	US-08-836-075A-205	Sequence 205, App
98	3	42.9	10	4	US-09-103-808-1	Sequence 1, Appli
99	3	42.9	10	4	US-09-348-265-3	Sequence 3, Appli
100	3	42.9	10	4	US-09-341-982-35	Sequence 35, Appli



## ALIGNMENTS

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RESULT 1
US-09-641-803-24
; Sequence 24, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-24

Query Match 100.0%; Score 7; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSMHQPP 7
Db 1 SSMHQPP 7

RESULT 2
US-08-870-529-3
; Sequence 3, Application US/08870529
; Patent No. 6080557
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Virca, G. Duke
; APPLICANT: Bird, Timothy A.
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: IL-1/TNF-(-ACTIVATED KINASE (ITAK),
; TITLE OF INVENTION: AND METHODS OF MAKING AND USING THE SAME
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/870,529
; FILING DATE: 06-JUN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McWaters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 480052.418
; TELECOMMUNICATION INFORMATION:

US-09-641-803-24

; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-870-529-3

Query Match 85.7%; Score 6; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.045; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSMHQPP 6
Db 12 SSMHQPP 17

RESULT 3
US-09-544-794-3
; Sequence 3, Application US/09544794
; Patent No. 6541232
; GENERAL INFORMATION:
; APPLICANT: Sims, John E.
; APPLICANT: Virca, G. Duke
; APPLICANT: Bird, Timothy A.
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: Polypeptides Having Kinase Activity
; FILE REFERENCE: 2005-B
; CURRENT APPLICATION NUMBER: US/09/544,794
; CURRENT FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 08/870,529
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/059,979
; PRIOR FILING DATE: 1996-06-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide substrate
US-09-544-794-3

Query Match 85.7%; Score 6; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.045; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSMHQPP 6
Db 12 SSMHQPP 17

RESULT 4
US-09-641-803-34
; Sequence 34, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 34
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-34

Query Match      71.4%; Score 5; DB 4; Length 15;
Best Local Similarity 100.0%; Pred.No. 0.81;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 MHQPP 7
Db      1 MHQPP 5

RESULT 5
US-09-149-476-689
; Sequence 689, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
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; EARLIER APPLICATION NUMBER: 60/038,621
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; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
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; EARLIER APPLICATION NUMBER: 60/040,336
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; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
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; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
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; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
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; EARLIER APPLICATION NUMBER: 60/056,662
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; EARLIER FILING DATE: 1997-08-22
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; EARLIER APPLICATION NUMBER: 60/056,637
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EARLIER APPLICATION NUMBER: 60/057,761  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/047,595  
EARLIER FILING DATE: 1997-05-23  
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EARLIER FILING DATE: 1997-05-23  
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EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,586  
EARLIER FILING DATE: 1997-05-23  
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EARLIER FILING DATE: 1997-05-23  
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EARLIER FILING DATE: 1997-05-23  
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EARLIER APPLICATION NUMBER: 60/047,614  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,578  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,576  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/047,501  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,670  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/056,632  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,664  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,876  
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EARLIER APPLICATION NUMBER: 60/056,881  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,909  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,875  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,862  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,887  
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EARLIER APPLICATION NUMBER: 60/056,908  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/057,650  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/056,884  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057,669  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/049,610  
EARLIER FILING DATE: 1997-06-13  
EARLIER APPLICATION NUMBER: 60/061,060

EARLIER FILING DATE: 1997-10-02  
Query Match 57.1%; Score 4; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 HOPP 7  
DB 1 HOPP 4  
RESULT 6  
US-09-205-258-773  
Sequence 773, Application US/09205258  
Patent No. 6525174  
GENERAL INFORMATION:  
APPLICANT: Young et al.  
TITLE OF INVENTION: 207 Human Secreted Proteins  
FILE REFERENCE: PZ007P1  
CURRENT APPLICATION NUMBER: US/09/205,258  
CURRENT FILING DATE: 1998-12-04  
EARLIER APPLICATION NUMBER: PCT/US98/11422  
EARLIER FILING DATE: 1998-06-04  
EARLIER APPLICATION NUMBER: 60/048,885  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,375  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,881  
EARLIER FILING DATE: 1997-06-06  
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EARLIER APPLICATION NUMBER: 60/048,895  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,884  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,894  
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EARLIER APPLICATION NUMBER: 60/048,893  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,900  
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EARLIER APPLICATION NUMBER: 60/048,901  
EARLIER FILING DATE: 1997-06-06  
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EARLIER APPLICATION NUMBER: 60/048,915  
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EARLIER APPLICATION NUMBER: 60/049,019  
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EARLIER APPLICATION NUMBER: 60/048,970  
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EARLIER FILING DATE: 1997-06-06  
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EARLIER APPLICATION NUMBER: 60/048,875  
EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/049,374  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,917  
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EARLIER APPLICATION NUMBER: 60/048,949  
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EARLIER APPLICATION NUMBER: 60/048,974  
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EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,897  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,898  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,962  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,963  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,877  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,878  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/070,923  
EARLIER FILING DATE: 1997-12-18  
EARLIER APPLICATION NUMBER: 60/092,921  
EARLIER FILING DATE: 1998-07-15  
EARLIER APPLICATION NUMBER: 60/094,657  
EARLIER FILING DATE: 1998-07-30  
NUMBER OF SEQ ID NOS: 1227  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 773  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-205-258-773

Query Match 57.1%; Score 4; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HOPP 7  
Db 1 HOPP 4

RESULT 7  
US-08-810-720-12  
Sequence 12, Application US/08810720  
Patent No. 6037327  
GENERAL INFORMATION:  
APPLICANT: Barton, Kenneth A.  
APPLICANT: Umbeck, Paul F.  
TITLE OF INVENTION: INSECTICIDAL COTTON PLANTS (AS AMENDED)  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Nicholas J. Seay  
STREET: One South Pinckney Street  
CITY: Madison  
STATE: WI  
COUNTRY: US  
ZIP: 53701-2113  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/810,720  
FILING DATE: 03-MAR-1997  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Seay, Nicholas J.  
REGISTRATION NUMBER: 27,386

REFERENCE/DOCKET NUMBER: 670513.90163  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 608/251-5000  
TELEFAX: 608/251-9166  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-810-720-12

Query Match 42.9%; Score 3; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7  
Db 2 QPP 4

RESULT 8  
US-08-014-979-52  
Sequence 52, Application US/08014979  
Patent No. 5510240  
GENERAL INFORMATION:  
APPLICANT: Lam, Kit S. et al.  
TITLE OF INVENTION: Random Bio-Oligomer Library, A Method of  
NUMBER OF SEQUENCES: 121  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/014,979  
FILING DATE: 19930208  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mirock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 7156-041  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212 790-9090  
TELEFAX: 212 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-014-979-52

Query Match 42.9%; Score 3; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 WMH 4  
Db 1 WMH 3

```
RESULT 9
US-07-946-421-4
; Sequence 4, Application US/07946421
; Patent No. 555864
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Kettlborough, Catherine A.
; APPLICANT: Saldanha, Jose
; TITLE OF INVENTION: Humanized and Chimeric Monoclonal
; TITLE OF INVENTION: Antibodies
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
; STREET: 2200 Clarendon Boulevard, Suite 1400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/946,421
; FILING DATE: 06-NOV-1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP92/00480
; FILING DATE: 04-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 911933892
; FILING DATE: 06-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hamlet-King, Diana
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: Merck 1430
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; TELEX: 64191
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-07-946-421-4

Query Match 42.9%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4
Db 3 WMH 5

RESULT 10
US-08-318-970B-1
; Sequence 1, Application US/08318970B
; Patent No. 5589573
; GENERAL INFORMATION:
; APPLICANT: Hideaki HAGIWARA, et al.
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF ANTI-IDIOYPIC
; TITLE OF INVENTION: ANTIBODIES AGAINST ANTI-CANCER HUMAN MONOCLONAL ANTIBODY
; TITLE OF INVENTION: AND DNA BASE SEQUENCES ENCODING THOSE SEQUENCES
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Office of Sherman and Shalloway
; STREET: 413 N. Washington Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA

Query Match 42.9%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4
Db 3 WMH 5

RESULT 11
US-08-672-345C-70
; Sequence 70, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
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; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: Dell System 210; Intel 80 285 Microprocessor
; OPERATING SYSTEM: MS DOS 3.3
; SOFTWARE: Word Perfect, Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,970B
; FILING DATE: October 6, 1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Richard A. Steinberg
; REGISTRATION NUMBER: 26,588
; REFERENCE/DOCKET NUMBER: S-2371
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 549-2282
; TELEFAX: (703) 836-0106
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: H-CDR1-1
; OTHER INFORMATION: hypervariable region
US-08-318-970B-1

Query Match 42.9%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4
Db 3 WMH 5

RESULT 11
US-08-672-345C-70
; Sequence 70, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
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TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-672-345C-70

Query Match 42.9%; Score 3; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0;

Qy 2 WMH 4  
Db 3 WMH 5

## RESULT 12

US-08-774-354B-2  
Sequence 2, Application US/08774354B  
Patent No. 6063427  
GENERAL INFORMATION:  
APPLICANT: Michiko WATANABE  
TITLE OF INVENTION: METHOD FOR PRODUCING A  
TITLE OF INVENTION: HYPOALLERGENIC WHEAT FLOUR  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 2033 K Street, N.W., Suite 800  
CITY: Washington, D.C.  
STATE:  
COUNTRY: U.S.A.  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1+  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/774,354B  
FILING DATE: December 27, 1996  
CLASSIFICATION: 426  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Matthew Jacob  
REGISTRATION NUMBER: 25,154  
REFERENCE/DOCKET NUMBER: 653-96F029US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 721-8200  
TELEFAX: (202) 721-8250  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
IMMEDIATE SOURCE:  
POSITION IN GENOME:  
FEATURE:  
PUBLICATION INFORMATION:

Query Match 42.9%; Score 3; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0;

Qy 5 QPP 7  
Db 3 QPP 5

## RESULT 13

US-09-258-754-278  
Sequence 278, Application US/09258754  
Patent No. 6174687  
GENERAL INFORMATION:  
APPLICANT: Ruoslahti, Erkki  
APPLICANT: Pasqualini, Renata  
APPLICANT: Rajotte, Daniel  
TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using  
TITLE OF INVENTION: Membrane Dipeptidase  
FILE REFERENCE: P-LJ 3443  
CURRENT APPLICATION NUMBER: US/09/258,754  
CURRENT FILING DATE: 1998-02-26  
EARLIER APPLICATION NUMBER: 09/042,107  
EARLIER FILING DATE: 1998-03-13  
NUMBER OF SEQ ID NOS: 452  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 278  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-258-754-278

Query Match 42.9%; Score 3; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQP 6  
Db 2 HQP 4

## RESULT 14

US-09-042-107-278  
Sequence 278, Application US/09042107  
Patent No. 6232287  
GENERAL INFORMATION:  
APPLICANT: Ruoslahti, Erkki  
APPLICANT: Pasqualini, Renata  
TITLE OF INVENTION: Molecules that Home to Various Selected Organs or  
TITLE OF INVENTION: Tissues  
FILE REFERENCE: P-LJ 2892  
CURRENT APPLICATION NUMBER: US/09/042,107  
CURRENT FILING DATE: 1998-03-13  
NUMBER OF SEQ ID NOS: 436  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 278  
LENGTH: 5  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-042-107-278

Query Match 42.9%; Score 3; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQP 6  
Db 2 HQP 4

## RESULT 15

US-08-811-463-26  
Sequence 26, Application US/08811463C  
Patent No. 6277375  
GENERAL INFORMATION:  
APPLICANT: Ward, Elizabeth S.

; TITLE OF INVENTION: IMMUNOGLOBIN-LIKE DOMAINS WITH INCREASED HALF LIVES  
; FILE REFERENCE: UTS0:483  
; CURRENT APPLICATION NUMBER: US/08/811,463C  
; CURRENT FILING DATE: 1997-03-03  
; EARLIER APPLICATION NUMBER: 60/013,563  
; EARLIER FILING DATE: 1996-03-18  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 26  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptides  
US-08-811-463-26

Query Match 42.9%; Score 3; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MHQ 5  
|||  
Db 2 MHQ 4

## RESULT 16

US-09-214-095D-70  
; Sequence 70, Application US/09214095D  
; Patent No. 6280987  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 51400-A-PCT-US  
; CURRENT APPLICATION NUMBER: US/09/214,095D  
; CURRENT FILING DATE: 1999-07-19  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 70  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Murinae gen. sp.  
US-09-214-095D-70

Query Match 42.9%; Score 3; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4  
|||  
Db 3 WMH 5

## RESULT 17

US-09-406-532-5  
; Sequence 5, Application US/09406532A  
; Patent No. 6365154  
; GENERAL INFORMATION:  
; APPLICANT: Connie L. Erickson-Miller  
; APPLICANT: Stephen D. Holmes  
; APPLICANT: James D. Winkler  
; TITLE OF INVENTION: TIE2 Agonist Antibodies  
; FILE REFERENCE: P50843  
; CURRENT APPLICATION NUMBER: US/09/406,532A  
; CURRENT FILING DATE: 1999-09-27  
; PRIOR APPLICATION NUMBER: 60/102,098  
; PRIOR FILING DATE: 1998-09-28  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Mus musculus

; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (1)...(5)  
; OTHER INFORMATION: 15B8 heavy chain CDR 1  
US-09-406-532-5

Query Match 42.9%; Score 3; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4  
|||  
Db 3 WMH 5

## RESULT 18

US-08-479-089A-7  
; Sequence 7, Application US/08479089A  
; Patent No. 6383487  
; GENERAL INFORMATION:  
; APPLICANT: Amlot, Peter L.  
; APPLICANT: Akbar, Arne N.  
; APPLICANT: Heinrich, Gunther  
; APPLICANT: Cammisuli, Salvatore  
; TITLE OF INVENTION: CD25 Binding Molecules  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 6383487artis Corporation  
; STREET: 564 Morris Avenue  
; CITY: Summit  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07901-1027  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/479,089A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/669,545  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9019323  
; FILING DATE: 05-SEP-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Furman, Diane E.  
; REGISTRATION NUMBER: 31,104  
; REFERENCE/DOCKET NUMBER: 100-7617  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908) 522-6924  
; TELEFAX: (908) 522-6955  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
US-08-479-089A-7

Query Match 42.9%; Score 3; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4  
|||  
Db 3 WMH 5

RESULT 19  
US-09-082-358B-31  
; Sequence 31, Application US/09082358B  
; Patent No. 6469153  
; GENERAL INFORMATION:  
; APPLICANT: Goff, Stephen P.  
; APPLICANT: Li, Xingquiang  
; TITLE OF INVENTION: EIP-1, EIP-3 GENES, ENVELOPE-INTERACTING PROTEINS,  
; TITLE OF INVENTION: EIP-1, and EIP-3  
; FILE REFERENCE: 0575/54804  
; CURRENT APPLICATION NUMBER: US/09/082,358B  
; CURRENT FILING DATE: 1998-05-20  
; NUMBER OF SEQ ID NOS: 106  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 31  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: murine  
US-09-082-358B-31

Query Match 42.9%; Score 3; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 OPP 7  
|||  
Db 2 QPP 4

RESULT 20  
US-07-669-545B-7  
; Sequence 7, Application US/07669545B  
; Patent No. 6521230  
; GENERAL INFORMATION:  
; APPLICANT: Amlot, Peter L.  
; APPLICANT: Akbar, Arne N.  
; APPLICANT: Heinrich, Gunther  
; APPLICANT: Cammisuli, Salvatore  
; TITLE OF INVENTION: CD25 Binding Molecules  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 6521230artis Corporation  
; STREET: 564 Morris Avenue  
; CITY: Summit  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07901-1027  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/669,545B  
; FILING DATE: 14-MAR-1991  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9005962  
; FILING DATE: 16-MAR-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9019323  
; FILING DATE: 05-SEP-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Furman, Diane E.  
; REGISTRATION NUMBER: 31,104  
; REFERENCE/DOCKET NUMBER: 100-7617  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908) 522-6924  
; TELEFAX: (908) 522-6955  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:

; LENGTH: 5 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
US-07-669-545B-7

Query Match 42.9%; Score 3; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4  
|||  
Db 3 WMH 5

RESULT 21  
5217869-43  
; Patent No. 5217869  
; APPLICANT: KAUFAR, LAWRENCE M.  
; TITLE OF INVENTION: METHOD TO PRODUCE IMMUNODIAGNOSTIC  
; REAGENTS  
; NUMBER OF SEQUENCES: 121  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/255,906  
; FILING DATE: 11-OCT-1988  
; SEQ ID NO:43  
; LENGTH: 5  
5217869-43

Query Match 42.9%; Score 3; DB 6; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4  
|||  
Db 1 WMH 3

RESULT 22  
5464756-28  
; Patent No. 5464756  
; APPLICANT: HENNER, DENNIS J.; VANDLEN, RICHARD L.; WILKINS,  
; JAMES A.; YANSURA, DANIEL G.  
; TITLE OF INVENTION: PROCESS AND COMPOSITIONS FOR THE  
; ISOLATION HUMAN RELAXIN  
; NUMBER OF SEQUENCES: 42  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/908,766  
; FILING DATE: 01-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 347,550  
; FILING DATE: 04-MAY-1989  
; SEQ ID NO:28  
; LENGTH: 5  
5464756-28

Query Match 42.9%; Score 3; DB 6; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SWM 3  
|||  
Db 2 SWM 4

RESULT 23  
US-08-253-854-40  
; Sequence 40, Application US/08253854  
; Patent No. 5504190  
; GENERAL INFORMATION:



```
;
; APPLICANT: Houghten, Richard A.
; APPLICANT: Cuervo, Julio H.
; APPLICANT: Pinilla, Clemencia
; APPLICANT: Appel Jr., Jon R.
; APPLICANT: Blondelle, Silvie
; TITLE OF INVENTION: Synthesis of Equimolar Multiple
; TITLE OF INVENTION: Oligomer Mixtures, Especially Of Oligopeptide Mixtures
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Shore, Sutker &
; ADDRESSEE: Milanow, Ltd.
; STREET: 180 No. 5504190th Stetson Avenue, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/253,854
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,391
; REFERENCE/DOCKET NUMBER: PRL.0003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)616-5400
; TELEFAX: (312)616-5460
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-253-854-40

Query Match 42.9%; Score 3; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4
   |||
Db 4 WMH 6

RESULT 24
US-08-127-499A-22
; Sequence 22, Application US/08127499A
; Patent No. 5510264
; GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
; TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,499A
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 51916/104/INBI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
;
US-08-482-847-22
Query Match 42.9%; Score 3; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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;
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 51916/102/INBI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
;
US-08-127-499A-22

Query Match 42.9%; Score 3; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
   |||
Db 2 QPP 4

RESULT 25
US-08-482-847-22
; Sequence 22, Application US/08482847
; Patent No. 5556757
; GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
; TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
; TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,847
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,499
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 51916/104/INBI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
;
US-08-482-847-22
Query Match 42.9%; Score 3; DB 1; Length 6;
```

```
; TITLE OF INVENTION: IMMUNOINFECTION CLUSTER VIRUS INFECTIONS
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 No. 5707626th Figueroa Street, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,170
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/029,850
; FILING DATE: 11-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Spitals, John P.
; REGISTRATION NUMBER: 29,215
; REFERENCE/DOCKET NUMBER: 1920-331
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 977-1001
; TELEFAX: (213) 977-1003
; INFORMATION FOR SEQ ID NO: 89:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-704-170-89

Query Match 42.9%; Score 3; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
Db 2 QPP 4

RESULT 28
US-08-460-269C-7
; Sequence 7, Application US/08460269C
; Patent No. 6197548
; GENERAL INFORMATION:
; APPLICANT: CLARE, JEFFREY J.
; ROMANOS, MICHAEL A.
; TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN YEAST
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
; STREET: 2200 Clarendon Blvd., Suite 1400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,269C
; FILING DATE: 02-Jun-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lebovitz, Richard M.
; REGISTRATION NUMBER: 37,067
```

```
; TITLE OF INVENTION: IMMUNOINFECTION CLUSTER VIRUS INFECTIONS
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 No. 5707626th Figueroa Street, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,170
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/029,850
; FILING DATE: 11-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Spitals, John P.
; REGISTRATION NUMBER: 29,215
; REFERENCE/DOCKET NUMBER: 1920-331
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 977-1001
; TELEFAX: (213) 977-1003
; INFORMATION FOR SEQ ID NO: 89:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-704-170-89

Query Match 42.9%; Score 3; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
Db 2 QPP 4

RESULT 26
US-08-237-716-7
; Sequence 7, Application US/08237716
; Patent No. 5589384
; GENERAL INFORMATION:
; APPLICANT: LIPSCOMBE, Martin J
; APPLICANT: CHARLES, Ian G
; APPLICANT: FAIRWEATHER, Neil F
; TITLE OF INVENTION: FUSION PROTEINS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vanderhye, P.C.
; STREET: 1100 No. 5589384th Glebe Road, 8th Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/237,716
; FILING DATE: 02-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/896,003
; FILING DATE: 11-JUN-1992
; APPLICATION NUMBER: GB 9112553.4
; FILING DATE: 11-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mary J
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 117-157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-237-716-7

Query Match 42.9%; Score 3; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
Db 4 QPP 6

RESULT 27
US-08-704-170-89
; Sequence 89, Application US/08704170
; Patent No. 5707626
; GENERAL INFORMATION:
; APPLICANT: Douvas, Angeline
; APPLICANT: Takehana, Yoshi
; APPLICANT: Ehresmann, Glenn
; TITLE OF INVENTION: THERAPEUTIC STRATEGIES FOR
```

```
; REFERENCE/DOCKET NUMBER: Popov-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 243-6333
; TELEFAX: (703) 243-6410
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-08-460-269C-7

Query Match 42.9%; Score 3; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
Db 4 QPP 6

RESULT 29
US-09-641-803-13
; Sequence 13, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-13

Query Match 42.9%; Score 3; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
Db 3 QPP 5

RESULT 30
PCT-US94-02631-89
; Sequence 89, Application PC/TUS9402631
; GENERAL INFORMATION:
; APPLICANT: Douvas, Angeline
; APPLICANT: Takehana, Yoshi
; APPLICANT: Ehresmann, Glenn
; TITLE OF INVENTION: THERAPEUTIC STRATEGIES FOR
; TITLE OF INVENTION: IMMUNOINFECTION CLUSTER VIRUS INFECTIONS
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 North Figueroa Street, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.

; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-08-460-269C-7

Query Match 42.9%; Score 3; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
Db 4 QPP 6

RESULT 29
US-09-641-803-13
; Sequence 13, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-13

Query Match 42.9%; Score 3; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7
Db 2 QPP 4

RESULT 31
US-08-169-524-3
; Sequence 3, Application US/08169524
; Patent No. 5496706
; GENERAL INFORMATION:
; APPLICANT: Kuusela, Pentti
; APPLICANT: Hilden, Pekka
; TITLE OF INVENTION: Methods and Materials for the
; TITLE OF INVENTION: Detection of
; TITLE OF INVENTION: Staphylococcus Aureus
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/169,524
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: 36,989
; REFERENCE/DOCKET NUMBER: 28113/31832
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
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; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 7 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 US-08-169-524-3

Query Match 42.9%; Score 3; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7  
 Db 1 QPP 3

RESULT 32  
 US-08-081-539-113  
 ; Sequence 113, Application US/08081539  
 ; Patent No. 5501962

; GENERAL INFORMATION:  
 ; APPLICANT: Braford-Goldberg, Sarah R.  
 ; APPLICANT: Easton, Alan M.  
 ; APPLICANT: Klein, Barbara K.  
 ; APPLICANT: McKearn, John P.  
 ; APPLICANT: Olins, Peter O.  
 ; TITLE OF INVENTION: Interleukin-3 (IL-3) Human/Murine  
 ; TITLE OF INVENTION: Chimeric Hybrid Polypeptides  
 ; NUMBER OF SEQUENCES: 121  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Mary Jo Kanady, G. D. Searle & Co., Corporate  
 ; ADDRESSEE: Patent Dept.  
 ; STREET: P. O. Box 5110  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: USA  
 ; ZIP: 60680

; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/081,539  
 ; FILING DATE: 19930621  
 ; CLASSIFICATION: 424  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Kanady, Mary J.  
 ; REGISTRATION NUMBER: 28623  
 ; REFERENCE/DOCKET NUMBER: 2724  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (708)470-6501  
 ; TELEFAX: (708)470-6881

; INFORMATION FOR SEQ ID NO: 113:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 7 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 US-08-081-539-113

Query Match 42.9%; Score 3; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7  
 Db 1 QPP 3

RESULT 33  
 US-08-127-499A-3

; Sequence 3, Application US/08127499A  
 ; Patent No. 5510264  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VAN ALSTYNE, Diane  
 ; APPLICANT: SHARMA, Lawrence Rajendra  
 ; TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED  
 ; TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES  
 ; NUMBER OF SEQUENCES: 40  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Foley & Lardner  
 ; STREET: 3000 K Street, N.W., Suite 500  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20007-5109

; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/127,499A  
 ; FILING DATE: 28-SEP-1993

; ATTORNEY/AGENT INFORMATION:  
 ; NAME: BENT, Stephen A.  
 ; REGISTRATION NUMBER: 29,768  
 ; REFERENCE/DOCKET NUMBER: 51916/102/INBI  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202)672-5300  
 ; TELEFAX: (202)672-5399  
 ; TELEX: 904136

; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 7 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: unknown  
 US-08-127-499A-3

Query Match 42.9%; Score 3; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7  
 Db 3 QPP 5

RESULT 34  
 US-08-127-499A-7  
 ; Sequence 7, Application US/08127499A  
 ; Patent No. 5510264  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VAN ALSTYNE, Diane  
 ; APPLICANT: SHARMA, Lawrence Rajendra

; TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED  
 ; TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES  
 ; NUMBER OF SEQUENCES: 40  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Foley & Lardner  
 ; STREET: 3000 K Street, N.W., Suite 500  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20007-5109

; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/127,499A  
 ; FILING DATE: 28-SEP-1993

ATTORNEY/AGENT INFORMATION:  
 NAME: BENT, Stephen A.  
 REGISTRATION NUMBER: 29,768  
 REFERENCE/DOCKET NUMBER: 51916/102/INBI  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202)672-5300  
 TELEFAX: (202)672-5399  
 TELEX: 904136  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 7 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: unknown  
 US-08-127-499A-7

Query Match 42.9%; Score 3; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7  
 |||  
 Db 3 QPP 5

RESULT 35  
 US-08-127-499A-10  
 ; Sequence 10, Application US/08127499A  
 ; Patent No. 5510264  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VAN ALSTYNE, Diane  
 ; APPLICANT: SHARMA, Lawrence Rajendra  
 ; TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED  
 ; TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES  
 ; NUMBER OF SEQUENCES: 40  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Foley & Lardner  
 ; STREET: 3000 K Street, N.W., Suite 500  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20007-5109  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/127,499A  
 ; FILING DATE: 28-SEP-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: BENT, Stephen A.  
 ; REGISTRATION NUMBER: 29,768  
 ; REFERENCE/DOCKET NUMBER: 51916/102/INBI  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202)672-5300  
 ; TELEFAX: (202)672-5399  
 ; TELEX: 904136  
 ; INFORMATION FOR SEQ ID NO: 10:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 7 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: unknown  
 US-08-127-499A-10

Query Match 42.9%; Score 3; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7  
 |||  
 Db 3 QPP 5

RESULT 36  
 US-08-127-499A-25  
 ; Sequence 25, Application US/08127499A  
 ; Patent No. 5510264  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VAN ALSTYNE, Diane  
 ; APPLICANT: SHARMA, Lawrence Rajendra  
 ; TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED  
 ; TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES  
 ; NUMBER OF SEQUENCES: 40  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Foley & Lardner  
 ; STREET: 3000 K Street, N.W., Suite 500  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20007-5109  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/127,499A  
 ; FILING DATE: 28-SEP-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: BENT, Stephen A.  
 ; REGISTRATION NUMBER: 29,768  
 ; REFERENCE/DOCKET NUMBER: 51916/102/INBI  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202)672-5300  
 ; TELEFAX: (202)672-5399  
 ; TELEX: 904136  
 ; INFORMATION FOR SEQ ID NO: 10:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 7 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: unknown  
 US-08-127-499A-10

Query Match 42.9%; Score 3; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7  
 |||  
 Db 3 QPP 5

RESULT 36  
 US-08-127-499A-25  
 ; Sequence 25, Application US/08127499A  
 ; Patent No. 5510264  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VAN ALSTYNE, Diane  
 ; APPLICANT: SHARMA, Lawrence Rajendra  
 ; TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED  
 ; TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES  
 ; NUMBER OF SEQUENCES: 40  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Foley & Lardner  
 ; STREET: 3000 K Street, N.W., Suite 500  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20007-5109  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/127,499A  
 ; FILING DATE: 28-SEP-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: BENT, Stephen A.  
 ; REGISTRATION NUMBER: 29,768  
 ; REFERENCE/DOCKET NUMBER: 51916/102/INBI  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202)672-5300  
 ; TELEFAX: (202)672-5399  
 ; TELEX: 904136  
 ; INFORMATION FOR SEQ ID NO: 25:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 7 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: unknown  
 US-08-127-499A-25

Query Match 42.9%; Score 3; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7  
 |||  
 Db 3 QPP 5

RESULT 37  
 US-08-466-647-113  
 ; Sequence 113, Application US/08466647  
 ; Patent No. 5543141  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Braford-Goldberg, Sarah R.  
 ; APPLICANT: Easton, Alan M.  
 ; APPLICANT: Klein, Barbara K.  
 ; APPLICANT: McKearn, John P.  
 ; APPLICANT: Olin, Peter O.  
 ; TITLE OF INVENTION: Interleukin-3 (IL-3) Human/Murine  
 ; TITLE OF INVENTION: Chimeric Hybrid Polypeptides  
 ; NUMBER OF SEQUENCES: 121  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Mary Jo Kanady, G. D. Searle & Co., Corporate  
 ; ADDRESSEE: Patent Dept.  
 ; STREET: P. O. Box 5110  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: USA  
 ; ZIP: 60680

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,647  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/081,539  
FILING DATE: 21-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Kanady, Mary J.  
REGISTRATION NUMBER: 28623  
REFERENCE/DOCKET NUMBER: 2724  
TELEPHONE: (708)470-6501  
TELEFAX: (708)470-6881  
INFORMATION FOR SEQ ID NO: 113:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-466-647-113

Query Match 42.9%; Score 3; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7  
Db 1 QPP 3

RESULT 38  
US-08-482-847-3  
Sequence 3, Application US/08482847  
Patent No. 5556757  
GENERAL INFORMATION:  
APPLICANT: VAN ALSTYNE, Diane  
APPLICANT: SHARMA, Lawrence Rajendra  
TITLE OF INVENTION: PETIDES REPRESENTING EPITOPIC SITES FOR  
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR  
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,847  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/127,499  
FILING DATE: 28-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 51916/104/INBI  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399

TELEX: 904136  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
US-08-482-847-3

Query Match 42.9%; Score 3; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7  
Db 3 QPP 5

RESULT 39  
US-08-482-847-7  
Sequence 7, Application US/08482847  
Patent No. 5556757  
GENERAL INFORMATION:  
APPLICANT: VAN ALSTYNE, Diane  
APPLICANT: SHARMA, Lawrence Rajendra  
TITLE OF INVENTION: PETIDES REPRESENTING EPITOPIC SITES FOR  
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR  
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,847  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/127,499  
FILING DATE: 28-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 51916/104/INBI  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
US-08-482-847-7

Query Match 42.9%; Score 3; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7  
Db 3 QPP 5

## RESULT 40

US-08-482-847-10  
 ; Sequence 10, Application US/08482847  
 ; Patent No. 5556757  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VAN ALSTYNE, Diane  
 ; APPLICANT: SHARMA, Lawrence Rajendra  
 ; TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR  
 ; TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR  
 ; TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF  
 ; NUMBER OF SEQUENCES: 40  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Foley & Lardner  
 ; STREET: 3000 K Street, N.W., Suite 500  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20007-5109  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/482,847  
 ; FILING DATE: 07-JUN-1995  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/127,499  
 ; FILING DATE: 28-SEP-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: BENT, Stephen A.  
 ; REGISTRATION NUMBER: 29,768  
 ; REFERENCE/DOCKET NUMBER: 51916/104/INBI  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202)672-5300  
 ; TELEFAX: (202)672-5399  
 ; TELEX: 904136  
 ; INFORMATION FOR SEQ ID NO: 10:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 7 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: unknown  
 ; US-08-482-847-10  
 ;  
 ; Query Match 42.9%; Score 3; DB 1; Length 7;  
 ; Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 ; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7

Db 3 QPP 5

## RESULT 41

US-08-482-847-25  
 ; Sequence 25, Application US/08482847  
 ; Patent No. 5556757  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VAN ALSTYNE, Diane  
 ; APPLICANT: SHARMA, Lawrence Rajendra  
 ; TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR  
 ; TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR  
 ; TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF  
 ; NUMBER OF SEQUENCES: 40  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Foley & Lardner  
 ; STREET: 3000 K Street, N.W., Suite 500  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20007-5109

; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/482,847  
 ; FILING DATE: 07-JUN-1995  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/127,499  
 ; FILING DATE: 28-SEP-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: BENT, Stephen A.  
 ; REGISTRATION NUMBER: 29,768  
 ; REFERENCE/DOCKET NUMBER: 51916/104/INBI  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202)672-5300  
 ; TELEFAX: (202)672-5399  
 ; TELEX: 904136  
 ; INFORMATION FOR SEQ ID NO: 25:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 7 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: unknown  
 ; US-08-482-847-25

Query Match 42.9%; Score 3; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7

Db 3 QPP 5

## RESULT 42

US-08-723-116-4  
 ; Sequence 4, Application US/08723116  
 ; Patent No. 5837248  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KIKUCHI, KIKICHI  
 ; APPLICANT: SATO, NORIYUKI  
 ; APPLICANT: SAHARA, HIROMITSU  
 ; APPLICANT: YASOJIMA, TAKAHIRO  
 ; APPLICANT: WADA, YOSHIMASA  
 ; APPLICANT: SUZUKI, MANABU  
 ; APPLICANT: HAMURO, JUNJI  
 ; TITLE OF INVENTION: PEPTIDE CAPABLE OF INDUCING IMMUNE  
 ; TITLE OF INVENTION: RESPONSE TO HUMAN GASTRIC CANCER AND AGENT FOR PREVENTING  
 ; TITLE OF INVENTION: OR TREATING HUMAN GASTRIC CANCER, CONTAINING THE PEPTIDE  
 ; NUMBER OF SEQUENCES: 4  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
 ; ADDRESSEE: P.C.  
 ; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
 ; CITY: ARLINGTON  
 ; STATE: VA  
 ; COUNTRY: USA  
 ; ZIP: 22202  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/723,116  
 ; FILING DATE: 30-SEP-1996  
 ; CLASSIFICATION: 530  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: JP 253491/1995  
 ; FILING DATE: 29-SEP-1995

Qy 5 QPP 7

Db 3 QPP 5

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: JP 217140/1996  
;; FILING DATE: 19-AUG-1996  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: OBLON, NORMAN F.  
;; REGISTRATION NUMBER: 24,618  
;; REFERENCE/DOCKET NUMBER: 10-821-0X  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 703-413-3000  
;; TELEFAX: 703-413-2220  
;; INFORMATION FOR SEQ ID NO: 4:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 7 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; ORIGINAL SOURCE:  
;; ORGANISM: HUMAN  
US-08-723-116-4

Query Match 42.9%; Score 3; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SWM 3  
|||  
Db 2 SWM 4

## RESULT 43

US-08-774-354B-4  
; Sequence 4, Application US/08774354B  
; Patent No. 6063427  
; GENERAL INFORMATION:  
; APPLICANT: Michiko WATANABE  
; TITLE OF INVENTION: METHOD FOR PRODUCING A  
; TITLE OF INVENTION: HYPOALLERGENIC WHEAT FLOUR  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 2033 K Street, N.W., Suite 800  
; CITY: Washington, D.C.  
; STATE:  
; COUNTRY: U.S.A.  
; ZIP: 20006

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1+  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/774,354B  
; FILING DATE: December 27, 1996  
; CLASSIFICATION: 426  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Matthew Jacob

REGISTRATION NUMBER: 25,154  
REFERENCE/DOCKET NUMBER: 653-96F029US  
TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 721-8200  
; TELEFAX: (202) 721-8250  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

;; HYPOTHETICAL:  
;; ANTI-SENSE:  
;; FRAGMENT TYPE:  
;; ORIGINAL SOURCE:  
;; IMMEDIATE SOURCE:  
;; POSITION IN GENOME:  
;; FEATURE:  
;; PUBLICATION INFORMATION:  
US-08-774-354B-4

Query Match 42.9%; Score 3; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7  
|||  
Db 4 QPP 6

## RESULT 44

US-09-103-808-4  
; Sequence 4, Application US/09103808  
; Patent No. 6368852  
; GENERAL INFORMATION:  
; APPLICANT: KIKUCHI, KOKICHI

; SATO, NORIYUKI  
; SAHARA, HIROMITSU  
; YASOJIMA, TAKAHIRO  
; WADA, YOSHIMASA  
; SUZUKI, MANABU  
; HAMURO, JUNJI

;; TITLE OF INVENTION: PEPTIDE CAPABLE OF INDUCING IMMUNE  
;; RESPONSE TO HUMAN GASTRIC CANCER AND AGENT FOR PREVENTIN  
;; OR TREATING HUMAN GASTRIC CANCER, CONTAINING THE PEPTIDE

;; NUMBER OF SEQUENCES: 4

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
;; P.C.

;; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

;; CITY: ARLINGTON

;; STATE: VA

;; COUNTRY: USA

;; ZIP: 22202

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/103,808

;; FILING DATE: 24-Jun-1998

;; CLASSIFICATION: <Unknown>

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: 08/723,116

;; FILING DATE: <Unknown>

;; APPLICATION NUMBER: JP 217140/1996

;; FILING DATE: 19-AUG-1996

;; ATTORNEY/AGENT INFORMATION:

;; NAME: OBLON, NORMAN F.

;; REGISTRATION NUMBER: 24,618

;; REFERENCE/DOCKET NUMBER: 10-821-0X

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 703-413-3000

;; TELEFAX: 703-413-2220

;; INFORMATION FOR SEQ ID NO: 4:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 7 amino acids

;; TYPE: amino acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; MOLECULE TYPE: peptide

;; ORIGINAL SOURCE: HUMAN



```
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-103-808-4
Query Match          42.9%; Score 3; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SWM 3
Db 2 SWM 4

RESULT 45
US-09-641-803-1
; Sequence 1, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-1

Query Match          42.9%; Score 3; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
Db 2 QPP 4

RESULT 46
US-07-872-644-35
; Sequence 35, Application US/07872644
; Patent No. 5389527
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; SEQUENCE CHARACTERISTICS:

; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-07-872-644-35
Query Match          42.9%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 WMH 4
Db 4 WMH 6

RESULT 47
US-08-291-349A-5
; Sequence 5, Application US/08291349A
; Patent No. 5545620
; GENERAL INFORMATION:
; APPLICANT: Mahl, Sharon M.
; APPLICANT: McCarthy, James B.
; APPLICANT: Furcht, Leo T.
; TITLE OF INVENTION: Synthetic Fibronection Fragments As
; TITLE OF INVENTION: Inhibitors of Retroviral Infection
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff
; STREET: 10 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/291,349A
; FILING DATE: 16 AUG 1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/006,121
; FILING DATE: 19 JAN 1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: McDonnell, John J.
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 92,673-B
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
```

; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1, 8  
; OTHER INFORMATION: /note= "FN5 (1892-1899)  
; OTHER INFORMATION: fibronectin fragment : FN-C/H-V"  
US-08-291-349A-5

Query Match 42.9%; Score 3; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7  
|||  
Db 2 QPP 4

RESULT 48  
US-08-297-494-35  
; Sequence 35, Application US/08297494  
; Patent No. 5580771  
; GENERAL INFORMATION:  
; APPLICANT: Beavo, Joseph A.  
; APPLICANT: Bentley, Kelley  
; APPLICANT: Charbonneau, Harry  
; APPLICANT: Sonnenburg, William K.  
; TITLE OF INVENTION: DNA Encoding Mammalian  
; TITLE OF INVENTION: Phosphodiesterases  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; ADDRESSEE: Bicknell  
; STREET: Two First National Plaza, 20 South Clark  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/297,494  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/688,356  
; FILING DATE: 04-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5580771and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27866/30822  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 346-5750  
; TELEFAX: (312) 984-9740  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 35:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-297-494-35

Query Match 42.9%; Score 3; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WHH 4  
|||  
Db 4 WHH 6

RESULT 49  
US-07-990-296-3  
; Sequence 3, Application US/07990296  
; Patent No. 5591719  
; GENERAL INFORMATION:  
; APPLICANT: Rucht, Leo T.  
; APPLICANT: Allen, Janice B.  
; APPLICANT: Wahl, Sharon M.  
; APPLICANT: McCarthy, James B.  
; TITLE OF INVENTION: Method for Treating Acute and  
; TITLE OF INVENTION: Chronic Inflammatory Disorders Using Polypeptides  
; TITLE OF INVENTION: with Fibronectin Activity  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant & Gould  
; STREET: 3100 No. 5591719west Center  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy Disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Wordperfect 5.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/990,296  
; FILING DATE: 19921210  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kowalchuk, Alan W.  
; REGISTRATION NUMBER: 31,535  
; REFERENCE/DOCKET NUMBER: 600.252-US-01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612-332-5300  
; TELEFAX: 612-332-9081  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acid residues  
; TYPE: AMINO ACID  
; TOPOLOGY: Linear  
; MOLECULE TYPE: Peptide  
; FRAGMENT TYPE: Internal Fragment  
; ORIGINAL SOURCE: Synthetically Derived  
; FEATURE:  
; NAME/KEY: Fragment of the 33 kD carboxy  
; NAME/KEY: terminal heparin-binding fragment of the A  
; NAME/KEY: chain of fibronectin  
; LOCATION: Represents isolated fibronectin  
; LOCATION: Residues 1892-1899 from all plasma isoforms  
; LOCATION: of fibronectin  
US-07-990-296-3

Query Match 42.9%; Score 3; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7  
|||  
Db 2 QPP 4

RESULT 50  
US-08-297-510-35  
; Sequence 35, Application US/08297510  
; Patent No. 5602019  
; GENERAL INFORMATION:

APPLICANT: Beavo, Joseph A.  
APPLICANT: Bentley, Kelley  
APPLICANT: Charbonneau, Harry  
APPLICANT: Sonnenburg, William K.  
TITLE OF INVENTION: DNA Encoding Mammalian  
TITLE OF INVENTION: Phosphodiesterases  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSEE: Bicknell  
STREET: Two First National Plaza, 20 South Clark  
STREET: Street  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/297,510  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/688,356  
FILING DATE: 04-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5602019and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/30822  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-297-510-35

Query Match 42.9%; Score 3; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4  
|||  
Db 4 WMH 6

RESULT 51  
US-08-479-532-35  
Sequence 35, Application US/08479532  
Patent No. 5776752  
GENERAL INFORMATION:  
APPLICANT: Beavo, Joseph A.  
APPLICANT: Bentley, Kelley  
APPLICANT: Charbonneau, Harry  
APPLICANT: Sonnenburg, William K.  
TITLE OF INVENTION: DNA Encoding Mammalian  
TITLE OF INVENTION: Phosphodiesterases  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSEE: Bicknell  
STREET: Two First National Plaza, 20 South Clark  
STREET: Street  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA

ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/479,532  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/297,494  
FILING DATE:  
APPLICATION NUMBER: US 07/688,356  
FILING DATE: 04-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5776752and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/30822  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-479-532-35

Query Match 42.9%; Score 3; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4  
|||  
Db 4 WMH 6

RESULT 52  
US-08-455-526-35  
Sequence 35, Application US/08455526  
Patent No. 5789553  
GENERAL INFORMATION:  
APPLICANT: Beavo, Joseph A.  
APPLICANT: Bentley, Kelley  
APPLICANT: Charbonneau, Harry  
APPLICANT: Sonnenburg, William K.  
TITLE OF INVENTION: DNA Encoding Mammalian  
TITLE OF INVENTION: Phosphodiesterases  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSEE: Bicknell  
STREET: Two First National Plaza, 20 South Clark  
STREET: Street  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,526  
FILING DATE: 31-MAY-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/297,494  
FILING DATE: 29-AUG-1994

```
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5789553and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-455-525-35

Query Match 42.9%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4
DB 4 WMH 6

RESULT 53
US-08-455-525-35
; Sequence 35, Application US/08455525
; Patent No. 5800987
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; City: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,525
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/297,494
; FILING DATE:
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5800987and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
```

```
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-455-525-35

Query Match 42.9%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4
DB 4 WMH 6

RESULT 54
US-08-723-116-3
; Sequence 3, Application US/08723116
; Patent No. 5837248
; GENERAL INFORMATION:
; APPLICANT: KIKUCHI, KOKICHI
; APPLICANT: SATO, NORIYUKI
; APPLICANT: SAHARA, HIROMITSU
; APPLICANT: YASOJIMA, TAKAHIRO
; APPLICANT: WADA, YOSHIMASA
; APPLICANT: SUZUKI, MANABU
; APPLICANT: HAMURO, JUNJI
; TITLE OF INVENTION: PEPTIDE CAPABLE OF INDUCING IMMUNE
; TITLE OF INVENTION: RESPONSE TO HUMAN GASTRIC CANCER AND AGENT FOR PREVENTING
; TITLE OF INVENTION: OR TREATING HUMAN GASTRIC CANCER, CONTAINING THE PEPTIDE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/723,116
; FILING DATE: 30-SEP-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 253491/1995
; FILING DATE: 29-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 217140/1996
; FILING DATE: 19-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-821-OX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: HUMAN
; US-08-723-116-3

Query Match 42.9%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
```

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SWM 3  
|||  
Db 2 SWM 4

RESULT 55  
US-08-480-133A-3  
; Sequence 3, Application US/08480133A  
; Patent No. 5840691  
; GENERAL INFORMATION:  
; APPLICANT: Furcht, Leo T.  
; APPLICANT: McCarthy, James B.  
; APPLICANT: Wahl, Sharon M.  
; APPLICANT: Allen, Janice B.  
; APPLICANT: Billups, Kevin L.  
; APPLICANT: Everett, Jeffrey E.  
; TITLE OF INVENTION: Method for Treating Inflammatory  
; TITLE OF INVENTION: Diseases Using Polypeptides with Fibronectin Activity  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant & Gould  
; STREET: 90 South 7th Street, 3100 No. 5840691west Center  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/480,133A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/139,903  
; FILING DATE: 21-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/990,296  
; FILING DATE: 10-DEC-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Carter, Charles G.  
; REGISTRATION NUMBER: 35,093  
; REFERENCE/DOCKET NUMBER: 600-308US01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612-332-5300  
; TELEFAX: 612-332-9081  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-480-133A-3

Query Match 42.9%; Score 3; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7  
|||  
Db 2 QPP 4

RESULT 56  
US-08-699-965-2  
; Sequence 2, Application US/08699965  
; Patent No. 5853744  
; GENERAL INFORMATION:  
; APPLICANT: MOORADIAN, DANIEL L.  
; APPLICANT: FIELDS, GREGG B.  
; TITLE OF INVENTION: METHOD FOR MODIFYING A SUBSTRATE SURFACE  
; TITLE OF INVENTION: TO INCLUDE A BIOMOLECULE  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MUEITING, RAASCH, GEBHARDT & SCHWAPPACH, P.A.  
; STREET: 119 No. 5853744th Fourth Street, Suite 203  
; CITY: Minneapolis  
; STATE: Minnesota  
; COUNTRY: USA  
; ZIP: 55401  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/699,965  
; FILING DATE: 20-AUG-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MUEITING, ANN M.  
; REGISTRATION NUMBER: 33,977  
; REFERENCE/DOCKET NUMBER: 110.00300101  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612-305-1217  
; TELEFAX: 612-305-1228  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-699-965-2

Query Match 42.9%; Score 3; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7  
|||  
Db 2 QPP 4

RESULT 57  
US-08-435-149-6  
; Sequence 6, Application US/08435149  
; Patent No. 5866402  
; GENERAL INFORMATION:  
; APPLICANT: INNIS, MICHAEL A.  
; APPLICANT: ZAROR, ISABEL  
; APPLICANT: CREASEY, ABLA A.  
; TITLE OF INVENTION: CHIMERIC MCP AND DAF PROTEINS WITH CELL  
; TITLE OF INVENTION: SURFACE LOCALIZING DOMAIN  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CHIRON CORPORATION  
; STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097  
; CITY: EMERYVILLE  
; STATE: CALIFORNIA  
; COUNTRY: U.S.A.  
; ZIP: 94662-8097  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/435,149  
; FILING DATE: 05-MAY-1995  
; CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:  
NAME: SAVERIDE, PAUL B.  
REGISTRATION NUMBER: 36,914  
REFERENCE/DOCKET NUMBER: 0989.001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 601-2585  
TELEFAX: (510) 655-3542  
TELEX: N/A  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-435-149-6

Query Match 42.9%; Score 3; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7  
Db 2 QPP 4

RESULT 58  
US-09-025-706-10  
Sequence 10, Application US/09025706  
Patent No. 5958874  
GENERAL INFORMATION:  
APPLICANT: Clark, Richard A  
APPLICANT: Greiling, Doris  
APPLICANT: Gailit, James  
TITLE OF INVENTION: RECOMBINANT FIBRONECTIN-BASED  
TITLE OF INVENTION: EXTRACELLULAR MATRIX FOR WOUND HEALING  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jaekie Fleischmann & Mugel, LLP  
STREET: 39 State Street  
CITY: Rochester  
STATE: New York  
COUNTRY: USA  
ZIP: 14614-1310  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,706  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Braman, Susan J  
REGISTRATION NUMBER: 34,103  
REFERENCE/DOCKET NUMBER: 87653.97R263  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 716-262-3640  
TELEFAX: 716-262-4133  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-025-706-10

Query Match 42.9%; Score 3; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7  
Db 2 QPP 4

RESULT 59  
US-08-394-748A-13  
Sequence 13, Application US/08394748A  
Patent No. 6013628  
GENERAL INFORMATION:  
APPLICANT: Skubitz, Amy P.N.  
APPLICANT: Furcht Leo T.  
APPLICANT: Balles, Mark  
APPLICANT: Gregerson, Dale S.  
APPLICANT: Agarwal, Anita  
APPLICANT: Wright, Martha M.  
APPLICANT: Murali, Shobana  
TITLE OF INVENTION: Method for Treating Conditions of the Eye  
TITLE OF INVENTION: Using Polypeptides  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merchant & Gould  
STREET: 3100 No. 6013628west Center  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/394,748A  
FILING DATE: 27-FEB-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/203,458  
FILING DATE: 28-FEB-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Carter, Charles G.  
REGISTRATION NUMBER: 35,093  
REFERENCE/DOCKET NUMBER: 600.307US01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-332-5300  
TELEFAX: 612-332-9081  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
STRAIN: FN-C/H-V  
US-08-394-748A-13

Query Match 42.9%; Score 3; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7  
Db 2 QPP 4

RESULT 60  
US-09-139-491-35  
Sequence 35, Application US/09139491  
Patent No. 6015677  
GENERAL INFORMATION:  
APPLICANT: Beavo, Joseph A.  
APPLICANT: Bentley, Kelley  
APPLICANT: Charbonneau, Harry

APPLICANT: Sonnenburg, William K.  
TITLE OF INVENTION: DNA Encoding Mammalian  
Phosphodiesterases  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSEE: Bicknell  
STREET: Two First National Plaza, 20 South Clark  
STREET: Street  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/139,491  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,525  
FILING DATE: 31-MAY-1995  
APPLICATION NUMBER: 08/297,494  
FILING DATE:  
FILING DATE: 04-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6015677and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/30822  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-139-491-35

Query Match 42.9%; Score 3; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 2 WMH 4  
Db 4 WMH 6

RESULT 61  
US-08-774-354B-5  
Sequence 5, Application US/08774354B  
Patent No. 6063427  
GENERAL INFORMATION:  
APPLICANT: Michiko WATANABE  
TITLE OF INVENTION: METHOD FOR PRODUCING A  
TITLE OF INVENTION: HYPOALLERGENIC WHEAT FLOUR  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 2033 K Street, N.W., Suite 800  
CITY: Washington, D.C.  
STATE:  
COUNTRY: U.S.A.  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1+  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/774,354B  
FILING DATE: December 27, 1996  
CLASSIFICATION: 426  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Matthew Jacob  
REGISTRATION NUMBER: 25,154  
REFERENCE/DOCKET NUMBER: 653-96F029US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 721-8200  
TELEFAX: (202) 721-8250  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
IMMEDIATE SOURCE:  
POSITION IN GENOME:  
FEATURE:  
PUBLICATION INFORMATION:  
US-08-774-354B-5

Query Match 42.9%; Score 3; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 5 QPP 7  
Db 5 QPP 7

RESULT 62  
US-08-916-913A-3  
Sequence 3, Application US/08916913A  
Patent No. 6121027  
GENERAL INFORMATION:  
APPLICANT: Clapper, David L.  
APPLICANT: Swanson, Melvin J.  
APPLICANT: Hu, Sheau-Ping  
APPLICANT: Amos, Richard A.  
APPLICANT: Everson, Terrence P.  
TITLE OF INVENTION: LATENT REACTIVE POLYMERS WITH  
BIOLOGICALLY ACTIVE MOIETIES  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fredrikson & Byron, P.A.  
STREET: 900 Second Avenue South  
CITY: Minneapolis  
STATE: Minnesota  
COUNTRY: USA  
ZIP: 55402-3397  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows-97  
SOFTWARE: ASCII files  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/916,913A  
FILING DATE: 15 August 1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:

```

; APPLICATION NUMBER: No. 6121027e
; FILING DATE: No. 6121027e
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Philip M.
; REGISTRATION NUMBER: 31,162
; REFERENCE/DOCKET NUMBER: 9896.116.0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 347-7088
; TELEFAX: (612) 347-7077
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acid residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-916-913A-3
Query Match 42.9%; Score 3; DB 3; Length 8;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
Db 2 QPP 4

RESULT 63
US-09-025-622-10
; Sequence 10, Application US/09025622
; Patent No. 6194378
; GENERAL INFORMATION:
; APPLICANT: Clark, Richard A
; TITLE OF INVENTION: FIBRONECTIN PEPTIDES-BASED EXTRACELLULAR
; TITLE OF INVENTION: MATRIX FOR WOUND HEALING
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jaackle Fleischmann & Muegel, LLP
; STREET: 39 State Street
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14614-1310
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,622
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Braman, Susan J
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 87653.97R270
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-262-3640
; TELEFAX: 716-262-4133
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-025-622-10
Query Match 42.9%; Score 3; DB 3; Length 8;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
Db 2 QPP 4

RESULT 64
US-08-847-065-11
; Sequence 11, Application US/08847065
; Patent No. 6245335
; GENERAL INFORMATION:
; APPLICANT: Masure, H. Robert
; APPLICANT: Rosenow, Carsten I.
; APPLICANT: Tuomanen, Elaine
; APPLICANT: Wizemann, Theresa M.
; TITLE OF INVENTION: CHOLINE BINDING PROTEINS FOR
; TITLE OF INVENTION: ANTI-PNEUMOCOCCAL VACCINES
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/847,065
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-158
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-847-065-11
Query Match 42.9%; Score 3; DB 3; Length 8;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
Db 2 QPP 4

RESULT 65
US-08-960-054A-6
; Sequence 6, Application US/08960054A
; Patent No. 6261537
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to
; TITLE OF INVENTION: diagnostic/therapeutic
; TITLE OF INVENTION: agents
; FILE REFERENCE: REF/Klaveness/054
; CURRENT APPLICATION NUMBER: US/08/960,054A
; CURRENT FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 31
```

```

Db 2 QPP 4

RESULT 64
US-08-847-065-11
; Sequence 11, Application US/08847065
; Patent No. 6245335
; GENERAL INFORMATION:
; APPLICANT: Masure, H. Robert
; APPLICANT: Rosenow, Carsten I.
; APPLICANT: Tuomanen, Elaine
; APPLICANT: Wizemann, Theresa M.
; TITLE OF INVENTION: CHOLINE BINDING PROTEINS FOR
; TITLE OF INVENTION: ANTI-PNEUMOCOCCAL VACCINES
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/847,065
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-158
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-847-065-11
Query Match 42.9%; Score 3; DB 3; Length 8;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QPP 7
Db 2 QPP 4

RESULT 65
US-08-960-054A-6
; Sequence 6, Application US/08960054A
; Patent No. 6261537
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to
; TITLE OF INVENTION: diagnostic/therapeutic
; TITLE OF INVENTION: agents
; FILE REFERENCE: REF/Klaveness/054
; CURRENT APPLICATION NUMBER: US/08/960,054A
; CURRENT FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 31
```



; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial  
; OTHER INFORMATION: Sequence:Fibronectin  
; OTHER INFORMATION: peptide  
US-08-960-054A-6

Query Match 42.9%; Score 3; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7  
|||  
Db 2 QPP 4

## RESULT 66

US-08-958-993A-6  
; Sequence 6, Application US/08958993A  
; Patent No. 6264917  
; GENERAL INFORMATION:  
; APPLICANT: Nycomed Imaging AS

; TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic  
; TITLE OF INVENTION: agents  
; FILE REFERENCE: REF/Klaveness/993  
; CURRENT APPLICATION NUMBER: US/08/958,993A  
; CURRENT FILING DATE: 1997-10-28  
; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 8

; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Fibronectin  
; OTHER INFORMATION: peptide

## US-08-958-993A-6

Query Match 42.9%; Score 3; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7  
|||  
Db 2 QPP 4

## RESULT 67

US-08-959-206A-2  
; Sequence 2, Application US/08959206A  
; Patent No. 6331289  
; GENERAL INFORMATION:  
; APPLICANT: Nycomed Imaging AS

; TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic  
; TITLE OF INVENTION: agents  
; FILE REFERENCE: REF/Klaveness/206  
; CURRENT APPLICATION NUMBER: US/08/959,206A  
; CURRENT FILING DATE: 1997-10-24  
; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 8

; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Fibronectin  
; OTHER INFORMATION: peptide

## US-08-959-206A-2

Query Match 42.9%; Score 3; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7  
|||  
Db 2 QPP 4

## RESULT 68

US-09-103-808-3  
; Sequence 3, Application US/09103808  
; Patent No. 6388852  
; GENERAL INFORMATION:  
; APPLICANT: KIKUCHI, KOKICHI

; SAITO, NORIYUKI  
; SAHARA, HIROMITSU  
; YASOJIMA, TAKAHIRO  
; WADA, YOSHIMASA  
; SUZUKI, MANABU  
; HAMURO, JUNJI

; TITLE OF INVENTION: PEPTIDE CAPABLE OF INDUCING IMMUNE  
; RESPONSE TO HUMAN GASTRIC CANCER AND AGENT FOR PREVENTING  
; OR TREATING HUMAN GASTRIC CANCER, CONTAINING THE PEPTID.

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; P.C.

; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
; CITY: ARLINGTON  
; STATE: VA

; COUNTRY: USA  
; ZIP: 22202

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/103,808

; FILING DATE: 24-Jun-1998

; CLASSIFICATION: <Unknown>

; PRIORITY INFORMATION DATA:

; APPLICATION NUMBER: 08/723,116

; FILING DATE: <Unknown>

; APPLICATION NUMBER: JP 217140/1996

; FILING DATE: 19-AUG-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: OBLON, NORMAN F.

; REGISTRATION NUMBER: 24,618

; REFERENCE/DOCKET NUMBER: 10-821-0X

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-413-3000

; TELEFAX: 703-413-2220

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; ORIGINAL SOURCE:

; ORGANISM: HUMAN

; SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-103-808-3

Query Match 42.9%; Score 3; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SWM 3  
|||  
Db 2 SWM 4

```

RESULT 69
US-09-101-751A-58
; Sequence 58, Application US/09101751A
; Patent No. 6465253
; GENERAL INFORMATION:
; APPLICANT: WICKHAM, THOMAS J.
; APPLICANT: KOVESDI, IMRE
; APPLICANT: BROUGH, DOUGLAS E.
; TITLE OF INVENTION: VECTORS AND METHODS FOR GENE TRANSFER TO CELLS
; FILE REFERENCE: 85710
; CURRENT APPLICATION NUMBER: US/09/101,751A
; CURRENT FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: WO 96US19150
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 08/700,846
; PRIOR FILING DATE: 1996-08-21
; PRIOR APPLICATION NUMBER: US 08/701,124
; PRIOR FILING DATE: 1996-08-21
; PRIOR APPLICATION NUMBER: US 08/563,368
; PRIOR FILING DATE: 1995-11-28
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 58
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: ( )..( )
; OTHER INFORMATION: Description of Unknown Organism: Artificial
; OTHER INFORMATION: Sequence
US-09-101-751A-58

Query Match 42.9%; Score 3; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 Qpp 7
Db 2 Qpp 4

RESULT 70
US-09-591-564-3
; Sequence 3, Application US/09591564
; Patent No. 6514734
; GENERAL INFORMATION:
; APPLICANT: Clapper, David L.
; Swanson, Melvin J.
; Hu, Sheau-Fing
; Amos, Richard A.
; Everson, Terrence P.
; TITLE OF INVENTION: LATENT REACTIVE POLYMERS WITH BIOLOGICALLY
; ACTIVE MOIETIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fredrikson & Byron, P.A.
; STREET: 900 Second Avenue South
; CITY: Minneapolis
; STATE: Minnesota
; COUNTRY: USA
; ZIP: 55402-3397
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows-97
; SOFTWARE: ASCII files
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/591,564
; FILING DATE: 09-Jun-2000
; CLASSIFICATION: <Unknown>

```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/916,913
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Philip M.
; REGISTRATION NUMBER: 31,162
; REFERENCE/DOCKET NUMBER: 9896.116.0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 347-7088
; TELEFAX: (612) 347-7077
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acid residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-591-564-3

Query Match 42.9%; Score 3; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 Qpp 7
Db 2 Qpp 4

RESULT 71
PCT-US92-03222-35
; Sequence 35, Application PC/TUS9203222
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/03222
; FILING DATE: 19920420
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear

```

MOLECULE TYPE: peptide  
PCT-US92-03222-35

Query Match 42.9%; Score 3; DB 5; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 WMH 4  
Db 4 WMH 6

## RESULT 72

PCT-US93-11781-3  
; Sequence 3, Application PC/TUS9311781  
; GENERAL INFORMATION:  
; APPLICANT: Regents of the University of Minnesota  
; APPLICANT: Morrill Hall  
; APPLICANT: 100 Church Street, S.E.  
; APPLICANT: Minneapolis, Minnesota 55455  
; APPLICANT: U.S.A.  
; APPLICANT: Represented By The Secretary of Health  
and Human Services  
; APPLICANT: 200 Independence Avenue S.W.  
; APPLICANT: Washington, D.C. 20201  
; APPLICANT: United States of America  
; TITLE OF INVENTION: Polypeptides Useful for Treating  
Inflammatory Disorders  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merchant & Gould  
STREET: 3100 Norwest Center  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55402  
; COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/11781  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/139,903  
FILING DATE: 21-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/990,296  
FILING DATE: 10-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Kowalchuk, Alan W.  
REGISTRATION NUMBER: 31,535  
REFERENCE/DOCKET NUMBER: 600.283-US-01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-332-5300  
TELEFAX: 612-332-9081  
; INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US93-11781-3

Query Match 42.9%; Score 3; DB 5; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7  
Db 2 QPP 4

## RESULT 73

PCT-US95-02478-13  
; Sequence 13, Application PC/TUS9502478  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Method for Treating Conditions  
Of the Eye Using Polypeptides  
; NUMBER OF SEQUENCES: 16  
; COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/02478  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/203,458  
FILING DATE: 28-FEB-1994  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
STRAIN: FN-C/H-V  
PCT-US95-02478-13

Query Match 42.9%; Score 3; DB 5; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QPP 7  
Db 2 QPP 4

## RESULT 74

US-08-139-054-7  
; Sequence 7, Application US/08139054  
; Patent No. 5578710  
; GENERAL INFORMATION:  
; APPLICANT: Ambrosius, Dorothea  
; APPLICANT: Dony, Carola  
; APPLICANT: Rudolph, Rainer  
; TITLE OF INVENTION: IMPROVED ACTIVATION OF RECOMBINANT  
PROTEINS  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram  
STREET: 1725 K. St. N.W. Suite 1000  
CITY: Washington, D.C.  
COUNTRY: USA  
ZIP: 20006  
; COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/139,054  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/837,779  
FILING DATE:  
APPLICATION NUMBER: DE P 41 05 480.6  
FILING DATE: 21-FEB-1991  
ATTORNEY/AGENT INFORMATION:

NAME: Murray, Robert B.  
REGISTRATION NUMBER: 22,980  
REFERENCE/DOCKET NUMBER: 920053  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)659-2930  
TELEFAX: (202)887-0357  
TELEX: 440142  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-139-054-7

Query Match 42.9%; Score 3; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 5 Qpp 7  
Db 7 Qpp 9

RESULT 75  
US-08-723-116-2  
Sequence 2, Application US/08723116  
Patent No. 5837248  
GENERAL INFORMATION:  
APPLICANT: KIKUCHI, KOKICHI  
APPLICANT: SATO, NORIYUKI  
APPLICANT: SAHARA, HIROMITSU  
APPLICANT: YASUJIMA, TAKAHIRO  
APPLICANT: WADA, YOSHIMASA  
APPLICANT: SUZUKI, MANABU  
APPLICANT: HAMURO, JUNJI  
TITLE OF INVENTION: PEPTIDE CAPABLE OF INDUCING IMMUNE  
TITLE OF INVENTION: RESPONSE TO HUMAN GASTRIC CANCER AND AGENT FOR PREVENTING  
TITLE OF INVENTION: OR TREATING HUMAN GASTRIC CANCER, CONTAINING THE PEPTIDE  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
ADDRESSEE: P.C.  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/723,116  
FILING DATE: 30-SEP-1996  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 253491/1995  
FILING DATE: 29-SEP-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 217140/1996  
FILING DATE: 19-AUG-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 10-821-0X  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: HUMAN  
US-08-723-116-2

Query Match 42.9%; Score 3; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SWM 3  
Db 2 SWM 4  
Search completed: November 25, 2003, 20:30:00  
Job time : 5.65698 secs

GenCore version 5.1.1.6

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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:28:30 ; Search time 6.86047 Seconds  
(without alignments)  
140.178 Million cell updates/sec

Title: US-09-641-801-25

Perfect score: 10

Sequence: 1 QLPPTVMFP 10

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size: 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database:

PIR 76:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	40.0	8	2	enamelin f - bovin
2	4	40.0	12	2	dystrophin-associa
3	4	40.0	13	2	deoxynucleotidyltr
4	4	40.0	19	2	Ig heavy chain DJ
5	4	40.0	20	2	tumor-derived adhe
6	3	30.0	8	2	hypothetical prote
7	3	30.0	9	2	Ig kappa chain C r
8	3	30.0	10	2	triacylglycerol li
9	3	30.0	10	2	probable glucosyl-6
10	3	30.0	10	2	sphingomyelinase -
11	3	30.0	11	1	bradykinin-potenti
12	3	30.0	11	2	seed protein ws-18
13	3	30.0	11	2	173K exoantigen -
14	3	30.0	13	2	inhibin alpha chai
15	3	30.0	13	2	actin 7 - soybean
16	3	30.0	13	2	cell surface glyco
17	3	30.0	14	2	18K iron-sulfur pr
18	3	30.0	14	2	223K exoantigen -
19	3	30.0	14	2	cerebrin 30 - huma
20	3	30.0	14	2	Ig heavy chain DJ
21	3	30.0	14	2	hypothetical prote
22	3	30.0	15	2	capsid protein VP1
23	3	30.0	15	2	hypothetical 1.5K
24	3	30.0	15	2	niagerithrin - besu
25	3	30.0	15	2	protein QF200037 -
26	3	30.0	15	2	alpha-glucosidase
27	3	30.0	16	2	chitinase (EC 3.2.
28	3	30.0	16	2	alpha-conotoxin Pn
29	3	30.0	16	2	alpha-conotoxin Pn

30	3	30.0	16	2	E58503	superoxide dismuta
31	3	30.0	16	2	S01104	hypothetical prote
32	3	30.0	17	2	S15754	actin 6 - soybean
33	3	30.0	17	2	S32587	L-ascorbate peroxi
34	3	30.0	17	2	S59481	hydroxyproline-ric
35	3	30.0	17	2	S56612	thyroid hormone re
36	3	30.0	18	2	S04229	N4-(beta-N-acetyl
37	3	30.0	18	2	PC2280	prolylendopeptida
38	3	30.0	18	2	S39845	2-aminobenzoate-Co
39	3	30.0	18	2	B45138	arsenite oxidase I
40	3	30.0	18	2	S10452	hypothetical prote
41	3	30.0	18	2	A54135	Na+/K+-exchanging
42	3	30.0	19	2	S60633	H+-transporting tw
43	3	30.0	19	2	C32735	thyroglobulin - pi
44	3	30.0	19	2	B32735	genome polypeptid
45	3	30.0	19	2	B61409	36K microfibrill-as
46	3	30.0	19	2	A34467	comaurin 7-monooxy
47	3	30.0	20	2	S21737	cytochrome P450 2C
48	3	30.0	20	2	S29817	notechis II-5b non
49	3	30.0	20	2	A39328	ribulose-bisphosph
50	3	30.0	20	2	A37111	tubulin alpha chai
51	3	30.0	20	2	A54519	acetyl-CoA synthet
52	3	30.0	20	2	T44453	alpha-amylase (EC
53	3	30.0	20	2	PH1380	gluc protein (B
54	3	30.0	20	2	S65605	interphotoreceptor
55	3	30.0	20	2	A61093	acidic fibroblast
56	3	30.0	20	2	F24417	somatotropin - syn
57	3	30.0	20	2	S03954	tyrosine protein k
58	3	30.0	20	4	153672	tyrosine-melanocyt
59	2	20.0	3	3	178890	starvation-induced
60	2	20.0	4	2	A32039	proctolin - Americ
61	2	20.0	4	2	S53508	peptidyl-dipeptida
62	2	20.0	5	1	HORCHA	flagellar protein
63	2	20.0	5	2	JN0860	ribulose-bisphosph
64	2	20.0	5	2	E42364	acid proteinase li
65	2	20.0	5	2	FS0324	proctolin - Atlant
66	2	20.0	5	2	B37988	27.5 kda structura
67	2	20.0	5	2	A60411	27.5 kda structura
68	2	20.0	5	2	G44817	27.5K structural p
69	2	20.0	5	2	144817	28.5K structural p
70	2	20.0	5	2	E44817	28K structural pro
71	2	20.0	5	2	C44817	halo-toxin - Pseud
72	2	20.0	5	2	A44817	contraction-inhibi
73	2	20.0	6	2	A61049	contraction-inhibi
74	2	20.0	6	2	A27696	transferrin - bovi
75	2	20.0	6	2	B27696	MHC H2-K-k cell su
76	2	20.0	6	2	A19780	hypothetical colla
77	2	20.0	6	2	I67345	Ig heavy chain V r
78	2	20.0	6	2	A35039	hypothetical prote
79	2	20.0	6	4	PH1408	tryptophyllin, bas
80	2	20.0	7	2	S08606	seed protein ws-5
81	2	20.0	7	2	A61081	ICL2 protein - Par
82	2	20.0	7	2	B61491	Ig heavy chain CRD
83	2	20.0	7	2	S71299	caldesquetrin, fas
84	2	20.0	7	2	PC1316	dihydrofolate redu
85	2	20.0	7	2	PT0283	DNA topoisomerase
86	2	20.0	7	2	B39040	glutathione S-tran
87	2	20.0	7	2	I48105	neural cell adhesi
88	2	20.0	7	2	I48086	carcacin U149 - Ca
89	2	20.0	7	2	S66442	Ig heavy chain V r
90	2	20.0	7	2	A39690	angiotensin-conver
91	2	20.0	7	2	A58718	neuropeptide B - b
92	2	20.0	7	2	S45648	tumor-associated a
93	2	20.0	8	2	PH1407	capsid protein VP-
94	2	20.0	8	2	A31570	cellulase (EC 3.2.
95	2	20.0	8	2	B24749	endoglycosylcerami
96	2	20.0	8	2	S43571	lectin - potato (f
97	2	20.0	8	2	PL0184	
98	2	20.0	8	2	S21273	
99	2	20.0	8	2	B39745	
100	2	20.0	8	2	S21288	

## ALIGNMENTS

RESULT 1  
S10783  
enamelin f - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)  
C>Date: 19-Mar-1997 #sequence\_revision 21-Nov-1998 #text\_change 21-Nov-1998  
C:Accession: S10783  
R;Strawich, E.; Glimcher, M.J.  
Eur. J. Biochem. 191, 47-56, 1990  
A:Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is albumin.  
A:Reference number: S10780; MUID:90336641; PMID:2379503  
A:Accession: S10783  
A:Molecule type: protein  
A:Residues: 1-8 <STR>  
C:Keywords: enamel; phosphoprotein

Query Match 40.0%; Score 4; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5  
|||  
DB 2 PLPP 5

RESULT 2  
PN0663  
dystrophin-associated glycoprotein A3a-II - rabbit (fragment)  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C>Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 07-May-1999  
C:Accession: PN0663  
R;Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.  
J. Biochem. 114, 634-639, 1993  
A:Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained in the trans-Golgi network.  
A:Reference number: PN0662; MUID:94156881; PMID:8113213  
A:Accession: PN0663  
A:Molecule type: protein  
A:Residues: 1-12 <YOS>  
C:Comment: This protein is retained in Duchenne type muscular dystrophy muscle.  
C:Keywords: glycoprotein; skeletal muscle

Query Match 40.0%; Score 4; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5  
|||  
DB 3 PLPP 6

RESULT 3  
I84603  
deoxynucleotidyltransferase - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 21-Jul-2000  
C:Accession: I84603  
R;Koizumi, O.; Kaneda, T.; Morishita, R.  
Biochem. Biophys. Res. Commun. 144, 185-190, 1987  
A:Title: Analysis of human terminal deoxynucleotidyl transferase cDNA expressible in man.  
A:Reference number: I45884; MUID:87213162; PMID:3579900  
A:Accession: I84603  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-13 <RES>  
A:Cross-references: GB:M26144; NID:9951194; PIDN:AAA74588.1; PID:9951195  
C:Genetics:  
A:Gene: GDB:DNTT  
A:Cross-references: GDB:119100; OMIM:187410  
A:Map position: 10q23-10q24

Query Match 40.0%; Score 4; DB 2; Length 13;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPLP 4  
|||  
DB 8 QPLP 11

RESULT 4  
PHI352  
Ig heavy chain DJ region (clone C100-115) - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C:Accession: PHI352  
R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
J. Exp. Med. 176, 1577-1581, 1992  
A:Title: Predominance of fetal type DJH joining in young children with B precursor 1;  
A:Reference number: PHI302; MUID:93094761; PMID:1460419  
A:Accession: PHI352  
A:Molecule type: DNA  
A:Residues: 1-19 <WAS>  
A>Note: The authors translated the stop codon for residue 2 as X  
C:Keywords: heterotetramer; immunoglobulin

Query Match 40.0%; Score 4; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPTV 7  
|||  
DB 8 PPTV 11

RESULT 5  
PC2030  
tumor-derived adhesion factor - human (fragment)  
N:Alternate names: 30K protein  
C:Species: Homo sapiens (man)  
C>Date: 14-Jul-1994 #sequence\_revision 14-Jul-1994 #text\_change 21-Jan-2000  
R;Akaogi, K.; Okabe, Y.; Funahashi, K.; Yoshitake, Y.; Nishikawa, K.; Yasumitsu, H.;  
Biochem. Biophys. Res. Commun. 198, 1046-1053, 1994  
A:Title: Cell adhesion activity of a 30-kDa major secreted protein from human bladder.  
A:Reference number: PC2030; MUID:94161713; PMID:8117260  
A:Accession: PC2030  
A:Molecule type: protein  
A:Residues: 1-20 <AKA>  
A:Experimental source: cell line EJ-1  
C:Comment: this protein relates with the aberrant cell adhesion of cancer cells.

Query Match 40.0%; Score 4; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5  
|||  
DB 16 PLPP 19

RESULT 6  
S16324  
Hypothetical protein 2 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 21-Nov-1993 #sequence\_revision 12-May-1995 #text\_change 21-Jul-2000  
C:Accession: S16324  
R;Ruberti, I.; Sessa, G.; Lucchetti, S.; Morelli, G.  
EMBO J. 10, 1787-1791, 1991  
A:Title: A novel class of plant proteins containing a homeodomain with a closely lin.  
A:Reference number: S16323; MUID:91266907; PMID:1675603  
A:Accession: S16324  
A>Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-8 <RUB>

A;Cross-references: EMBL:X58821; NID:gi16327; PIDN:CAA41624.1; PID:g579259

Query Match 30.0%; Score 3; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5  
|||  
Db 6 LPP 8

# RESULT 7

B38740  
Ig kappa chain C region (PY20) - mouse (fragment)

C;Species: Mus musculus (house mouse)  
C;Date: 19-Mar-1997 #sequence\_revision 13-Mar-1998 #text\_change 13-Mar-1998

C;Accession: B38740

R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.

J. Biol. Chem. 266, 6607-6613, 1991

A;Title: Heavy and light chain variable region sequences and antibody properties of anti

A;Reference number: B38740; MUID:91177923; PMID:1708720

A;Accession: B38740

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-9 <RUF>

Query Match 30.0%; Score 3; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PTV 7  
|||  
Db 5 PTV 7

# RESULT 8

PC2171  
triacylglycerol lipase (EC 3.1.1.3) I A chain - Rhizopus niveus (strain IFO 4759) (fragm

C;Species: Rhizopus niveus

C;Date: 03-May-1994 #sequence\_revision 07-Oct-1994 #text\_change 07-May-1999

C;Accession: PC2171

R;Kobno, M.; Kugimiya, W.; Hashimoto, Y.; Morita, Y.

Biosci. Biotechnol. Biochem. 58, 1007-1012, 1994

A;Title: Purification, characterization, and crystallization of two types of lipase from

A;Reference number: PC2171; MUID:94319059; PMID:7765029

A;Accession: PC2171

A;Molecule type: protein

A;Residues: 1-10 <KOH>

C;Comment: This enzyme catalyzes the hydrolysis of the ester bonds.

C;Keywords: carboxylic ester hydrolase

Query Match 30.0%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5  
|||  
Db 5 LPP 7

# RESULT 9

S18396  
Probable glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) - Acetobacter hansenii (fragm

C;Species: Acetobacter hansenii

C;Date: 19-Mar-1997 #sequence\_revision 01-Feb-1999 #text\_change 01-Feb-1999

C;Accession: S18396

R;Levy, H.R.; Cook, C.

Arch. Biochem. Biophys. 291, 161-167, 1991

A;Title: Purification and properties of NADP-linked glucose-6-phosphate dehydrogenase fr

A;Reference number: S18396; MUID:92027789; PMID:1929428

A;Accession: S18396

A;Molecule type: protein

A;Residues: 1-10 <LEV>

A;Keywords: carboxylic ester hydrolase

A;Keywords: carboxylic ester hydrolase

A;Keywords: carboxylic ester hydrolase

A;Keywords: carboxylic ester hydrolase

A;Keywords: carboxylic ester hydrolase

A;Keywords: carboxylic ester hydrolase

A;Keywords: carboxylic ester hydrolase

A;Keywords: carboxylic ester hydrolase

A;Experimental source: ATCC 23769

C;Function:

A;Description: catalyzes reduction of glucose-6-phosphate to gluconolactone 6-phospha

A;Pathway: pentose phosphate pathway

C;Keywords: oxidoreductase; homotetramer; NADP; pentose phosphate pathway

Query Match 30.0%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5  
|||  
Db 3 LPP 5

# RESULT 10

C39745  
sphingomyelinase - Rhodococcus sp. (fragment)

C;Species: Rhodococcus sp.

C;Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 30-Sep-1993

C;Accession: C39745

R;Ito, M.; Ikegami, Y.; Yamagata, T.

J. Biol. Chem. 266, 7919-7926, 1991

A;Title: Activator proteins for glycosphingolipid hydrolysis by endoglycoceramidas.

ble using these activator proteins.

A;Reference number: A39745; MUID:91210321; PMID:1850427

A;Accession: C39745

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <ITO>

A;Residues: 1-10 <ITO>

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A;Residues: 1-10 <ITO>

A;Residues: 1-10 <ITO>

A;Residues: 1-10 <ITO>

A;Residues: 1-10 <ITO>

A;Residues: 1-10 <ITO>

A;Residues: 1-10 <ITO>

A;Residues: 1-10 <ITO>

A;Residues: 1-10 <ITO>

A;Residues: 1-10 <ITO>

A;Residues: 1-10 <ITO>

A;Residues: 1-10 <ITO>

A;Residues: 1-10 <ITO>

A;Residues: 1-10 <ITO>

A;Residues: 1-10 <ITO>

A;Residues: 1-10 <ITO>

A;Residues: 1-10 <ITO>

J. Protein Chem. 8, 115-130, 1989

A:Title: Microsequence analysis of winged bean seed proteins electrophoretically separated from two-dimensional gel electrophoresis  
A:Reference number: A61491; MUID:89351606; PMID:2765119  
A:Accession: C61497  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-11 <HIR>  
C:Keywords: glycoprotein; seed

Query Match 30.0%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PTV 7  
|||  
Db 3 PTV 5

#### RESULT 13

I33098  
173K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)  
C:Species: Plasmodium falciparum  
C:Date: 24-Aug-1990 #sequence\_revision 24-Aug-1990 #text\_change 09-Jun-2000  
C:Accession: I33098

R.Nichols, J.H.; Hager, L.P.  
submitted to the Protein Sequence Database, May 1990  
A:Reference number: A33098  
A:Accession: I33098  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-11 <NIC>

Query Match 30.0%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5  
|||  
Db 2 LPP 4

#### RESULT 14

A60856  
inhibin alpha chain - sheep (fragment)  
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C:Accession: A60856  
R:Leversha, L.J.; Robertson, D.W.; de Vos, F.L.; Morgan, F.J.; Hearn, M.T.W.; Wettenhall, J.  
A:Title: Isolation of inhibin from ovine follicular fluid.  
A:Reference number: A60856; MUID:87224684; PMID:3585232  
A:Accession: A60856  
A:Molecule type: protein  
A:Residues: 1-13 <LEV>

C:Comment: Inhibin suppresses follicle-stimulating hormone secretion.  
C:Superfamily: inhibin  
C:Keywords: disulfide bond; glycoprotein; gonad; heterodimer; hormone

Query Match 30.0%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4  
|||  
Db 4 PLP 6

#### RESULT 15

S15755  
actin 7 - soybean (fragment)  
C:Species: Glycine max (soybean)  
C:Date: 20-Feb-1995 #sequence\_revision 29-May-1998 #text\_change 13-Aug-1999  
C:Accession: S15755

R:Pearson, L.; Meagher, R.B.  
Plant Mol. Biol. 14, 513-526, 1990  
A:Title: Diverse soybean actin transcripts contain a large intron in the 5' untranslated region  
A:Reference number: S15754; MUID:91346640; PMID:2102831  
A:Accession: S15755  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-13 <PEA>

C:Cross-references: EMBL:X17120; NID:G18527; PIDN:CAA34980.1; PID:G18528  
C:Superfamily: actin  
C:Keywords: cytoskeleton; structural protein

Query Match 30.0%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPL 3  
|||  
Db 8 QPL 10

#### RESULT 16

A40207  
cell surface glycoprotein gp150 - slime mold (Dictyostelium discoideum) (fragment)  
C:Species: Dictyostelium discoideum  
C:Date: 28-Aug-1992 #sequence\_revision 28-Aug-1992 #text\_change 31-Dec-1993  
C:Accession: A40207

R:Gao, E.N.; Shier, P.; Siu, C.H.  
J. Biol. Chem. 267, 9409-9415, 1992  
A:Title: Purification and partial characterization of a cell adhesion molecule (gp150) from Dictyostelium discoideum  
A:Reference number: A40207; MUID:92250549; PMID:1577768  
A:Accession: A40207

A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-13 <GAO>  
C:Keywords: glycoprotein

Query Match 30.0%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPT 6  
|||  
Db 3 PPT 5

#### RESULT 17

PQ0152  
18K iron-sulfur protein - Chlamydomonas reinhardtii chloroplast (fragment)  
N:Alternate names: frxB homolog  
C:Species: chloroplast Chlamydomonas reinhardtii  
C:Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 30-Sep-1993  
C:Accession: PQ0152  
R:Wu, M.; Nie, Z.Q.; Yang, J.

Plant Cell 1, 551-557, 1989  
A:Title: The 18-KD protein that binds to the chloroplast DNA replicative origin is a component of the 18-KD protein complex  
A:Reference number: PQ0152; MUID:92404720; PMID:2562513  
A:Accession: PQ0152

A:Molecule type: protein  
A:Residues: 1-14 <WUM>  
C:Genetics:  
A:Genome: chloroplast  
C:Keywords: chloroplast

Query Match 30.0%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 MFP 10  
|||  
Db 1 MFP 3



## RESULT 18.

C33098  
223K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)  
C:Species: Plasmodium falciparum  
C:Date: 24-Aug-1990 #sequence\_revision 24-Aug-1990 #text\_change 09-Jun-2000  
C:Accession: C33098

R:Nichols, J.H.; Hager, L.P.  
submitted to the Protein Sequence Database, May 1990

A:Reference number: A33098

A:Accession: C33098

A>Status: Preliminary

A:Molecule type: protein

A:Residues: 1-14 <NIC>

Query Match 30.0%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LPP 5  
|||  
Db 2 LPP 4

## RESULT 19

PH1566

cerebrin 30 - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 05-Aug-1994 #sequence\_revision 05-Aug-1994 #text\_change 07-May-1999

C:Accession: PH1566

R:Leone, M.G.; Saso, L.; Vecchio, A.D.; Mo, M.; Silvestrini, B.; Cheng, C.Y.

J. Neurochem. 61, 533-540, 1993

A:Title: Micropurification of two human cerebrospinal fluid proteins by high performance

A:Reference number: PH1566; MUID:93329419; PMID:8336140

A:Accession: PH1566

A:Molecule type: protein

A:Residues: 1-14 <LEO>

Query Match 30.0%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPL 3  
|||  
Db 9 QPL 11

## RESULT 20

PH1348

Ig heavy chain DJ region (clone C100-106) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999

C:Accession: PH1348

R:Wasserman, R.; Galli, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.

J. Exp. Med. 176, 1577-1581, 1992

A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph

A:Reference number: PH1302; MUID:93094761; PMID:1460419

A:Accession: PH1348

A:Molecule type: DNA

A:Residues: 1-14 <WAS>

C:Keywords: heterotetramer; immunoglobulin

Query Match 30.0%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPT 6  
|||  
Db 4 PPT 6

## RESULT 21

H83778

hypothetical protein BH1032 [imported] - Bacillus halodurans (strain C-125)

C:Species: Bacillus halodurans  
C:Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001  
C:Accession: H83778  
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H  
Nucleic Acids Res. 28, 4317-4331, 2000  
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a  
submitted to the Protein Sequence Database, May 1990  
A:Reference number: A83650; MUID:20512582; PMID:11058132  
A:Accession: H83778  
A>Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-14 <STO>  
A:Cross-references: GB:AP001510; GB:BA000004; NID:GI0173440; PIDN:BA04751.1; GSPDB:C  
A:Experimental source: strain C-125  
C:Genetics:  
A:Gene: BH1032

Query Match 30.0%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TVM 8  
|||  
Db 8 TVM 10

## RESULT 22

PQ0545

capsid protein VP19C - human herpesvirus 1 (fragment)

C:Species: human herpesvirus 1

C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 07-May-1999

C:Accession: PQ0545

R:Davidson, M.D.; Rixon, F.J.; Davidson, A.J.

J. Gen. Virol. 73, 2709-2713, 1992

A:Title: Identification of genes encoding two capsid proteins (VP24 and VP26) of herp

A:Reference number: PQ0544; MUID:93019027; PMID:1328483

A:Accession: PQ0545

A:Molecule type: protein

A:Residues: 1-15 <DAV>

A:Experimental source: strain 17

C:Genetics:

A:Gene: UL38

C:Keywords: capsid protein

Query Match 30.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLP 4  
|||  
Db 5 PLP 7

## RESULT 23

B39109

hypothetical 1.5K protein - hepatitis C virus

N:Alternate names: hypothetical protein 2

C:Species: hepatitis C virus

C:Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 07-May-1999

C:Accession: B39109; JQ1585

R:Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Tek

Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991

A:Title: Characterization of the terminal regions of hepatitis C viral RNA: identific

A:Reference number: A39109; MUID:91156678; PMID:1705704

A:Accession: B39109

A>Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-15 <HAN>

A:Cross-references: GB:M58406

R:Kumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.

J. Gen. Virol. 73, 1521-1525, 1992

A:Title: Cloning and sequencing of the structural region and expression of putative c

A:Reference number: JQ1584; MUID:92300349; PMID:1318944

A:Accession: JQ1585

A:Molecule type: genomic RNA  
A:Residues: 1-15 <KUM>  
A:Experimental source: strain U.K.

Query Match 30.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4  
|||  
Db 10 PLP 12

## RESULT 24

S29386

nigerythrins - Desulfovibrio vulgaris

C:Species: Desulfovibrio vulgaris

C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 17-Mar-1999

C:Accession: S29386

R:Pierik, A.J.; Wolbert, R.B.G.; Portier, G.L.; Verhagen, M.F.J.M.; Hagen, W.R.

Eur. J. Biochem. 212, 237-245, 1993

A:Title: Nigerythrins and rubrerythrins from Desulfovibrio vulgaris each contain two monon

A:Reference number: S29385; PMID:93185629; PMID:8383040

A:Accession: S29386

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-15 <PIE>

Query Match 30.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PTV 7  
|||  
Db 8 PTV 10

## RESULT 25

PA0060

protein QF200037 - fungus (Fusarium sporotrichioides) (fragment)

C:Species: Fusarium sporotrichioides

C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001

C:Accession: PA0060

R:Chow, L.P.; Fukaya, N.; Sugiyama, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.

submitted to JIPID, October 1994

A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich

A:Reference number: PA0051

A:Accession: PA0060

A:Molecule type: protein

A:Residues: 1-15 <CHO>

Query Match 30.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4  
|||  
Db 4 PLP 6

## RESULT 26

B61457

alpha-glucosidase (EC 3.2.1.20) - Tetrahymena pyriformis (strain W) (fragment)

C:Species: Tetrahymena pyriformis

C>Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 07-Dec-1999

C:Accession: B61457

R:Banno, Y.; Sasaki, N.; Yoshino, T.; Mochizuki, J.I.; Hirata, H.; Nozawa, Y.

J. Protozool. 36, 562-567, 1989

A:Title: A thermostable acid alpha-glucosidase from Tetrahymena thermophila: purification

A:Reference number: A61457; PMID:90095988; PMID:2689637

A:Accession: B61457

A:Molecule type: protein

A:Residues: 1-15 <BAN>

C:Genetics:

A:Genetic code: SGCS

C:Keywords: extracellular protein; glycoprotein; glycosidase; hydrolase; lysosome; m

Query Match 30.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5  
|||  
Db 2 LPP 4

## RESULT 27

F44908

chitinase (EC 3.2.1.14), 23.4K - Streptomyces olivaceoviridis (fragment)

C:Species: Streptomyces olivaceoviridis

C>Date: 01-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 26-May-2000

C:Accession: F44908

R:Romaguera, A.; Menge, U.; Breves, R.; Diekmann, H.

J. Bacteriol. 174, 3450-3454, 1992

A:Title: Chitinases of Streptomyces olivaceoviridis and significance of processing f

A:Reference number: A44908; PMID:92276319; PMID:1592803

A:Accession: F44908

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-16 <ROM>

A:Experimental source: ATCC 11238

A>Note: sequence extracted from NCBI backbone (NCBI:104594)

C:Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology

C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 30.0%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 MFP 10  
|||  
Db 6 MFP 8

## RESULT 28

AS4877

alpha-conotoxin Pn1A [validated] - cone shell (Conus pennaceus)

N:Alternate names: alpha-CTX-Pn1A

C:Species: Conus pennaceus

C>Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 15-Sep-2000

C:Accession: AS4877

R:Fainzilber, M.; Hasson, A.; Oren, R.; Burlingame, A.L.; Gordon, D.; Spira, M.E.; Z

Biochemistry 33, 9523-9529, 1994

A:Title: New mollusc-specific alpha-conotoxins block Aplysia neuronal acetylcholine

A:Reference number: AS4877; PMID:94347719; PMID:8068627

A:Accession: AS4877

A:Molecule type: protein

A:Residues: 1-16 <PAI>

R:Hu, S.H.; Gehrmann, J.; Guddat, L.W.; Alewood, P.F.; Craik, D.J.; Martin, J.L.

submitted to the Brookhaven Protein Data Bank, January 1996

A:Reference number: A66355; PDB:1PEN

A:Contents: annotation; X-ray crystallography, 1.1 angstroms; residues 1-16

C:Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsy

C:Superfamily: alpha-conotoxin

C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic ne

F16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 30.0%; Score 3; DB 2; Length 16;

Best Local Similarity 100.0%; Pred. No. 2.4e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5  
|||  
Db 5 LPP 7

## RESULT 29

B54877  
 A:Gene: Cs  
 A:Cross-references: FlyBase:FBgn0002036  
 C:Species: Conus pennaceus  
 C:Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 23-May-1997  
 C:Accession: B54877  
 R:Faizilber, M.; Hasson, A.; Oren, R.; Burlingame, A.L.; Gordon, D.; Spira, M.E.; Zlotk  
 Biochemistry 33, 9523-9529, 1994  
 A:Title: New mollusc-specific alpha-conotoxins block Aplysia neuronal acetylcholine rece  
 A:Reference number: A54877; MUID:94347719; PMID:8068627  
 A:Accession: B54877  
 A:Molecule type: protein  
 A:Residues: 1-16 <EAL>  
 C:Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynap  
 C:Superfamily: alpha-conotoxin  
 C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuro  
 F:2-6,3-16/Disulfide bonds: #status experimental  
 F:16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 30.0%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LPP 5  
 ||||  
 Db 5 LPP 7

## RESULT 30

B58503  
 A:Gene: Cs  
 A:Cross-references: EMBL:X05991; NID:g7759; PIDN:CAA29407.1; PID:g7762  
 C:Species: unidentified bacterium  
 C:Date: 07-Feb-1997 #sequence\_revision 07-Feb-1997 #text\_change 05-Mar-1999  
 C:Accession: B58503  
 R:Binette, J.P.; Binette, M.B.  
 submitted to the Protein Sequence Database, October 1996  
 A:Description: The proteins of kidney and gallbladder stones.  
 A:Reference number: A58501  
 A:Accession: B58503  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-16 <BIN>  
 A:Experimental source: human bladder and kidney stones  
 C:Function:  
 A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen  
 C:Keywords: metalloprotein; oxidoreductase

Query Match 30.0%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LPP 5  
 ||||  
 Db 5 LPP 7

## RESULT 31

S01104  
 A:Gene: Cs  
 A:Cross-references: EMBL:X05991; NID:g7759; PIDN:CAA29407.1; PID:g7762  
 C:Species: Drosophila melanogaster  
 C:Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 21-Jul-2000  
 C:Accession: S01104  
 R:Evaleth, D.D.; Marsh, J.L.  
 Mol. Gen. Genet. 209, 290-298, 1987  
 A:Title: Overlapping transcription units in Drosophila: sequence and structure of the Cs  
 A:Reference number: S01102; MUID:88038375; PMID:3478553  
 A:Accession: S01104  
 A:Molecule type: DNA  
 A:Residues: 1-16 <EVE>  
 A:Cross-references: EMBL:X05991; NID:g7759; PIDN:CAA29407.1; PID:g7762  
 C:Genetics:

## A:Gene: Cs

A:Cross-references: FlyBase:FBgn0002036

## Query Match

Best Local Similarity 30.0%; Score 3; DB 2; Length 16;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PTV 7  
 ||||

Db 13 PTV 15

## RESULT 32

S15754  
 A:Gene: Cs  
 A:Cross-references: EMBL:X17119; NID:g18525; PIDN:CAA34979.1; PID:g18526  
 C:Species: Glycine max (soybean)  
 C:Date: 04-Dec-1992 #sequence\_revision 04-Dec-1992 #text\_change 13-Aug-1999  
 C:Accession: S15754; S08049  
 R:Pearson, L.; Mesgher, R.B.  
 Plant Mol. Biol. 14, 513-526, 1990  
 A:Title: Diverse soybean actin transcripts contain a large intron in the 5' untransla  
 A:Reference number: S15754; MUID:91346640; PMID:2102831  
 A:Accession: S15754  
 A:Molecule type: DNA  
 A:Residues: 1-17 <PEA>  
 A:Cross-references: EMBL:X17119; NID:g18525; PIDN:CAA34979.1; PID:g18526  
 C:Superfamily: actin  
 C:Keywords: cytoskeleton

Query Match 30.0%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPL 3  
 ||||

Db 8 QPL 10

## RESULT 33

S32587  
 A:Gene: Cs  
 A:Cross-references: EMBL:X17119; NID:g18525; PIDN:CAA34979.1; PID:g18526  
 C:Species: Spinacia oleracea (spinach)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 30-Sep-1993  
 C:Accession: S32587; S15878  
 R:Kubo, A.; Saji, H.; Tanaka, K.; Kondo, N.  
 Plant Mol. Biol. 18, 691-701, 1992  
 A:Title: Cloning and sequencing of a cDNA encoding ascorbate peroxidase from Arabidop  
 A:Reference number: S20866; MUID:92216045; PMID:11558944  
 A:Accession: S32587  
 A:Molecule type: protein  
 A:Residues: 1-17 <KUB>  
 A:Note: this is a revision to the sequence from reference S15878  
 R:Tanaka, K.; Takeuchi, E.; Kubo, A.; Sakaki, T.; Haraguchi, K.; Kawamura, Y.  
 Arch. Biochem. Biophys. 286, 371-375, 1991  
 A:Title: Two immunologically different isoforms of ascorbate peroxidase from spinach  
 A:Reference number: S15878; MUID:91378325; PMID:1897962  
 A:Accession: S15878  
 A:Molecule type: protein  
 A:Residues: 1,3-17 <TAN>  
 A:Note: this sequence has been revised in reference S20866  
 C:Keywords: chloroplast; oxidoreductase

Query Match 30.0%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PTV 7  
 ||||

Db 5 PTV 7

## RESULT 34

S59481

hydroxyproline-rich cell wall glycoprotein, 230K - kidney bean (fragment)  
 C:Species: Phaseolus vulgaris (kidney bean)  
 C>Date: 27-Apr-1996 #sequence\_revision 19-Jul-1996 #text\_change 05-Dec-1998  
 C:Accession: S59481  
 R:Wojtaszek, P.; Trethowan, J.; Bolwell, G.P.  
 Plant Mol. Biol. 28, 1075-1087, 1995

A:Title: Specificity in the immobilisation of cell wall proteins in response to different  
 A:Reference number: S59481; MUID:96011753; PMID:7548825  
 A:Accession: S59481  
 A:Molecule type: protein  
 A:Residues: 1-17 <WOL>  
 C:Keywords: glycoprotein; hydroxyproline  
 F;6,8,9,10,11/Modified site: hydroxyproline (Pro) #status experimental

Query Match 30.0%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5  
 |||  
 Db 4 LPP 6

## RESULT 35

I55612  
 thyroid hormone receptor beta - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999  
 C:Accession: I55612  
 R:Adams, M.; Matthews, C.; Collingwood, T.N.; Tone, Y.; Beck-Peccoz, P.; Chatterjee, K.K.  
 J. Clin. Invest. 94, 506-515, 1994

A:Title: Genetic analysis of 29 kindreds with generalized and pituitary resistance to th  
 A:Reference number: I55612; MUID:94314950; PMID:8040303  
 A:Accession: I55612  
 A>Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-17 <RES>  
 A:Cross-references: GB:S72623; NID:G633779; PIDN:AAB31420.1; PID:G633780  
 C:Genetics:  
 A:Gene: TRbeta

Query Match 30.0%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5  
 |||  
 Db 5 LPP 7

## RESULT 36

S04229  
 N4-(beta-N-acetylglucosaminyl)-L-asparaginase (EC 3.5.1.26) 24K chain - rat (fragment)

A:Alternate names: glycosylasparaginase  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 30-Sep-1993  
 C:Accession: S04229

R:Tollersrud, O.K.; Aronson Jr., N.N.  
 Biochem. J. 260, 101-108, 1989  
 A:Title: Purification and characterization of rat liver glycosylasparaginase.  
 A:Reference number: S04228; MUID:89374025; PMID:2775174

A:Accession: S04229  
 A:Molecule type: protein  
 A:Residues: 1-18 <TOL>  
 C:Superfamily: N4-(beta-N-acetylglucosaminyl)-L-asparaginase  
 C:Keywords: hydrolase

Query Match 30.0%; Score 3; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4  
 |||

Db 3 PLP 5

## RESULT 37

PC2280  
 prollylendopeptidase-inhibiting peptide - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)  
 C>Date: 28-Feb-1995 #sequence\_revision 05-Apr-1995 #text\_change 09-May-1997  
 C:Accession: PC2280  
 R:Ohmori, T.; Nakagami, T.; Tanaka, H.; Maruyama, S.  
 Biochem. Biophys. Res. Commun. 202, 809-815, 1994  
 A:Title: Isolation of prollylendopeptidase-inhibiting peptides from bovine brain.  
 A:Reference number: PC2280; MUID:94324971; PMID:8048952

A:Accession: PC2280  
 A:Molecule type: protein  
 A:Residues: 1-18 <OHM>  
 A:Experimental source: brain  
 C:Superfamily: cytoskeletal keratin

Query Match 30.0%; Score 3; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4  
 |||  
 Db 4 PLP 6

## RESULT 38

S39845  
 2-aminobenzoate-CoA ligase, anaerobic - Pseudomonas sp. (strain KB740) (fragment)  
 C:Species: Pseudomonas sp.  
 C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 13-Jan-1995  
 C:Accession: S39845  
 R:Altenschmidt, U.; Fuchs, G.  
 Eur. J. Biochem. 205, 721-727, 1992  
 A:Title: Novel aerobic 2-aminobenzoate metabolism. Purification and characterization  
 from a denitrifying Pseudomonas sp.  
 A:Reference number: S22402; MUID:92241310; PMID:1315272

A:Accession: S39845  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-10, 'X', 12-14, 'X', 16-18 <ALT>

Query Match 30.0%; Score 3; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5  
 |||  
 Db 12 LPP 14

## RESULT 39

B45138  
 arsenite oxidase I - Alcaligenes faecalis (fragment)

C:Species: Alcaligenes faecalis  
 C>Date: 30-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 04-Dec-1994  
 C:Accession: B45138  
 R:Anderson, G.L.; Williams, J.; Hille, R.  
 J. Biol. Chem. 267, 23674-23682, 1992

A:Title: The purification and characterization of arsenite oxidase from Alcaligenes  
 A:Reference number: A45138; MUID:93054722; PMID:1331097

A:Accession: B45138  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-18 <AND>

A>Note: sequence extracted from NCBI backbone (NCBIP:118543)

Query Match 30.0%; Score 3; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy . 3 LPP 5  
|||  
Db 9 LPP 11

## RESULT 40

S10452  
hypothetical protein (bpha 5' region) - Aspergillus niger  
C;Species: Aspergillus niger  
C;Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 09-Sep-1997  
C;Accession: S10452  
R;van Gorcom, R.F.M.; Boschloo, J.G.; Kuijvenhoven, A.; Lange, J.; Bos, C.J.; van Balken  
submitted to the EMBL Data Library, March 1990  
A;Reference number: S10452  
A;Accession: S10452  
A;Molecule type: DNA  
A;Residues: 1-18 <VAN>  
A;Cross-references: EMBL:X52521; NID:g2336; PID:g2337

Query Match 30.0%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPL 3  
|||  
Db 4 QPL 6

## RESULT 41

A54195  
Na+/K+-exchanging ATPase (EC 3.6.3.9) - spiny dogfish (fragment)  
C;Species: Squalus acanthias (spiny dogfish)  
C;Date: 13-Oct-1994 #sequence\_revision 18-Nov-1994 #text\_change 19-Apr-2002  
C;Accession: A54195  
R;Esmann, M.; Karlisch, S.J.; Sottrup-Jensen, L.; Marsh, D.  
Biochemistry 33, 8044-8050, 1994

A;Title: Structural integrity of the membrane domains in extensively trypsinized Na,K-ATPase  
A;Reference number: A54195; MUID:94297020; PMID:8025109  
A;Accession: A54195  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-18 <ESM>  
A;Experimental source: rectal gland  
A;Note: sequence extracted from NCBI backbone (NCBIP:149363)  
C;Keywords: hydrolase

Query Match 30.0%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPT 6  
|||  
Db 9 PPT 11

## RESULT 42

S60633  
H+-transporting two-sector ATPase [EC 3.6.3.14] protein 8 - brine shrimp mitochondrion  
C;Species: mitochondrion Artemia sp. (brine shrimp)  
A;Variety: strain La Mata  
C;Date: 27-Apr-1996 #sequence\_revision 13-Mar-1997 #text\_change 03-Jun-2002  
C;Accession: S60633  
R;Perez, M.L.; Valverde, J.R.; Batuecas, B.; Amat, F.; Marco, R.; Garesse, R.  
J. Mol. Evol. 38, 156-168, 1994

A;Title: Speciation in the Artemia genus: mitochondrial DNA analysis of bisexual and parthenogenetic strains  
A;Reference number: S60624; MUID:94223692; PMID:8169960  
A;Accession: S60633  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-19 <PER>  
A;Cross-references: EMBL:X67263; NID:g11210; PIDN:CAA47685.1; PID:g11211  
A;Experimental source: strain La Mata  
A;Note: the source is designated as Artemia parthenogenetica

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992  
C;Genetics:  
A;Gene: ATP8  
A;Genome: mitochondrion  
A;Genetic code: SGC4  
C;Superfamily: H+-transporting ATP synthase protein 8  
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion;

Query Match 30.0%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLP 4  
|||  
Db 6 PLP 8

## RESULT 43

C32735  
thyroglobulin - pig (fragment)  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 20-Jul-1990 #sequence\_revision 20-Jul-1990 #text\_change 11-Apr-1997  
C;Accession: C32735  
R;Rawitch, A.B.; Litwer, M.R.; Gregg, J.; Turner, C.D.; Rouse, J.B.; Hamilton, J.W.  
Biochem. Biophys. Res. Commun. 118, 423-429, 1984  
A;Title: The isolation of identical thyroxine containing amino acid sequences from bovine thyroglobulin  
A;Reference number: A32735; MUID:84153804; PMID:6704086  
A;Accession: C32735  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-19 <RAW>  
C;Superfamily: thyroglobulin; cholinesterase homology; thyroglobulin type I repeat homology  
C;Keywords: dimer; glycoprotein; iodine; thyroid gland; thyroid hormone biosynthesis  
F;5/Modified site: thyroxine (Tyr) #status predicted

Query Match 30.0%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPL 3  
|||  
Db 10 QPL 12

## RESULT 44

B32735  
thyroglobulin - sheep (fragment)  
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C;Date: 20-Jul-1990 #sequence\_revision 20-Jul-1990 #text\_change 11-Apr-1997  
C;Accession: B32735  
R;Rawitch, A.B.; Litwer, M.R.; Gregg, J.; Turner, C.D.; Rouse, J.B.; Hamilton, J.W.  
Biochem. Biophys. Res. Commun. 118, 423-429, 1984  
A;Title: The isolation of identical thyroxine containing amino acid sequences from bovine thyroglobulin  
A;Reference number: A32735; MUID:84153804; PMID:6704086  
A;Accession: B32735  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-19 <RAW>  
C;Superfamily: thyroglobulin; cholinesterase homology; thyroglobulin type I repeat homology  
C;Keywords: dimer; glycoprotein; iodine; thyroid gland; thyroid hormone biosynthesis  
F;5/Modified site: thyroxine (Tyr) #status predicted

Query Match 30.0%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPL 3  
|||  
Db 10 QPL 12

## RESULT 45

B61409

```

genome polypeptide (clone L3/S2) - Skalica virus (fragment)
C:Species: Skalica virus
C:Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 17-Nov-2000
C:Accession: B61409
R:Guirakhoo, F.; Heinz, F.X.; Mandl, C.W.; Holzmann, H.; Kunz, C.; Griesikova, M.
J. Gen. Virol. 72, 333-338, 1991
A:Title: The relationship between the flaviviruses Skalica and Langat as revealed by mon
A:Reference number: A61409; MUID:91132129; PMID:1847173
A:Accession: B61409
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: genomic RNA
A:Residues: 1-19 <GUI>
C:Superfamily: yellow fever virus genome polypeptide

Query Match 30.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
Db 1 LPP 3

RESULT 46
A34467
36K microfibril-associated protein - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 08-Jun-1990 #sequence_revision 08-Jun-1990 #text_change 18-Jun-1993
C:Accession: A34467
R:Kobayashi, R.; Tashima, Y.; Masuda, H.; Shozawa, T.; Numata, Y.; Miyauchi, K.; Hayakawa
J. Biol. Chem. 264, 17437-17444, 1989
A:Title: Isolation and characterization of a new 36-kDa microfibril-associated glycoprotein
A:Reference number: A34467; MUID:90008913; PMID:2793866
A:Accession: A34467
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-19 <KOB>

Query Match 30.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPL 3
Db 16 QPL 18

RESULT 47
S21737
coulmarin 7-monoxygenase (EC 1.14.14.-) cytochrome P450 2A7 - western baboon (fragment)
N:Alternate names: coumarin 7-hydroxylase
C:Species: Papio papio (western baboon)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Mar-1999
C:Accession: S21737
R:Dalet-Beluche, I.; Boulenc, X.; Fabre, G.; Maurel, P.; Bonfils, C.
Eur. J. Biochem. 204, 641-648, 1992
A:Title: Purification of two cytochrome P450 isozymes related to CYP2A and CYP3A gene fa
A:Reference number: S21176; MUID:92174920; PMID:1541278
A:Accession: S21737
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <DAL>
C:Genetics:
A:Gene: CYP2A7
C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C:Keywords: heme; microsome; monooxygenase; oxidoreductase; transmembrane protein

Query Match 30.0%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TVM 8
Db 1

```

```

Db 16 TVM 18

RESULT 48
S29817
cytochrome P450 2C23 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 05-Mar-1999
C:Accession: S29817
R:Marie, S.; Rousset, F.; Cresteil, T.
Biochim. Biophys. Acta 1172, 124-130, 1993
A:Title: Age- and tissue-dependent expression of CYP2C23 in the rat.
A:Reference number: S29817; MUID:93176794; PMID:7679925
A:Accession: S29817
A:Molecule type: mRNA
A:Residues: 1-20 <MAR>
C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C:Keywords: heme; transmembrane protein

Query Match 30.0%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4
Db 4 PLP 6

RESULT 49
A39328
notechis II-5b nontoxic venom protein - common tiger snake (fragment)
C:Species: Notechis scutatus (common tiger snake, mainland tiger snake)
C:Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 30-Sep-1993
C:Accession: A39328
R:Yang, C.C.; Chang, L.S.; Wu, F.S.
Toxicol. 29, 1337-1344, 1991
A:Title: Venom constituents of Notechis scutatus (Australian tiger snake) f;
A:Reference number: A39328; MUID:92263371; PMID:1814009
A:Accession: A39328
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <YAN>
C:Superfamily: phospholipase A2

Query Match 30.0%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPL 3
Db 17 QPL 19

RESULT 50
A37111
ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain - spinach (fragment)
C:Species: Spinacia oleracea (spinach)
C:Date: 15-Feb-1991 #sequence_revision 15-Feb-1991 #text_change 12-Apr-1995
C:Accession: A37111
R:Sato, M.H.; Hisabori, T.; Yoshida, M.
J. Biol. Chem. 265, 13419-13422, 1990
A:Title: The 55-kDa polypeptide released from spinach thylakoid membranes with 1 M L
A:Reference number: A37111; MUID:90337936; PMID:2143183
A:Accession: A37111
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <SAT>
C:Superfamily: ribulose-bisphosphate carboxylase small chain
C:Keywords: carbon-carbon lyase; carboxy-lyase

Query Match 30.0%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 3 LPP 5  
Db 18 LPP 20

RESULT 51  
A54519  
tubulin alpha chain - Leishmania enriettii (fragment)  
C:Species: Leishmania enriettii  
C>Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 13-Aug-1999  
C:Accession: A54519  
R:Wirth, D.F.; Slater, C.  
Mol. Biochem. Parasitol. 9, 83-92, 1993  
A:Title: Isolation and characterization of an alpha-tubulin gene from Leishmania enriettii  
A:Reference number: A54519; MUID:84142075; PMID:6321982  
A:Accession: A54519  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-20 <WIR>  
A:Cross-references: GB:M28001; NID:g159409; PIDN:AAA29273.1; PID:g159410  
C:Superfamily: tubulin

Query Match 30.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PTV 7  
Db 2 PTV 4

RESULT 52  
T44453  
acetyl-CoA synthetase [imported] - Pseudomonas aeruginosa (fragment)  
C:Species: Pseudomonas aeruginosa  
C>Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jul-2000  
C:Accession: T44453  
R:Nishijyo, T.; Park, S.M.; Lu, C.D.; Itoh, Y.; Abdelal, A.T.  
J. Bacteriol. 180, 5559-5566, 1998  
A:Title: Molecular characterization and regulation of an operon encoding a system for the  
A:Reference number: 222777; MUID:99008987; PMID:9791103  
A:Accession: T44453  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-20 <NIS>  
A:Cross-references: EMBL:AF012537; NID:g2668593; PIDN:AAC71069.1; PID:g2668594  
A:Experimental source: strain PAO1

Query Match 30.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLP 4  
Db 11 PLP 13

RESULT 53  
PH1380  
alpha-amylase (EC 3.2.1.1) (Haim sensitive) - Bacillus sp. (fragment)  
C:Species: Bacillus sp.  
C>Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 07-May-1999  
C:Accession: PH1380  
R:Kawaguchi, T.; Nagae, H.; Murao, S.; Arai, M.  
Biosci. Biotechnol. Biochem. 56, 1792-1796, 1992  
A:Title: Purification and some properties of a Haim-sensitive alpha-amylase from newly  
A:Reference number: PH1380; MUID:93113087; PMID:1369074  
A:Accession: PH1380  
A:Molecule type: protein  
A:Residues: 1-20 <KAW>  
A:Experimental source: strain NO.195  
C:Comment: This enzyme has an optimum pH of 7.0.

C:Function:  
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds  
A:Pathway: glycogen/starch degradation  
C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 30.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VMF 9  
Db 11 VMF 13

RESULT 54  
S65605  
dimeric protein (BDP) - barley (fragment)  
C:Species: Hordeum vulgare (barley)  
C>Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 25-Apr-1997  
C:Accession: S65605  
R:Garcia-Casado, G.; Armentia, A.; Sanchez-Monge, R.; Sanchez, L.M.; Lopez-Otin, C.;  
FEBS Lett. 364, 36-40, 1995  
A:Title: A major baker's asthma allergen from rye flour is considerably more active t  
A:Reference number: S65604; MUID:95269763; PMID:7750539  
A:Accession: S65605  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-20 <GAR>

Query Match 30.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLP 4  
Db 18 PLP 20

RESULT 55  
A61093  
glue protein - California mussel (fragments)  
A:Alternate names: adhesive polyphenolic protein  
C:Species: Mytilus californianus (California mussel)  
C>Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 07-May-1999  
C:Accession: A61093  
R:Waite, J.H.  
J. Comp. Physiol. B 156, 491-496, 1986  
A:Title: Mussel glue from Mytilus californianus Conrad: a comparative study.  
A:Reference number: A61093; MUID:86279063; PMID:3734192  
A:Accession: A61093  
A:Molecule type: protein  
A:Residues: 1-20 <WAI>  
A:Note: the amino terminal residue was tentatively identified as Ser  
A:Note: 12-Ser was also found  
C:Comment: This glue protein is a component of the adhesive plaque of the byssus, the

Query Match 30.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPT 6  
Db 4 PPT 6

RESULT 56  
F24417

interphotoreceptor retinoid-binding protein - bush baby (fragment)  
 N:Alternate names: interstitial retinol-binding protein  
 C:Species: Galago sp. (bush baby)  
 C:Date: 21-May-1988 #sequence\_revision 21-May-1988 #text\_change 18-Jun-1993  
 C:Accession: F24417  
 R:Fong, S.L.; Cook, R.G.; Alvarez, R.A.; Liou, G.I.; Landers, R.A.; Bridges, C.D.B.  
 FEBS Lett. 205, 309-312, 1986  
 A:Title: N-terminal sequence homologies in interstitial retinol-binding proteins from 10  
 A:Reference number: A91365; MUID:86301171; PMID:3743780  
 A:Accession: F24417  
 A:Molecule type: protein  
 A:Residues: 1-20 <FON>

Query Match 30.0%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPL 3  
 |||  
 Db 5 QPL 7

RESULT 57  
 S03954  
 acidic fibroblast growth factor - pig (fragment)  
 N:Alternate names: alpha-endothelial cell growth factor  
 C:Species: Sus scrofa domestica (domestic pig)  
 C:Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 18-Jun-1993  
 C:Accession: S03954  
 R:Quinkler, W.; Masberg, M.; Bernotat-Danielowski, S.; Luethe, N.; Sharma, H.S.; Schape  
 Eur. J. Biochem. 181, 67-73, 1989  
 A:Title: Isolation of heparin-binding growth factors from bovine, porcine and canine hea  
 A:Reference number: S03953; MUID:89231704; PMID:2714282  
 A:Accession: S03954  
 A:Molecule type: protein  
 A:Residues: 1-20 <QUI>  
 C:Keywords: growth factor

Query Match 30.0%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5  
 |||  
 Db 3 LPP 5

RESULT 58  
 I53672  
 somatotropin - synthetic  
 C:Species: synthetic  
 C:Date: 07-Jun-1996 #sequence\_revision 31-Jul-1997 #text\_change 19-May-2000  
 C:Accession: I53672  
 R:Bogossian, G.; Bilyeu, K.; O'Neil, J.P.  
 Gene 133, 17-22, 1993  
 A:Title: Genome rearrangements by residual IS10 elements in strains of Escherichia coli  
 A:Reference number: I53672; MUID:94040791; PMID:8224890  
 A:Accession: I53672  
 A>Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-20 <BOG>  
 A:Cross-references: GB:S67119; NID:g455674; PIDN:AB28847.1; PID:g455675  
 A>Note: partial sequence of bovine somatotropin synthesized and expressed in Escherichia

Query Match 30.0%; Score 3; DB 4; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 MFP 10  
 |||  
 Db 1 MFP 3

RESULT 59  
 I78890  
 tyrosine protein kinase - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
 C:Accession: I78890  
 R:Chow, L.M.; Davidson, D.; Fournel, M.; Gosselin, P.; Lemieux, S.; Lyu, M.S.; Kozak,  
 Oncogene 9, 3437-3448, 1994  
 A:Title: Two distinct protein isoforms are encoded by ntK, a csk-related tyrosine pr  
 A:Reference number: I58407; MUID:95060800; PMID:7970703  
 A:Accession: I78890  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-3 <RES>  
 A:Cross-references: GB:L33339; NID:g609536; PIDN:AAA64432.1; PID:g609538  
 C:Genetics:  
 A:Gene: p52ntk

Query Match 20.0%; Score 2; DB 3; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PT 6  
 |||  
 Db 2 PT 3

RESULT 60  
 A32039  
 tyrosine-melanocyte-stimulating hormone release-inhibiting factor 1 - bovine  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 31-Jul-1989 #sequence\_revision 31-Jul-1989 #text\_change 18-Aug-2000  
 C:Accession: A32039  
 R:Horvath, A.; Kastin, A.J.  
 J. Biol. Chem. 264, 2175-2179, 1989  
 A:Title: Isolation of tyrosine-melanocyte-stimulating hormone release-inhibiting fac  
 A:Reference number: A32039; MUID:89123285; PMID:2563371  
 A:Accession: A32039  
 A:Molecule type: protein  
 A:Residues: 1-4 <HOR>  
 A:Experimental source: brain  
 C:Superfamily: unassigned animal peptides  
 C:Keywords: amidated carboxyl end  
 F:4/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 20.0%; Score 2; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PL 3  
 |||  
 Db 2 PL 3

RESULT 61  
 S53508  
 starvation-induced ribonuclease - tomato  
 C:Species: Lycopersicon esculentum (tomato)  
 C:Date: 01-Aug-1995 #sequence\_revision 01-Sep-1995 #text\_change 07-May-1999  
 C:Accession: S53508  
 R:Koeck, M.; Loeffler, A.; Abel, S.; Glund, K.  
 Plant Mol. Biol. 27, 477-485, 1995  
 A:Title: cDNA structure and regulatory properties of a family of starvation-induced  
 A:Reference number: S53506; MUID:95201242; PMID:7894013  
 A:Accession: S53508  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-4 <ROE>

Query Match 20.0%; Score 2; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Qy 5 PT 6  
||  
Db 2 PT 3

## RESULT 62

HOROHA

proctolin - American cockroach  
C;Species: Periplaneta americana (American cockroach)  
C;Date: 29-Jul-1981 #sequence\_revision 29-Jul-1981 #text\_change 23-Aug-1996  
C;Accession: A01644  
R;Starratt, A.N.; Brown, B.E.  
Life Sci. 17, 1253-1256, 1975  
A;Title: Structure of the pentapeptide proctolin, a proposed neurotransmitter in insects  
A;Reference number: A93048; MUID:76074708; PMID:576  
A;Accession: A01644  
A;Molecule type: protein  
A;Residues: 1-5 <STA>  
A;Note: the synthetic peptide had the same chromatographic, electrophoretic, and pharmacological properties as the natural peptide.  
R;O'Shea, M.; Adams, M.E.  
Science 213, 567-569, 1981  
A;Title: Pentapeptide (proctolin) associated with an identified neuron.  
A;Reference number: A94260; MUID:81225865; PMID:6113690  
A;Contents: annotation; biological source  
A;Comment: This peptide is found in the lateral white neurons, which occur (in the cockroach) innervate the striated hindgut muscles in insects and stimulate contraction of these muscles.  
A;Superfamily: proctolin  
C;Keywords: neuropeptide

Query Match 20.0%; Score 2; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LP 4  
||  
Db 3 LP 4

## RESULT 63

JN0860

peptidyl-dipeptidase A inhibitory peptide C107 - striped bonito  
C;Species: Sarda orientalis (striped bonito)  
C;Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 07-May-1999  
C;Accession: JN0860  
R;Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.  
Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993  
A;Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory peptide from striped bonito.  
A;Reference number: JN0859; MUID:94080036; PMID:7764272  
A;Accession: JN0860  
A;Molecule type: protein  
A;Residues: 1-5 <MAT>  
A;Experimental source: intestine  
A;Comment: The carboxyl-terminus is essential for the protein's expression of angiotensin I-converting enzyme inhibitory peptide.  
C;Superfamily: bradykinin-potentiating peptide  
C;Keywords: angiotensin-converting enzyme inhibitor

Query Match 20.0%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LP 4  
||  
Db 2 LP 3

## RESULT 64

E42364

flagellar protein flir - Salmonella typhimurium (fragment)  
C;Species: Salmonella typhimurium  
C;Date: 24-Jul-1992 #sequence\_revision 24-Jul-1992 #text\_change 30-Sep-1993  
C;Accession: E42364  
R;Vogler, A.P.; Homma, M.; Irikura, V.M.; Macnab, R.M.  
J. Bacteriol. 173, 3564-3572, 1991

A;Title: Salmonella typhimurium mutants defective in flagellar filament regrowth and flagellar assembly  
A;Reference number: A42364; MUID:91258342; PMID:1646201  
A;Accession: E42364  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-5 <VOG>  
A;Cross-references: GB:M62408

Query Match 20.0%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LP 4  
||  
Db 4 LP 5

## RESULT 65

PS0324

ribulose-bisphosphate carboxylase activase III - rice (strain Nihonbare) (fragment)  
C;Species: Oryza sativa (rice)  
C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 02-Jul-1998  
C;Accession: PS0324  
R;Tsugita, A.  
Submitted to JIPID, April 1993  
A;Reference number: PS0206  
A;Accession: PS0324  
A;Molecule type: protein  
A;Residues: 1-5 <TSU>  
A;Experimental source: leaf, chlorophyll

Query Match 20.0%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PT 6  
||  
Db 4 PT 5

## RESULT 66

B37988

acid proteinase light chain - slime mold (Physarum polycephalum) (fragment)  
C;Species: Physarum polycephalum  
C;Date: 28-Jun-1991 #sequence\_revision 28-Jun-1991 #text\_change 30-Sep-1993  
C;Accession: B37988  
R;Murakami-Murofushi, K.; Takahashi, T.; Minowa, Y.; Iino, S.; Takeuchi, T.; Kitagaki, J.  
J. Biol. Chem. 265, 19898-19903, 1990  
A;Title: Purification and characterization of a novel intracellular acid proteinase from Physarum polycephalum.  
A;Reference number: A37988; MUID:91060608; PMID:2246266  
A;Accession: B37988  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-5 <MUR>

Query Match 20.0%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PP 5  
||  
Db 3 PP 4

## RESULT 67

A60411

proctolin - Atlantic horseshoe crab  
C;Species: Limulus polyphemus (Atlantic horseshoe crab)  
C;Date: 03-Feb-1993 #sequence\_revision 03-Feb-1993 #text\_change 17-Mar-1999  
C;Accession: A60411  
R;Groome, J.R.; Willingham, E.K.; Townley, M.A.; Vetrovs, A.; Watson III, W.H.; Hunt, J.  
Peptides 11, 205-211, 1990  
A;Title: Identification of proctolin in the central nervous system of the horseshoe crab.

A:Reference number: A60411; MUID:90287800; PMID:2356151  
 A:Accession: A60411  
 A:Molecule type: protein  
 A:Residues: 1-5 <ARE>  
 C:Comment: This neuropeptide stimulates cardiac output and hindgut motility in the horse  
 C:Keywords: neuropeptide

Query Match 20.0%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LP 4  
 ||  
 Db 3 LP 4

## RESULT 68

G44817  
 27.5 kda structural protein - Leuconostoc oenos phase P32 (fragment)  
 C:Species: Leuconostoc oenos phase P32  
 C:Date: 31-Mar-1993 #sequence\_revision 22-May-1998 #text\_change 22-May-1998  
 C:Accession: G44817  
 R:Arendt, E.K.; Lonvaud, A.; Hammes, W.P.  
 J. Gen. Microbiol. 137, 2135-2139, 1991  
 A:Title: Lysogeny in Leuconostoc oenos.  
 A:Reference number: A44817; MUID:92085033; PMID:1748868  
 A:Accession: G44817  
 A:Molecule type: protein  
 A:Residues: 1-5 <ARE>  
 A:Note: sequence extracted from NCBI backbone (NCBIP:70333)

Query Match 20.0%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TV 7  
 ||  
 Db 2 TV 3

## RESULT 69

I44817  
 27.5K structural protein - Leuconostoc oenos phase P37 (fragment)  
 C:Species: Leuconostoc oenos phase P37  
 C:Date: 31-Mar-1993 #sequence\_revision 22-May-1998 #text\_change 22-May-1998  
 C:Accession: I44817  
 R:Arendt, E.K.; Lonvaud, A.; Hammes, W.P.  
 J. Gen. Microbiol. 137, 2135-2139, 1991  
 A:Title: Lysogeny in Leuconostoc oenos.  
 A:Reference number: A44817; MUID:92085033; PMID:1748868  
 A:Accession: I44817  
 A:Molecule type: protein  
 A:Residues: 1-5 <ARE>  
 A:Note: sequence extracted from NCBI backbone (NCBIP:70330)

Query Match 20.0%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TV 7  
 ||  
 Db 2 TV 3

## RESULT 70

E44817  
 27.5K structural protein - Leuconostoc oenos phase P54 (fragment)  
 C:Species: Leuconostoc oenos phase P54  
 C:Date: 31-Mar-1993 #sequence\_revision 22-May-1998 #text\_change 22-May-1998  
 C:Accession: E44817  
 R:Arendt, E.K.; Lonvaud, A.; Hammes, W.P.  
 J. Gen. Microbiol. 137, 2135-2139, 1991  
 A:Title: Lysogeny in Leuconostoc oenos.

A:Reference number: A44817; MUID:92085033; PMID:1748868  
 A:Accession: E44817  
 A:Molecule type: protein  
 A:Residues: 1-5 <ARE>  
 A:Note: sequence extracted from NCBI backbone (NCBIP:70336)

Query Match 20.0%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TV 7  
 ||  
 Db 2 TV 3

## RESULT 71

C44817  
 28.5K structural protein - Leuconostoc oenos phase PAT5-12 (fragment)  
 C:Species: Leuconostoc oenos phase PAT5-12  
 C:Date: 31-Mar-1993 #sequence\_revision 22-May-1998 #text\_change 22-May-1998  
 C:Accession: C44817  
 R:Arendt, E.K.; Lonvaud, A.; Hammes, W.P.  
 J. Gen. Microbiol. 137, 2135-2139, 1991  
 A:Title: Lysogeny in Leuconostoc oenos.  
 A:Reference number: A44817; MUID:92085033; PMID:1748868  
 A:Accession: C44817  
 A:Molecule type: protein  
 A:Residues: 1-5 <ARE>  
 A:Note: sequence extracted from NCBI backbone (NCBIP:70341)

Query Match 20.0%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TV 7  
 ||  
 Db 2 TV 3

## RESULT 72

A44817  
 28K structural protein - Leuconostoc oenos phase PZT11-15 (fragment)  
 C:Species: Leuconostoc oenos phase PZT11-15  
 C:Date: 31-Mar-1993 #sequence\_revision 22-May-1998 #text\_change 22-May-1998  
 C:Accession: A44817  
 R:Arendt, E.K.; Lonvaud, A.; Hammes, W.P.  
 J. Gen. Microbiol. 137, 2135-2139, 1991  
 A:Title: Lysogeny in Leuconostoc oenos.  
 A:Reference number: A44817; MUID:92085033; PMID:1748868  
 A:Accession: A44817  
 A:Molecule type: protein  
 A:Residues: 1-5 <ARE>  
 A:Note: sequence extracted from NCBI backbone (NCBIP:70343)

Query Match 20.0%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TV 7  
 ||  
 Db 2 TV 3

## RESULT 73

A61049  
 halo-toxin - Pseudomonas syringae pv. mori  
 C:Species: Pseudomonas syringae pv. mori  
 A:Note: host mulberry tree  
 C:Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 21-Jan-1997  
 C:Accession: A61049  
 R:Kajimoto, T.; Yokomizo, K.; Yahiro, K.; Umeda, T.; Shoji, S.; Kubota, Y.; Shibata, Chem. Lett. 00, 679-680, 1989  
 A:Title: Structure of halo-toxin produced by phytopathogenic bacterium, Pseudomonas

A:Reference number: A61049  
A:Accession: A61049  
A:Molecule type: protein  
A:Residues: 1-6 <KAJ>  
A>Note: sequence confirmed by synthesis  
C:Comment: This toxin is one of the etiological agents of halo bright disease in mulberry  
C:Keywords: toxin

Query Match 20.0%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 FP 10  
||  
Db 2 FP 3

## RESULT 74

A27696  
contraction-inhibiting peptide I - blue mussel  
C:Species: Mytilus edulis (blue mussel)  
C>Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 08-Dec-1995  
C:Accession: A27696  
R:Hirata, T.; Kubota, I.; Iwasawa, N.; Takabatake, I.; Ikeda, T.; Muneoka, Y.  
Biochem. Biophys. Res. Commun. 152, 1376-1382, 1988  
A>Title: Structures and actions of Mytilus inhibitory peptides.  
A:Reference number: A90142; MUID:88240357; PMID:3377776  
A:Accession: A27696  
A:Molecule type: protein  
A:Residues: 1-6 <HIR>  
C:Keywords: amidated carboxyl end  
F:6/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 20.0%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 MF 9  
||  
Db 4 MF 5

## RESULT 75

B27696  
contraction-inhibiting peptide II - blue mussel  
C:Species: Mytilus edulis (blue mussel)  
C>Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 08-Dec-1995  
C:Accession: B27696  
R:Hirata, T.; Kubota, I.; Iwasawa, N.; Takabatake, I.; Ikeda, T.; Muneoka, Y.  
Biochem. Biophys. Res. Commun. 152, 1376-1382, 1988  
A>Title: Structures and actions of Mytilus inhibitory peptides.  
A:Reference number: A90142; MUID:88240357; PMID:3377776  
A:Accession: B27696  
A:Molecule type: protein  
A:Residues: 1-6 <HIR>  
C:Keywords: amidated carboxyl end  
F:6/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 20.0%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 MF 9  
||  
Db 4 MF 5

Search completed: November 25, 2003, 19:36:10  
Job time : 7.86047 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:17:40 ; Search time 3.54651 Seconds  
(without alignments)  
132.600 Million cell updates/sec

Title: US-09-641-801-25  
Perfect score: 10  
Sequence: 1 QPUPPTVMFP 10

Scoring table:  
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3  
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	30.0	8	1	CPD1_ENTPA
2	3	30.0	9	1	RT33_BOVIN
3	3	30.0	11	1	BPP2_AKHA
4	3	30.0	11	1	TIN4_HOPII
5	3	30.0	12	1	TIN2_HOPII
6	3	30.0	12	1	TIN3_HOPII
7	3	30.0	13	1	ACT7_SOYBN
8	3	30.0	14	1	ECDC_LYMDI
9	3	30.0	16	1	CXAA_CONPE
10	3	30.0	16	1	CXAB_CONPE
11	3	30.0	17	1	ACT6_SOYBN
12	3	30.0	18	1	UC21_MAIZE
13	3	30.0	20	1	BULB_NARPS
14	3	30.0	20	1	CPA7_PAPSP
15	2	20.0	5	1	E104_LITRU
16	2	20.0	5	1	PAP2_FARMA
17	2	20.0	5	1	PRCT_PERAM
18	2	20.0	6	1	CIP1_MYTED
19	2	20.0	6	1	CIP2_MYTED
20	2	20.0	6	1	TMOF_SARBU
21	2	20.0	6	1	TRPI_PSEPU
22	2	20.0	6	1	VF19_HSVIK
23	2	20.0	7	1	LANC_CARUI
24	2	20.0	7	1	TPFY_PACDA
25	2	20.0	7	1	TPFY_PACDA
26	2	20.0	7	1	UF04_MOUSE
27	2	20.0	7	1	UN06_PINPS
28	2	20.0	8	1	ACI_THUAL
29	2	20.0	8	1	ALL5_CALVO
30	2	20.0	8	1	ALL6_CVDPO
31	2	20.0	8	1	COW2_CONPU
32	2	20.0	8	1	NPB_BOVIN
33	2	20.0	8	1	PPK2_PERAM

RESULT 1

ALIGNMENTS

34	2	20.0	9	1	AL10_CARMA
35	2	20.0	9	1	COXE_THUOB
36	2	20.0	9	1	FAR3_PENMO
37	2	20.0	9	1	FAR3_PENMO
38	2	20.0	9	1	FAR5_ASCSU
39	2	20.0	9	1	FAR9_ACSU
40	2	20.0	9	1	FLA2_TREHY
41	2	20.0	9	1	FRF1_SARBU
42	2	20.0	9	1	KNL3_BOMVA
43	2	20.0	9	1	LMT3_LOCMI
44	2	20.0	9	1	OXYA_SQUAC
45	2	20.0	9	1	OXYT_EISFO
46	2	20.0	9	1	OXYT_RABIT
47	2	20.0	9	1	SAMP_MUSCA
48	2	20.0	9	1	TKC1_CALVO
49	2	20.0	9	1	UPA3_HUMAN
50	2	20.0	9	1	YBFR_AZOVI
51	2	20.0	10	1	AL15_CARMA
52	2	20.0	10	1	BPP2_BOTIN
53	2	20.0	10	1	BPP2_BOTIN
54	2	20.0	10	1	BPP2_BOTIN
55	2	20.0	10	1	BPP2_BOTIN
56	2	20.0	10	1	BPP2_BOTIN
57	2	20.0	10	1	BPP2_BOTIN
58	2	20.0	10	1	BPP2_BOTIN
59	2	20.0	10	1	BPP2_BOTIN
60	2	20.0	10	1	BPP2_BOTIN
61	2	20.0	10	1	BPP2_BOTIN
62	2	20.0	10	1	BPP2_BOTIN
63	2	20.0	10	1	BPP2_BOTIN
64	2	20.0	10	1	BPP2_BOTIN
65	2	20.0	10	1	BPP2_BOTIN
66	2	20.0	10	1	BPP2_BOTIN
67	2	20.0	10	1	BPP2_BOTIN
68	2	20.0	10	1	BPP2_BOTIN
69	2	20.0	10	1	BPP2_BOTIN
70	2	20.0	10	1	BPP2_BOTIN
71	2	20.0	10	1	BPP2_BOTIN
72	2	20.0	10	1	BPP2_BOTIN
73	2	20.0	10	1	BPP2_BOTIN
74	2	20.0	10	1	BPP2_BOTIN
75	2	20.0	10	1	BPP2_BOTIN
76	2	20.0	10	1	BPP2_BOTIN
77	2	20.0	10	1	BPP2_BOTIN
78	2	20.0	10	1	BPP2_BOTIN
79	2	20.0	10	1	BPP2_BOTIN
80	2	20.0	10	1	BPP2_BOTIN
81	2	20.0	10	1	BPP2_BOTIN
82	2	20.0	10	1	BPP2_BOTIN
83	2	20.0	10	1	BPP2_BOTIN
84	2	20.0	10	1	BPP2_BOTIN
85	2	20.0	10	1	BPP2_BOTIN
86	2	20.0	10	1	BPP2_BOTIN
87	2	20.0	10	1	BPP2_BOTIN
88	2	20.0	10	1	BPP2_BOTIN
89	2	20.0	10	1	BPP2_BOTIN
90	2	20.0	10	1	BPP2_BOTIN
91	2	20.0	10	1	BPP2_BOTIN
92	2	20.0	10	1	BPP2_BOTIN
93	2	20.0	10	1	BPP2_BOTIN
94	2	20.0	10	1	BPP2_BOTIN
95	2	20.0	10	1	BPP2_BOTIN
96	2	20.0	10	1	BPP2_BOTIN
97	2	20.0	10	1	BPP2_BOTIN
98	2	20.0	10	1	BPP2_BOTIN
99	2	20.0	10	1	BPP2_BOTIN
100	2	20.0	10	1	BPP2_BOTIN

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CPD1_ENTFA
ID CPD1_ENTFA STANDARD; PRT; 8 AA.
AC P13269;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Sex pheromone cPD1.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE.
RX MEDLINE=85040398; PubMed=6436978;
RA Suzuki A., Mori M., Sagakami Y., Isogai A., Fujino M., Kitada C.,
RA Craig R.A., Clewell D.B.;
RT "Isolation and structure of bacterial sex pheromone, cPD1.";
RL Science 226:849-850(1984).
CC -!- FUNCTION: CPD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
CC BACTERIOTICIN PLASMID PPD1.
KW Pheromone.
SQ SEQUENCE 8 AA; 913 MW; 8665B729C682C729 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VNF 9
DB 3 VNF 5

RESULT 2
RT33_BOVIN
ID RT33_BOVIN STANDARD; PRT; 9 AA.
AC P82926;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mitochondrial 28S ribosomal protein S33 (S33mt) (MRP-S33) (Fragment).
GN MRPS33.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX TISSUE=Liver;
RX MEDLINE=21276436; PubMed=11279123;
RA Koc B.C., Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;
RT "The small subunit of the mammalian mitochondrial ribosome:
RT Identification of the full complement of ribosomal proteins present.";
RL J. Biol. Chem. 276:19363-19374(2001).
CC -!- SUBUNIT: Component of the mitochondrial ribosome small subunit
CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.
CC -!- SUBCELLULAR LOCATION: Mitochondrial.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1032 MW; D341D73776DB05B9 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPL 3
DB 5 QPL 7

RESULT 3
BPPB_AKGHA
ID BPPB_AKGHA STANDARD; PRT; 11 AA.

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AC P01021;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide B (Angiotensin-converting
DE enzyme inhibitor).
OS Agkistrodon halys blomhoffi (Mamushi) (Gloydius blomhoffii).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Agkistrodon.
OX NCBI_TaxID=61300;
RN [1]
RP SEQUENCE.
RX TISSUE=Venom;
RA Kato H., Suzuki T.;
RT "Amino acid sequence of bradykinin-potentiating peptide isolated from
RT the venom of Agkistrodon halys blomhoffii.";
RL Proc. Jpn. Acad. B, Phys. Biol. Sci. 46:176-181(1970).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; A01254; XASNBA.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1199 MW; 295CBF0627741777 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
DB 3 LPP 5

RESULT 4
TIN4_HOPTI
ID TIN4_HOPTI STANDARD; PRT; 11 AA.
AC P82654;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tigerin-4.
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae;
OC Hoplobatrachus.
OX NCBI_TaxID=103373;
RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
RX TISSUE=Skin secretion;
RX PubMed=11031261;
RA Purna Sai K., Jagannadham M.V., Vairamani M., Raju N.P.,
RA Devi A.S., Nagaraj R., Sitaram N.;
RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
RT tigerina.";
RL J. Biol. Chem. 276:2701-2707(2001).
CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST B.SUBTILIS, E.COLI,
CC S.AUREUS, M.LUTEUS, P.PUTIDA AND S.CEREVISIAE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=1247; METHOD=MALDI.
KW Amphibian defense peptide; Antibiotic.
FT DISULFID 3 11
SQ SEQUENCE 11 AA; 1248 MW; 117D8EFD37605DCB CRC64;

Query Match 30.0%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4
DB 2 PLP 4

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Db          7 PLP 9
RESULT 5
TIN2 HOPTI
ID TIN2 HOPTI STANDARD; PRT; 12 AA.
AC P82652;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tigerin-2.
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;
OC Hoplobatrachus.
OX NCBI_TaxID=103373;
[1]
RN SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
RC TISSUE=Skin secretion;
RX PubMed=11031261;
RA Purna Sai K., Jagannadham M.V., Vairamani M., Raju N.P.,
RA Devi A.S., Nagaraj R., Sitarum N.;
RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
RT tigerina.";
RL J. Biol. Chem. 276:2701-2707(2001).
CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST B.SUBTILIS, E.COLI,
CC S.AUREUS, M.LUTEUS, P.PUTIDA AND S.CEREVISIAE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=1368; METHOD=MALDI.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT DISULFID 3 11
FT MOD RES 12 12 AMIDATION.
FT SEQUENCE 12 AA; 1369 MW; C2627D8EFD37605D CRC64;

Query Match 30.0%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLP 4
Db 7 PLP 9

RESULT 6
TIN3 HOPTI
ID TIN3 HOPTI STANDARD; PRT; 12 AA.
AC P82653;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tigerin-3.
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;
OC Hoplobatrachus.
OX NCBI_TaxID=103373;
[1]
RN SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
RC TISSUE=Skin secretion;
RX PubMed=11031261;
RA Purna Sai K., Jagannadham M.V., Vairamani M., Raju N.P.,
RA Devi A.S., Nagaraj R., Sitarum N.;
RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
RT tigerina.";
RL J. Biol. Chem. 276:2701-2707(2001).
CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST B.SUBTILIS, E.COLI,
CC S.AUREUS, M.LUTEUS, P.PUTIDA AND S.CEREVISIAE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=1409; METHOD=MALDI.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT DISULFID 3 11
FT MOD RES 12 12 AMIDATION.
FT SEQUENCE 12 AA; 1369 MW; C2627D8EFD37605D CRC64;

Query Match 30.0%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLP 4
Db 7 PLP 9

RESULT 6
TIN3 HOPTI
ID TIN3 HOPTI STANDARD; PRT; 12 AA.
AC P82653;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tigerin-3.
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;
OC Hoplobatrachus.
OX NCBI_TaxID=103373;
[1]
RN SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
RC TISSUE=Skin secretion;
RX PubMed=11031261;
RA Purna Sai K., Jagannadham M.V., Vairamani M., Raju N.P.,
RA Devi A.S., Nagaraj R., Sitarum N.;
RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
RT tigerina.";
RL J. Biol. Chem. 276:2701-2707(2001).
CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST B.SUBTILIS, E.COLI,
CC S.AUREUS, M.LUTEUS, P.PUTIDA AND S.CEREVISIAE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=1409; METHOD=MALDI.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT DISULFID 3 11
FT MOD RES 12 12 AMIDATION.
FT SEQUENCE 12 AA; 1369 MW; C2627D8EFD37605D CRC64;

Query Match 30.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPL 3
Db 8 QPL 10

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FT MOD RES 12 12 AMIDATION.
FT SEQUENCE 12 AA; 1411 MW; C0717D8EFD37605D CRC64;

Query Match 30.0%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLP 4
Db 7 PLP 9

RESULT 7
ACT7 SOYBN
ID ACT7 SOYBN STANDARD; PRT; 13 AA.
AC P15987;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Actin 7 (Fragment).
GN SAC7.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=cv. Wayne.
RX MEDLINE=91346640; PubMed=2102831;
RA Pearson L., Meagher R.B.;
RT "Diverse soybean actin transcripts contain a large intron in the 5'
RT untranslated leader: structural similarity to vertebrate muscle actin
RT genes.";
RL Plant Mol. Biol. 14:513-526(1990).
CC -!- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED
CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBIQUITOUSLY EXPRESSED
CC IN ALL EUKARYOTIC CELLS.
CC -!- FUNCTION: ESSENTIAL COMPONENT OF CELL CYTOSKELETON; PLAYS AN
CC IMPORTANT ROLE IN CYTOPLASMIC STREAMING, CELL SHAPE DETERMINATION,
CC CELL DIVISION, ORGANELLE MOVEMENT AND EXTENSION GROWTH.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- MISCELLANEOUS: THERE ARE AT LEAST 16 ACTIN GENES IN SOYBEAN.
CC -!- SIMILARITY: Belongs to the actin family.

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EMBL; X17120; CAA34980.1; -.
PIR; S15755; S15755.
InterPro; IPR004001; Actin.
InterPro; IPR004000; Actin_like.
PROSITE; PS00406; ACTINS_1; PARTIAL.
PROSITE; PS00432; ACTINS_2; PARTIAL.
PROSITE; PS01132; ACTINS_ACT LIKE; PARTIAL.
KW Structural protein; Multigene family.
FT NON TER 13 13
FT SEQUENCE 13 AA; 1420 MW; 8BEFF3C6D4FD05A CRC64;

Query Match 30.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPL 3
Db 8 QPL 10

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RT	"The 1.1 A crystal structure of the neuronal acetylcholine receptor antagonist, alpha-conotoxin PnIA from Conus pennaceus.";
RL	Structure 4:417-423(1996).
CC	- - FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS INHIBIT THEM. IN CONTRAST TO OTHER ALPHA-CONOTOXINS, WHICH ARE SELECTIVE FOR VERTEBRATE SKELETAL MUSCLE NACHR, THE CONUS PENNAECUS ALPHA-CONOTOXINS BLOCK NACHR IN MOLLUSKS.
CC	- - SUBCELLULAR LOCATION: Secreted.
CC	- - TISSUE SPECIFICITY: Expressed by the venom duct.
CC	- - SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE FAMILY.
PIR	A54877; A54877.
PDB	1PEN; 21-APR-97.
KW	Postsynaptic neurotoxin; Neurotoxin; Toxin;
KW	Acetylcholine receptor inhibitor; Amidation; Sulfation; 3D-structure.
FT	DISULFID 2 8
FT	DOSULFID 3 16
FT	MOD_RES 15 15
FT	SULFATION.
FT	AMIDATION.
FT	HELIX 2 4
FT	HELIK 6 11
FT	TURN 13 16
SQ	SEQUENCE 16 AA; 1628 MW; 05310FF95SEC99005 CRC64;
Query Match	30.0%; Score 3; DB 1; Length 16;
Best Local Similarity	100.0%; Pred.No.1.le+03;
Matches	3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	3 LPP 5
Db	
	5 LPP 7
RESULT 10	
CXAB_CONPE	STANDARD; PRT; 16 AA.
ID_CXAB_CONPE	
AC_P50985	(Rel. 34, Created)
DT_01-OCT-1996	(Rel. 34, Last sequence update)
DT_01-OCT-1996	(Rel. 34, Last annotation update)
DT_28-FEB-2003	(Rel. 41, Last annotation update)
DE_Alpha-conotoxin PnIB.	
OS_Conus pennaceus (Feathered cone).	
OC_Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;	
OC_Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsgastropoda;	
OC_Neogastropoda; Conoidea; Conidae; Conus.	
OX_NCBI_TaxID=37335;	
RN [1]	
RP_SEQUENCE.	
RC_TISSUE=Venom;	
RX_MEDLINE=94347719; PubMed=8068627;	
RA_Fainzilber M., Hasson A., Oren R., Burlingame A.L., Gordon D., Spira M.E., Zlotkin E.;	
RA "New mollusc-specific alpha-conotoxins block Aplysia neuronal acetylcholine receptors."	
RT_Biochemistry 33:9523-9529(1994).	
RN [2]	
RP_SULFATION OF TYR-15.	
RX_MEDLINE=9242956; PubMed=10226369;	
RA_Wolfender J.L., Chu F., Ball H., Wolfender F., Fainzilber M., Baldwin M.A., Burlingame A.L.;	
RA "Identification of tyrosine sulfation in Conus pennaceus conotoxins alpha-PnIA and alpha-PnIB: further investigation of labile sulfo- and phosphopeptides by electrospray, matrix-assisted laser desorption/ionization (MALDI) and atmospheric pressure MALDI mass spectrometry."	
RT_J. Mass Spectrom. 34:447-454(1999).	
RN [3]	
RP_X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).	
RX_MEDLINE=97444322; PubMed=9298951;	
RA_Hu S.H., Gehrmann J., Alewood P.F., Craik D.J., Martin J.L.;	
RA "Crystal structure at 1.1-A resolution of alpha-conotoxin PnIB: comparison with alpha-conotoxins PnIA and G;"	

RL Biochemistry 36:11323-11330(1997).  
CC -!- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY  
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS  
CC INHIBIT THEM. IN CONTRAST TO OTHER ALPHA-CONOTOXINS, WHICH ARE  
CC SELECTIVE FOR VERTEBRATE SKELETAL MUSCLE NACHR, THE CONUS  
CC PENNACEUS ALPHA-CONOTOXINS BLOCK NACHR IN MOLLUSKS.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.  
CC -!- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE  
CC FAMILY.  
DR PIR: B54877; B54877.  
DR PDB: 1AKG; 20-MAY-98.  
KW Postsynaptic neurotoxin; Neurotoxin; Toxin;  
KW Acetylcholine receptor inhibitor; Amidation; Sulfation; 3D-structure.  
FT DISULFID 2 8  
FT MOD\_RES 3 16 SULFATION.  
FT MOD\_RES 15 15  
FT MOD\_RES 16 16 AMIDATION.  
FT HELIX 2 4  
FT HELIX 6 11  
FT TURN 13 16  
SQ SEQUENCE 16 AA; 1643 MW; 05310FF95ED86AF5 CRC64;  
  
Query Match 30.0%; Score 3; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 3 LPP 5  
Db 5 LPP 7  
  
RESULT 11  
ACT6\_SOYBN STANDARD; PRT; 17 AA.  
AC P15986;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Actin 6 (Fragment).  
GN SAG6.  
OS Glycine max (Soybean).  
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
CC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
CC NCBI\_TaxID=3847;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Wayne;  
RX MEDLINE=91346640; PubMed=21028311;  
RA Pearson L., Meagher R.B.;  
RT "Diverse soybean actin transcripts contain a large intron in the 5'  
RT untranslated leader: structural similarity to vertebrate muscle actin  
RT genes";  
RL Plant Mol. Biol. 14:513-526(1990).  
CC -!- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED  
CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBIQUITOUSLY EXPRESSED  
CC IN ALL EUKARYOTIC CELLS.  
CC -!- FUNCTION: ESSENTIAL COMPONENT OF CELL CYTOSKELETON; PLAYS AN  
CC IMPORTANT ROLE IN CYTOPLASMIC STREAMING, CELL SHAPE DETERMINATION,  
CC CELL DIVISION, ORGANELLE MOVEMENT AND EXTENSION GROWTH.  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -!- MISCELLANEOUS: THERE ARE AT LEAST 16 ACTIN GENES IN SOYBEAN.  
CC -!- SIMILARITY: Belongs to the actin family.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----

DR EMBL: X17119; CAA34979.1; -.  
DR PIR: S15754; S15754.  
DR InterPro: IPR004001; Actin.  
DR InterPro: IPR004000; Actin\_like.  
DR Pfam: PF00022; actin; 1.  
DR PROSITE: PS00406; ACTINS\_1; PARTIAL.  
DR PROSITE: PS00432; ACTINS\_2; PARTIAL.  
DR PROSITE: PS01132; ACTINS\_ACT\_LIKE; PARTIAL.  
KW Structural protein; Multigene family.  
FT NON\_TER 17  
FT NON\_TER 17  
SQ SEQUENCE 17 AA; 1749 MW; 38F4970D4BEFF3C3 CRC64;  
  
Query Match 30.0%; Score 3; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 QPL 3  
Db 8 QPL 10  
  
RESULT 12  
UC21\_MAIZE STANDARD; PRT; 18 AA.  
ID UC21\_MAIZE STANDARD; PRT; 18 AA.  
AC P80627;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 443)  
DE (Fragment).  
OS Zea mays (Maize).  
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
CC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
CC NCBI\_TaxID=4577;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Coleoptile;  
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,  
RA Pernollet J.-C., Zivy M., de Vienne D.;  
RT "The maize two dimensional gel protein database: towards an integrated  
RT genome analysis program";  
RL Theor. Appl. Genet. 93:997-1005(1996).  
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 5.9, ITS MW IS: 26.5 kDa.  
CC -!- SIMILARITY: TO L-ASCORBATE PEROXIDASES.  
DR Maize-2DPAGE; P80627; COLEOPTILE.  
DR MaizeDB; 123953; -.  
FT NON\_TER 1  
FT NON\_TER 18  
FT NON\_TER 18  
SQ SEQUENCE 18 AA; 1938 MW; F32F6FEF038BAB8A CRC64;  
  
Query Match 30.0%; Score 3; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 5 PTV 7  
Db 5 PTV 7  
  
RESULT 13  
BULB\_NARPS STANDARD; PRT; 20 AA.  
ID BULB\_NARPS STANDARD; PRT; 20 AA.  
AC P80554;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE Bulb protein (Fragment).  
OS Narcissus pseudonarcissus (Daffodil).  
CC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;  
CC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae;  
CC Narcissus.



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OX NCBI_TaxID=39639;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. Golden Harvest; TISSUE=Bulb;
RA Partis M.D., Barker P., Thomas B.;
RL Submitted (FEB-1996) to the SWISS-PROT data bank.
FT UNSURE 2 2 OR N.
FT NON TER 20 20
SQ SEQUENCE 20 AA; 2077 MW; 76213FF3A468AD38 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
DB 13 LPP 15

RESULT 14
CPA7 PAPSP STANDARD; PRT; 20 AA.
AC P80055;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Cytochrome P450 2A7 (BC 1.14.14.1) (CYP11A7) (P450 FI) (Coumarin 7-
DE hydroxylase) (Fragment).
GN CYP2A7.
OS Papio sp. (Baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Papio.
OX NCBI_TaxID=61183;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=92174920; PubMed=1541278;
RA Dalet-Beluche I., Boulenc X., Fabre G., Maurel P., Bonfils C.;
RT "Purification of two cytochrome P450 isozymes related to CYP2A and
RT CYP3A gene families from monkey (baboon, Papio papio) liver
RT microsomes. Cross reactivity with human forms."
RL Eur. J. Biochem. 204:641-648(1992).
CC -!- FUNCTION: EXHIBITS A HIGH COUMARIN 7-HYDROXYLASE ACTIVITY.
CC -!- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC oxidized flavoprotein + H(2)O.
CC -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC -!- INDUCTION: By phenobarbital.
CC -!- SIMILARITY: Belongs to the cytochrome P450 family.
DR InterPro; IPR001128; Cytochrome P450.
DR PROSITE; PS00086; CYTOCHROME P450; PARTIAL.
KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW Microsome; Endoplasmic reticulum.
FT UNSURE 14 14
FT NON TER 20 20
SQ SEQUENCE 20 AA; 2045 MW; 693102A1F0B50C96 CRC64;

Query Match 30.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TVM 8
DB 16 TVM 18

RESULT 15
EI04 LITRU STANDARD; PRT; 5 AA.
AC P82100;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)

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DE Electrin 4.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella."
RL Aust. J. Chem. 52:639-645(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD_RES 5 5 AMIDATION.
FT NON TER 5 5
SQ SEQUENCE 5 AA; 616 MW; 61F2D1A059A00000 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TV 7
DB 3 TV 4

RESULT 16
PAP2_PAPMA STANDARD; PRT; 5 AA.
ID P81864;
AC P81864;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pardaxin II (PXII) (Fragment).
OS Pardachirus marmoratus (Red sea mores sole).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Soleiidae; Soleidae; Pardachirus.
OX NCBI_TaxID=31087;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=87057369; PubMed=3782138;
RA Lazarovici P., Primor N., Loew L.M.;
RT "Purification and pore-forming activity of two hydrophobic
RT polypeptides from the secretion of the Red sea mores sole (Pardachirus
RT marmoratus).";
RL J. Biol. Chem. 261:16704-16713(1986).
CC -!- FUNCTION: Exhibits unusual shark repellent and surfactant
CC properties. Forms voltage-dependent, ion-permeable channels
CC in membranes. At high concentration causes cell membrane lysis.
CC -!- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE PARDAXIN FAMILY.
KW TOXIN.
FT NON TER 5 5
SQ SEQUENCE 5 AA; 614 MW; 7769C9C9C8100000 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 FP 10
DB 4 FP 5

RESULT 17
PRCT_PERAM

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ID PRCT\_PERAM STANDARD; PRT; 5 AA.  
 AC P01373;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 01-FEB-1995 (Rel. 31, Last annotation update)  
 DE Proctolin.  
 OS Periplaneta americana (American cockroach),  
 OS Limulus polyphemus (Atlantic horseshoe crab), and  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
 OC Blattidae; Periplaneta.  
 OX NCBI\_TaxID=6978, 6850, 6759;  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES=P.americana;  
 RX MEDLINE=76074708; PubMed=576;  
 RA Starratt A.N., Brown B.E.;  
 RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter  
 RT in insects.";  
 RL Life Sci. 17:1253-1256(1975).  
 RN [2]  
 RP BIOLOGICAL SOURCE.  
 RC SPECIES=P.americana;  
 RX MEDLINE=81225865; PubMed=6113690;  
 RA O'Shea M., Adams M.E.;  
 RT "Pentapeptide (proctolin) associated with an identified neuron.";  
 RL Science 213:567-569(1981).  
 RN [3]  
 RP SEQUENCE.  
 RC SPECIES=L.polyphemus;  
 RX MEDLINE=90287800; PubMed=2356151;  
 RA Groomer J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,  
 RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,  
 RA Shabanowitz J.;  
 RT Identification of proctolin in the central nervous system of the  
 RT horseshoe crab, Limulus polyphemus.";  
 RL Peptides 11:205-211(1990).  
 RN [4]  
 RP SEQUENCE.  
 RC SPECIES=C.maenas;  
 RX MEDLINE=86232789; PubMed=2872861;  
 RA Stangler J., Dirksen H., Keller R.;  
 RT "Identification and immunocytochemical localization of proctolin in  
 RT pericardial organs of the shore crab, Carcinus maenas.";  
 RL Peptides 7:67-72(1986).  
 CC -!- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY.  
 CC MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.  
 CC -!- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN  
 CC THE CRAB PERICARDIAL ORGANS.  
 DR PIR; A01644; HOROHA.  
 DR PIR; A60411; A60411.  
 KW Neuropeptide.  
 SQ SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;  
 Query Match 20.0%; Score 2; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 3 LP 4  
 Db 3 LP 4  
 RESULT 18  
 CIP1\_MYTED STANDARD; PRT; 6 AA.  
 AC P13736;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Contraction-inhibiting peptide I (MIP I).  
 OS Mytilus edulis (Blue mussel).

OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;  
 OC Mytiloidea; Mytilidae; Mytilus.  
 OX NCBI\_TaxID=6550;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Pedal ganglion;  
 RX MEDLINE=88240357; PubMed=3377776;  
 RA Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;  
 RA "Structures and actions of Mytilus inhibitory peptides.";  
 RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).  
 CC -!- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN  
 CC MUSCLES.  
 CC -!- SIMILARITY: TO MIP II.  
 DR PIR; A27696; A27696.  
 KW Hormone; Amidation.  
 FT MOD RES 6 6 AMIDATION.  
 SQ SEQUENCE 6 AA; 637 MW; 72C9C68775B81000 CRC64;  
 Query Match 20.0%; Score 2; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 8 MF 9  
 Db 4 MF 5  
 RESULT 19  
 CIP2\_MYTED STANDARD; PRT; 6 AA.  
 ID -CIP2\_MYTED STANDARD; PRT; 6 AA.  
 AC P13737;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Contraction-inhibiting peptide II (MIP II).  
 OS Mytilus edulis (Blue mussel).  
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;  
 OC Mytiloidea; Mytilidae; Mytilus.  
 OX NCBI\_TaxID=6550;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Pedal ganglion;  
 RX MEDLINE=88240357; PubMed=3377776;  
 RA Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;  
 RA "Structures and actions of Mytilus inhibitory peptides.";  
 RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).  
 CC -!- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN  
 CC MUSCLES.  
 CC -!- SIMILARITY: TO MIP I.  
 DR PIR; B27696; B27696.  
 KW Hormone; Amidation.  
 FT MOD RES 6 6 AMIDATION.  
 SQ SEQUENCE 6 AA; 621 MW; 72C9C6876DD81000 CRC64;  
 Query Match 20.0%; Score 2; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 8 MF 9  
 Db 4 MF 5  
 RESULT 20  
 TMOF\_SARBU STANDARD; PRT; 6 AA.  
 ID -TMOF\_SARBU STANDARD; PRT; 6 AA.  
 AC P41495;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE Trypsin-modulating oostatic factor (TMOF).  
 OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 OC Sarcophagidae; Sarcophaga.  
 OX NCBI\_TaxID=7385;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Ovary;  
 RX MEDLINE=94211930; PubMed=8159807;  
 RA Bylemans D., Borovsky D., Hunt D.F., Shabanowitz J., Grauwels L.,  
 de Loof A.;  
 RT "Sequencing and characterization of trypsin modulating oostatic  
 factor (IMOF) from the ovaries of the grey fleshfly, Neobellieria  
 (Sarcophaga) bullata.";  
 RL Regul. Pept. 50:61-72(1994).  
 CC -!- FUNCTION: HAS AN OOSTATIC ACTIVITY. INHIBITS TRYPSIN BIOSYNTHESIS  
 IN THE MIDGUT WHICH INDIRECTLY REDUCES THE VITELLOGENIN  
 CONCENTRATION IN THE HEMOLYPH RESULTING IN INHIBITION OF OOCYTE  
 DEVELOPMENT.  
 CC -!- DEVELOPMENTAL STAGE: SYNTHESIZED AND RELEASED FROM FOLLICULAR  
 EPITHELIUM AFTER A BLOOD MEAL.  
 KW Hormone.  
 SQ SEQUENCE 6 AA; 695 MW; 61E72451B7642000 CRC64;  
 Query Match 20.0%; Score 2; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 PT 6  
 DB 2 PT 3  
 RESULT 21  
 TRPI\_PSEPU  
 ID TRPI\_PSEPU STANDARD; PRT; 6 AA.  
 AC F36414;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-FEB-1995 (Rel. 31, Last annotation update)  
 DE TrpBA operon transcriptional activator (Fragment).  
 GN TRPI  
 OS Pseudomonas putida.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxID=303;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PG1 C18;  
 RX MEDLINE=89335826; PubMed=2503057;  
 RA Eberly L., Crawford I.P.;  
 RT "DNA sequence of the tryptophan synthase genes of Pseudomonas  
 putida.";  
 RL Biochimie 71:521-531(1989).  
 CC -!- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPBA GENES ENCODING  
 THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE  
 INDUCER (INDOLEGLYCEROL PHOSPHATE), TRPI BINDS UPSTREAM OF THE  
 TRPAB OPERON, OVERLAPPING ITS OWN PROMOTER REGION.  
 CC -!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL  
 REGULATORS.  
 CC -----  
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 CC -----  
 CC EMBL; X13299; CAA31660.1; -;  
 DR InterPro: IPR000847; HTH LysR.  
 DR PROSITE: PS00044; HTH LYSR\_FAMILY; PARTIAL.  
 KW Tryptophan biosynthesis; Transcription regulation; Activator;  
 KW DNA-binding.  
 RN NON\_TER 6  
 RP SEQUENCE.

SQ SEQUENCE 6 AA; 693 MW; 77672AA1EDD6F000 CRC64;  
 Query Match 20.0%; Score 2; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 LP 4  
 DB 5 LP 6  
 RESULT 22  
 VP19\_HSVIK  
 ID VP19\_HSVIK STANDARD; PRT; 6 AA.  
 AC P23210;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 01-DEC-1992 (Rel. 24, Last annotation update)  
 DE Capsid assembly and DNA maturation protein (Virion protein UL38)  
 DE (Capsid protein VP19C) (Fragment).  
 GN UL38.  
 OS Herpes simplex virus (type 1 / strain KOS).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Alphaherpesvirinae; Simplexvirus.  
 OX NCBI\_TaxID=10306;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91101287; PubMed=1846198;  
 RA Flanagan W.M., Papavassiliou A.G., Rice M., Hecht L.B.,  
 Silverstein S., Wagner E.K.;  
 RT "Analysis of the herpes simplex virus type 1 promoter controlling the  
 expression of UL38, a true late gene involved in capsid assembly.";  
 RL J. Virol. 65:769-786(1991).  
 CC -!- FUNCTION: COMPONENT OF THE BASAL LAYER IN WHICH THE CAPSIDS ARE  
 EMBEDDED. BINDS DNA.  
 CC -!- SIMILARITY: TO OTHER HERPESVIRUSES CAPSID PROTEIN VP19C.  
 CC -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; M57646; AAA45830.1; -;  
 DR Capsid assembly; Coat protein; DNA-binding.  
 FT NON\_TER 6  
 SQ SEQUENCE 6 AA; 703 MW; 67376451A336F000 CRC64;  
 Query Match 20.0%; Score 2; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 PL 3  
 DB 5 PL 6  
 RESULT 23  
 LANC\_CARUI  
 ID LANC\_CARUI STANDARD; PRT; 7 AA.  
 AC P36960;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Lantibiotic carnocin UI49 (Fragment).  
 OS Carnobacterium sp. (strain UI49).  
 OC Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;  
 OC Carnobacterium.  
 OX NCBI\_TaxID=35782;  
 RN [1]  
 RP SEQUENCE.

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RX MEDLINE=92321768; PubMed=1622206;
RA Nes I.P.;
RA Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,
RT "Purification and characterization of a new bacteriocin isolated from
RT a Carnobacterium sp.";
RL Appl. Environ. Microbiol. 58:1417-1422(1992).
CC -!- FUNCTION: LANTHIONINE-CONTAINING PEPTIDE ANTIBIOTIC (LANTIBIOTIC).
CC ACTIVE ON GRAM-POSITIVE BACTERIA.
KW Antibiotic; Bacteriocin; Lantibiotic.
FT NON_TER 7
SQ SEQUENCE 7 AA; 786 MW; 741776D05B05B810 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QP 2
DB 5 QP 6

RESULT 24
MNPI_LBPDE
ID MNPI_LBPDE STANDARD; PRT; 7 AA.
AC P42984;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Myotropic neuropeptide 1 (Led-MNP-I).
OS Leptinotarsa decemlineata (Colorado potato beetle).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
OC Phycophaga; Chrysomeloidea; Chrysomelidae; Chrysomelinae;
OC Chrysomelini; Leptinotarsa.
OX NCBI_TaxID=7539;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RX MEDLINE=95380343; PubMed=7651886;
RA Spittaels K., Vankeerberghen A., Schoofs L., Torrekens S.,
RA Grauwels L., van Leeuwen F., de Loof A.;
RT "Identification, characterization, and immunological localization of
RT a novel myotropic neuropeptide in the Colorado potato beetle,
RT Leptinotarsa decemlineata.";
RL Peptides 16:365-374(1995).
CC -!- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE
CC OVIDUCT.
KW Neuropeptide; Amidation.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 705 MW; 6DD73768745B5DB0 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PL 3
DB 5 PL 6

RESULT 25
TPFY_PACDA
ID TPFY_PACDA STANDARD; PRT; 7 AA.
AC P83455;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tryptophyllin-1 (PdT-1).
OS Pachymedusa dactyloides (Giant mexican leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Phyllomedusinae; Pachymedusa.
OX NCBI_TaxID=75988;

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[1]
RP SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF
RP PRO-7.
RA TISSUE=Skin secretion;
RA Chen T.B., Orr D.F., Shaw C.;
RT "Pachymedusa dactyloides tryptophyllin-1 (PdT-1): structural
RT characterization, pharmacological activity and cloning of precursor
RT cDNA.";
RL Submitted (SEP-2002) to the SWISS-PROT data bank.
CC -!- FUNCTION: Myoactive. Has selective relaxing activity on vascular
CC smooth muscle.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=809.2; METHOD=MALDI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0045986; P:negative regulation of smooth muscle contra. .; NAS.
KW Amphibian defense peptide; Amidation; Hydroxylation.
FT MOD_RES 3
FT MOD_RES 7
FT MOD_RES 7
SQ SEQUENCE 7 AA; 794 MW; 7772D37DC7776350 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
DB 2 PP 3

RESULT 26
UF04_MOUSE
ID UF04_MOUSE STANDARD; PRT; 7 AA.
AC P38642;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P46) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast; PubMed=7523108;
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.0, ITS MW IS: 46 kDa.
FT NON_TER 7
FT NON_TER 7
SQ SEQUENCE 7 AA; 766 MW; 68640AB777632700 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
DB 3 PP 4

RESULT 27
UN06_PINPS
ID UN06_PINPS STANDARD; PRT; 7 AA.
AC P81675;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of needles (N141) (Fragment).
OS Pinus pinaster (Maritime pine).

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OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.  
 RN NCBI\_TaxID=71647;  
 [1] \_SEQUENCE.  
 RP TISSUE=Needle;  
 RC MEDLINE=99274088; PubMed=10344291;  
 RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,  
 RA Frigerio J.-M., Plomion C.;  
 RT "Separation and characterization of needle and xylem maritime pine  
 RT proteins.";  
 RL Electrophoresis 20:1098-1108(1999).  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC  
 CC  
 FT NON TER 1 1  
 FT NON TER 7 7  
 SQ SEQUENCE 7 AA; 823 MW; 69D76724486B5740 CRC64;  
 Query Match 20.0%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 LP 4  
 Db 5 LP 6  
 RESULT 28  
 ACI\_THUAL  
 ID \_ACI\_THUAL STANDARD; PRT; 8 AA.  
 AC P18591;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 01-NOV-1990 (Rel. 16, Last annotation update)  
 DE Angiotensin-converting enzyme inhibitor.  
 OS Thunnus albacares (Yellowfin tuna) (Neothunnus macropterus).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;  
 OC Scombridae; Thunnus.  
 OC NCBI\_TaxID=8236;  
 RN [1] \_SEQUENCE.  
 RP TISSUE=Muscle;  
 RC MEDLINE=88326322; PubMed=3415688;  
 RA Kohana Y., Matsumoto S., Oka H., Teramoto T., Okabe M., Mimura T.;  
 RT "Isolation of angiotensin-converting enzyme inhibitor from tuna  
 RT muscle.";  
 RL Biochem. Biophys. Res. Commun. 155:332-337(1988).  
 DR PIR; A31570; A31570.  
 SQ SEQUENCE 8 AA; 953 MW; 6AA863733051F1B7 CRC64;  
 Query Match 20.0%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 PT 6  
 Db 1 PT 2  
 RESULT 29  
 ALL5\_CALVO  
 ID \_ALL5\_CALVO STANDARD; PRT; 8 AA.  
 AC P41841;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Calliostatin 5 (Met-calliostatin 1) ([Hyp3]Met-calliostatin).  
 OS Calliphora vomitoria (Blue blowfly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 OC Calliphoridae; Calliphora.

OX NCBI\_TaxID=27454;  
 RN [1] \_SEQUENCE.  
 RP MEDLINE=93211980; PubMed=8460157;  
 RA Duve H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.,  
 RA Thorpe A.;  
 RT "Calliostatins: neuropeptides from the blowfly Calliphora vomitoria  
 RT with sequence homology to cockroach allatostatins.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).  
 RN [2]  
 RP CHARACTERIZATION, AND HYDROXYLATION.  
 RC TISSUE=Head;  
 RC MEDLINE=94342269; PubMed=8063725;  
 RA Duve H., Johnsen A.H., Scott A.G., East P., Thorpe A.;  
 RA "[Hyp3]Met-calliostatin. Identification and biological properties of  
 RT a novel neuropeptide from the blowfly Calliphora vomitoria.";  
 RL J. Biol. Chem. 269:21059-21066(1994).  
 CC -!- FUNCTION: MAY ACT AS A NEUOTRANSMITTER OR NEUROMODULATOR AND PLAY  
 CC A ROLE IN THE INTEGRATION OF INFORMATION WITHIN THE BRAIN. MAY BE  
 CC INVOLVED IN THE CONTROL OF VISCERAL MUSCLES DUE TO ITS ABILITY TO  
 CC BEHAVE AS POTENT INHIBITORS OF PERISTALTIC MOVEMENTS. MAY ALSO  
 CC FULFILL A NEUROHORMONAL ROLE ON MUSCLES OF THE GUT AND HEART.  
 CC -!- TISSUE SPECIFICITY: NEURONS WITHIN BRAIN AND ABDOMINAL GANGLION.  
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 DR PIR; E47393; E47393.  
 KW Neuropeptide; Amidation; Hydroxylation.  
 FT MOD\_RES 3 3 HYDROXYLATION (20%).  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 883 MW; 7D9879CABB477768 CRC64;  
 Query Match 20.0%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 PP 5  
 Db 2 PP 3  
 RESULT 30  
 ALL6\_CVDPO  
 ID \_ALL6\_CVDPO STANDARD; PRT; 8 AA.  
 AC P821E7;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Cydiaastatin 6.  
 OS Cydia pomonella (Codling moth).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 OC Tortricoidae; Tortricidae; Olethreutinae; Cydia.  
 OC NCBI\_TaxID=82600;  
 RN [1] \_SEQUENCE.  
 RP TISSUE=Larva;  
 RC MEDLINE=98054539; PubMed=9392829;  
 RA Dave H., Johnsen A.H., Maestri J.-L., Scott A.G., Winstanley D.,  
 RA Davey M., East P.D., Thorpe A.;  
 RT "Lepidopteran peptides of the allatostatin superfamily.";  
 RL Peptides 18:1301-1309(1997).  
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;  
 Query Match 20.0%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 LP 4  
 Db 1 LP 2

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RESULT 31
COW2_CONPU STANDARD; PRT; 8 AA.
ID P58785;
AC 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leu-contryphan-P.
OS Conus purpurascens (Purple cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=41690;
RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC STRAIN=Clipperton Island; TISSUE=Venom;
RA MEDLINE=9938839; PubMed=10461743;
RA Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,
RA Olivera B.M.;
RT "A novel D-leucine-containing Conus peptide: diverse conformational
RT dynamics in the contryphan family.";
RL J. Pept. Res. 54:93-99(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- MASS SPECTROMETRY: MW=888.4; METHOD=LSIMS.
CC -!- SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY.
KW Toxin; Hydroxylation; D-amino acid.
FT DISULFID 2
FT MOD RES 4 4 D-LEUCINE.
SQ SEQUENCE 8 AA; 890 MW; 75A367672732CEB8 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LP 4
Db 5 LP 6

RESULT 32
NPB_BOVIN STANDARD; PRT; 8 AA.
ID NP507;
AC 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuropeptide B.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=86067985; PubMed=3865193;
RA Yang H.-Y.T., Fratta W., Majane E.A., Costa E.;
RT "Isolation, sequencing, synthesis, and pharmacological
RT characterization of two brain neuropeptides that modulate the action
RT of morphine.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).
CC -!- FUNCTION: MODULATES THE ACTION OF MORPHINE.
DR PIR; B24749; B24749.
KW Neuropeptide; Amidation.
FT MOD RES 8
FT SEQUENCE 8 AA; 1082 MW; 87D416C776D9C729 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 QP 2
Db 4 QP 5

RESULT 33
PPK2_PERAM STANDARD; PRT; 8 AA.
ID PPK2_PERAM STANDARD; PRT; 8 AA.
AC P82692;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinin-2 (Pea-PK-2) (FXPRL-amide).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pserygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Corpora cardiaca; PubMed=9210163;
RX MEDLINE=9735392; PubMed=9210163;
RA Predel R., Kellner R., Kaufmann R., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of two pyrokinins from the
RT retrocerebral complex of the American cockroach.";
RL Peptides 18:473-478(1997).
RN [2]
RP TISSUE SPECIFICITY.
RX MEDLINE=2018984; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Tagma-specific distribution of FXPRLamides in the nervous system of
RT the American cockroach.";
RL J. Comp. Neurol. 419:352-363(2000).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC -!- (MYOTROPIC ACTIVITY).
CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.
CC -!- MASS SPECTROMETRY: MW=883; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; FALSE_NEG.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD RES 8
FT SEQUENCE 8 AA; 884 MW; C834176DD9D7775 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PP 5
Db 2 PP 3

RESULT 34
AL10_CARMA STANDARD; PRT; 9 AA.
ID AL10_CARMA STANDARD; PRT; 9 AA.
AC P81813;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 10.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubranchyura; Portunioidea; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the

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RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -|- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -|- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
FW Neuropeptide; Amidation; Multigene family.
FT MOD RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 963 MW; 372D79DCB4776C7 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QP 2
DB 3 QP 4

RESULT 35
COXE THUOB STANDARD; PRT; 9 AA.
AC P80975;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Cytochrome c oxidase polypeptide Via (SC 1.9.3.1) (Fragment).
OS Thunus obesus (Bigeye tuna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8241;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=97454291; PubMed=9310366;
RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
RA Kadenbach B.;
RT "The subunit structure of cytochrome-c oxidase from tuna heart and
RT liver.";
RL Eur. J. Biochem. 248:99-103(1997).
CC -|- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -|- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -|- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -|- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIA FAMILY.
DR InterPro; IPR001349; COX6A.
DR PROSITE; PS01329; COX6A; PARTIAL.
KW Oxidoreductase; Inner membrane; Mitochondrion.
FT NON_TER 1 1
FT NON_TER 9 9
FT SEQUENCE 9 AA; 1136 MW; 62E072C9CB0776DB CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QP 2
DB 3 QP 4

RESULT 36
FAR3 PENMO STANDARD; PRT; 9 AA.
AC P83318;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRFamide-like neuropeptide FLFP3 (AQPSMRLRF-amide).
OS Penaeus monodon (Penaeid shrimp).

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OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupum J., Krungkarn C., Longyant S.,
RA Chaiyuthangura P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Penaeus monodon.";
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- MASS SPECTROMETRY: MW=1121.2; METHOD=MALDI.
CC -|- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1105 MW; CDD107340685A776 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QP 2
DB 2 QP 3

RESULT 37
FAR4 PENMO STANDARD; PRT; 9 AA.
AC P83319;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRFamide-like neuropeptide FLFP4 (SQPSMRLRF-amide).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupum J., Krungkarn C., Longyant S.,
RA Chaiyuthangura P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Penaeus monodon.";
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- MASS SPECTROMETRY: MW=1119.8; METHOD=MALDI.
CC -|- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1121 MW; DA0B07340685A776 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QP 2
DB 2 QP 3

RESULT 38
FAR5 ASCSU STANDARD; PRT; 9 AA.
ID "FAR5 ASCSU
AC P43170;

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DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last annotation update)  
DE FMRFamide-like neuropeptide AF5.  
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;  
OC Ascarididae; Ascaris.  
OX NCBI\_TaxID=6253;  
RN (1)  
RP SEQUENCE.  
RX MEDLINE=95380362; PubMed=7651904;  
RA Cowden C., Stretton A.O.W.;  
RT "Eight novel FMRFamide-like neuropeptides isolated from the nematode  
AScaris suum.";  
RL Peptides 16:491-500(1995).  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD RES 9  
SQ SEQUENCE 9 AA; 1052 MW; 340B0059D1B76338 CRC64;  
  
Query Match 20.0%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 5 PT 6  
Db 4 PT 5  
  
RESULT 39  
FAR9 ASCSU STANDARD; PRT; 9 AA.  
AC P43172;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last annotation update)  
DE FMRFamide-like neuropeptide AF9.  
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;  
OC Ascarididae; Ascaris.  
OX NCBI\_TaxID=6253;  
RN (1)  
RP SEQUENCE.  
RX MEDLINE=95380362; PubMed=7651904;  
RA Cowden C., Stretton A.O.W.;  
RT "Eight novel FMRFamide-like neuropeptides isolated from the nematode  
AScaris suum.";  
RL Peptides 16:491-500(1995).  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD RES 9  
SQ SEQUENCE 9 AA; 1012 MW; 524F073774176877 CRC64;  
  
Query Match 20.0%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 PL 3  
Db 6 PL 7  
  
RESULT 40  
FLA2 TREHY STANDARD; PRT; 9 AA.  
AC P80159;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Flagellar filament outer layer protein flaa2 (35 kDa sheath protein)  
(Fragment).

GN FLAA2.  
OS Treponema hyodysenteriae (Serpulina hyodysenteriae).  
OC Bacteria; Spirochaetes; Spirochaetales; Brachyspiraceae; Brachyspira.  
OX NCBI\_TaxID=159;  
RN (1)  
RP SEQUENCE.  
RX STRAIN=CS;  
RX MEDLINE=93139764; PubMed=1487733;  
RA Koopman M.B.H., Baats E., van Vorstenbosch C.J.A.H.V.,  
van der Zeijst B.A.M., Kusters J.G.;  
RT "The periplasmic flagella of Serpulina (Treponema) hyodysenteriae are  
composed of two sheath proteins and three core proteins.";  
RL J. Gen. Microbiol. 138:2697-2706(1992).  
CC -!- FUNCTION: COMPONENT OF THE OUTER LAYER OF THE FLAGELLA.  
CC -!- SUBUNIT: THE FLAGELLUM CONSISTS OF AN OUTER LAYER COMPOSED OF TWO  
SHEATH PROTEINS, FLAA1 (44 kDa) AND FLAA2 (35 kDa) AROUND A CORE  
THAT CONTAINS THREE PROTEINS FLAB1 (37 kDa), FLAB2 (34 kDa) AND  
FLAB3 (32 kDa).  
CC -!- SUBCELLULAR LOCATION: Periplasmic flagellum.  
KW Flagella; Periplasmic.  
FT UNSURE 2  
FT UNSURE 2  
FT NON TER 9  
SQ SEQUENCE 9 AA; 1129 MW; 855A19C68B4772D1 CRC64;  
  
Query Match 20.0%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 6 TV 7  
Db 2 TV 3  
  
RESULT 41  
FRF1 SARBU STANDARD; PRT; 9 AA.  
ID FRF1 SARBU  
AC P83350;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Neb-FMRFamide 1.  
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Sarcophagidae; Sarcophaga.  
OX NCBI\_TaxID=7385;  
RN (1)  
RP SEQUENCE, AMIDATION, AND FUNCTION.  
RC TISSUE=CNS;  
RX MEDLINE=22342733; PubMed=12438685;  
RA Meusen T., Mertens I., Clynen E., Baggerman G., Nichols R.,  
Nachman R.J., Huybrechts R., De Loof A., Schoofs L.;  
RT "Identification in Drosophila melanogaster of the invertebrate G  
protein-coupled FMRFamide receptor.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).  
CC -!- FUNCTION: Has modulatory actions at skeletal neuromuscular  
junctions.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.  
FT MOD RES 1  
FT MOD RES 1  
FT MOD RES 9  
SQ SEQUENCE 9 AA; 1155 MW; 2D810699CAB6C5A7 CRC64;  
  
Query Match 20.0%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 QP 2  
Db 1 QP 2



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RESULT 42
ID_KNL3_BOMVA STANDARD; PRT; 9 AA.
AC P83058;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE [Thr6]bradykinin.
OS Bombina variegata (Yellow-bellied toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=8348;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC TISSUE=Skin secretion;
RA Chen T.B., Orr D.F., Bjourson A.J., McClean S., Rao P.F., Shaw C.;
RT "Cloning and post-translational processing of frog skin kininogens.";
RL Submitted (JUL-2001) to the SWISS-PROT data bank.
CC -!- FUNCTION: [Thr6]bradykinin produces in vitro relaxation of rat
CC arterial smooth muscle and constriction of intestinal smooth
CC muscle.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
KW Amphibian defense peptide; Vasodilator; Bradykinin.
SQ SEQUENCE 9 AA; 1074 MW; 3393D771A9C86777 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 4 PP 5
DB 2 PP 3

RESULT 43
ID_LMT3_LOCMI STANDARD; PRT; 9 AA.
AC P41459;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Locustamyotropin 3 (LOM-MT-3).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,
RA de Loof A.;
RT "Isolation, identification and synthesis of locustamyotropin III and
RT IV, two additional neuropeptides of Locusta migratoria: members of the
RT locustamyotropin peptide family.";
RL Insect Biochem. Mol. Biol. 22:447-452 (1992).
CC -!- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR PIR; A61620; A61620.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1140 MW; D5AE1772C9D776C6 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
DB 2 PP 3

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QY 1 QP 2
DB 3 QP 4

RESULT 44
ID_OXYA_SQUAC STANDARD; PRT; 9 AA.
AC P42999;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Aspartocin (Aspartocin).
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.
OX NCBI_TaxID=7797;
RN [1]
RP SEQUENCE.
RX MEDLINE=73031727; PubMed=5083097;
RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Phylogeny of the neurohypophysial hormones. Two new active peptides
RT isolated from a cartilaginous fish, Squalus acanthias.";
RL Eur. J. Biochem. 29:12-19 (1972).
RN [2]
RP SEQUENCE.
RX MEDLINE=72128038; PubMed=4622083;
RA Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
RT "Identification of 2 new neurohypophysial hormones, valitocin (Val8-
RT oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the
RT spiny dog-fish (Squalus acanthias).";
RL C. R. Acad. Sci., D, Sci. Nat. 274:313-316 (1972).
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro; IPR000981; Neurohyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 996 MW; 17F8376EB44404B CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

QY 2 PL 3
DB 7 PL 8

RESULT 45
ID_OXYT_EISFO STANDARD; PRT; 9 AA.
AC P42998;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Annetocin.
OS Eisenia foetida (Common branding worm) (Common dung-worm).
OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
OC Lumbricina; Lumbricidae; Eisenia.
OX NCBI_TaxID=6396;
RN [1]
RP SEQUENCE.
RC TISSUE=Pituitary;
RX MEDLINE=94121660; PubMed=8292046;
RA Umi T., Ukena K., Matsushima O., Ikeda T., Fujita T., Minakata H.,
RA Nomoto K.;
RT "Annetocin: an oxytocin-related peptide isolated from the earthworm,
RT Eisenia foetida.";
RL Biochem. Biophys. Res. Commun. 198:393-399 (1994).
CC -!- FUNCTION: POTENTIATES SPONTANEOUS CONTRACTIONS OF THE GUT AND ALSO

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CC      . PULSATORY CONTRACTIONS AND BLADDER-SHAKING MOVEMENT OF THE
CC      NEPHRIDIA. MAY BE INVOLVED IN OSMOREGULATION OF THE ANIMAL THROUGH
CC      NEPHRIDIAL FUNCTION.
CC      -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR      PIR; PC2021; PC2021.
DR      InterPro; IPR000981; Neurhyp_horm.
DR      Pfam; PF00220; hormone4; 1.
DR      PROSITE; PS00264; NEUROHYPOPHYS_HORM; FALSE_NEG.
KW      Hormone; Amidation.
FT      DISULFID 1 6
FT      MOD RES 9 9
FT      MOD RES 9 9
SQ      SEQUENCE 9 AA; 996 MW; D4EEB76EB4542C9 CRC64;

Query Match      20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 PT 6
DB      7 PT 8

RESULT 46
OXYT RABIT
ID _OXYT RABIT STANDARD; PRT; 9 AA.
AC P32878; P01188;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Oxytocin (Oxytocin).
OS Oryctolagus cuniculus (Rabbit).
OS Hippopotamus amphibius (Hippopotamus).
OS Balaenoptera physalus (Finback whale), (Common rorqual),
OS Tachyglossus aculeatus aculeatus (Australian echidna), and
OS Hydrolagus collieri (Spotted ratfish) (Pacific ratfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986, 9833, 9770, 49271, 7873;
RN [1]
RP SEQUENCE.
RC SPECIES=Rabbit;
RX MEDLINE=72215060; PubMed=5150741;
RA Chauvet J., Chauvet M.-T., Acher R.;
RT "Evolution of neurohypophyseal hormones: isolation of active
RT principles from rabbits and rats.";
RL Biochimie 53:1099-1104(1971).
RN [2]
RP SEQUENCE.
RC SPECIES=H. amphibius;
RX MEDLINE=71232719; PubMed=5406007;
RA Ferguson D.R., Pickering B.T.;
RT "Arginine and lysine vasopressins in the hippopotamus
RT neurohypophysis.";
RL Gen. Comp. Endocrinol. 13:425-429(1969).
RN [3]
RP SEQUENCE.
RC SPECIES=B. physalus;
RX MEDLINE=73233515; PubMed=4515919;
RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Isolation of finback whale oxytocin and vasopressin.";
RL Nature 201:191-192(1964).
RN [4]
RP SEQUENCE.
RC SPECIES=A. aculeatus;
RX MEDLINE=73233515; PubMed=4515919;
RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Neurohypophyseal hormones and evolution of tetrapods.";
RL Nature New Biol. 244:124-126(1973).
RN [5]
RP SEQUENCE.
RC SPECIES=H. collieri;
RX MEDLINE=70088110; PubMed=5366118;
RA Pickering B.T., Heller H.;
RT "Oxytocin as a neurohypophyseal hormone in the holocephalian

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RT      elasmobranch fish, Hydrolagus collei.";
RL      J. Endocrinol. 45:597-606(1969).
CC      -!- FUNCTION: OXYTOCIN CAUSES CONTRACTION OF THE SMOOTH MUSCLE OF THE
CC      UTERUS AND OF THE MAMMARY GLAND.
CC      -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR      PIR; A91466; A91466.
DR      PIR; A92774; A92774.
DR      PIR; A93147; A93147.
DR      PIR; A93408; A93408.
DR      PIR; B90667; B90667.
DR      PDB; 1XY1; 15-OCT-90.
DR      InterPro; IPR000981; Neurhyp_horm.
DR      Pfam; PF00220; hormone4; 1.
DR      PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW      Hormone; Hypothalamus; Amidation; 3D-structure.
FT      DISULFID 1 6
FT      MOD RES 9 9
FT      MOD RES 9 9
SQ      SEQUENCE 9 AA; 1010 MW; 17F8376EB456D04B CRC64;

Query Match      20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PL 3
DB      7 PL 8

RESULT 47
SAMP MUSCA
ID _SAMP MUSCA STANDARD; PRT; 9 AA.
AC P19035;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serum amyloid P-component (SAP) (Fragment).
OS Mustelus canis (Smooth dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carchariniiformes; Triakidae;
OC Mustelus.
OX NCBI_TaxID=7812;
RN [1]
RP SEQUENCE.
RX MEDLINE=83160932; PubMed=6403520;
RA Robey F.A., Tanaka T., Liu T.-Y.;
RT "Isolation and characterization of two major serum proteins from the
RT dogfish, Mustelus canis, C-reactive protein and amyloid P
RT component.";
RL J. Biol. Chem. 258:3889-3894(1983).
CC      -!- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTRAXIN) HAVE A DISCOID
CC      ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.
CC      -!- SUBCELLULAR LOCATION: Secreted.
CC      -!- DISEASE: SAP IS A PRECURSOR OF AMYLOID COMPONENT P WHICH IS FOUND
CC      IN BASEMENT MEMBRANE AND ASSOCIATED WITH AMYLOID DEPOSITS.
CC      -!- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
DR      PIR; B20569; B20569.
DR      InterPro; IPR001759; Pentaxin.
DR      PROSITE; PS00289; PENTAXIN; PARTIAL.
KW      Lectin; Amyloid; Glycoprotein; Plasma; Pentaxin.
FT      DOMAIN 1 >9
FT      NON_TER 9 9
SQ      SEQUENCE 9 AA; 965 MW; D05B5735B3386769 CRC64;

Query Match      20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 FP 10
DB      2 FP 3

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RESULT 48
TKC1 CALVO STANDARD; PRT; 9 AA.
ID AC P41517;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Callitachykinin I.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX MEDLINE=95075727; PubMed=7984492;
RA Lundquist C.T., Clottens F.L., Holman G.M., Nichols R., Nachman R.J.,
RA Naessel D.R.;
RT "Callitachykinin I and II, two novel myotropic peptides isolated from
RT the blowfly, Calliphora vomitoria, that have resemblances to
RT tachykinins."
RL Peptides 15:761-768(1994).
CC -!- FUNCTION: MYOACTIVE PEPTIDE.
CC -!- SUBCELLULAR LOCATION: Secreted
CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD RES 9 AMIDATION.
SQ SEQUENCE 9 AA; 981 MW; 2417C86B59DC1B7 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PT 6
Db 2 PT 3

RESULT 49
ID UP3 HUMAN STANDARD; PRT; 9 AA.
AC P30089;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 11) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tisot J.-D., Bjellqvist B.,
RA Hochrasser D.F.;
RT "Plasma protein map: an update by microsequencing."
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.6, ITS MW IS: 46 kDa.
DR SWISS-2DPAGE; P30089; HUMAN.
FT NON TER 1
FT NON TER 9
SQ SEQUENCE 9 AA; 1056 MW; 26F2B1BAF769C737 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PL 3
Db 2 PL 3

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RESULT 50
YBFR AZOVI STANDARD; PRT; 9 AA.
ID AC P25825;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in bfr 3' region (Fragment).
OS Azotobacter vinelandii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Azotobacter.
OX NCBI_TaxID=354;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92196129; PubMed=1549605;
RA Grossman M.J., Hinton S.M., Minak-Bernero V., Slaughter C.,
RA Stiefel E.I.;
RT "Unification of the ferritin family of proteins."
RT Proc. Natl. Acad. Sci. U.S.A. 89:2419-2423(1992).
RL -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M83692; AAA22122.1; -
DR PIR; B41983; B41983.
KW Hypothetical protein.
FT NON TER 9
SQ SEQUENCE 9 AA; 947 MW; DF98B5A1B41776D CRC64;

Query Match 20.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
Db 3 PP 4

RESULT 51
AH3 PRUSE STANDARD; PRT; 10 AA.
ID AC P29261;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Amygdalin beta-glucosidase II (EC 3.2.1.117) (Amygdalin hydrolase
DE isozyme II) (AH II) (Fragment).
OS Prunus serotina (Black cherry).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot; Rosidae;
OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=23207;
RN [1]
RP SEQUENCE.
RX TISSUE=Seed;
RX Li C.P., Swain E., Poulton J.E.;
RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase.";
RL Plant Physiol. 100:282-290(1992).
CC -!- CATALYTIC ACTIVITY: (R)-amygdalin + H(2)O = (R)-prunasin + D-
CC glucose.
CC -!- SUBUNIT: Monomer.
CC -!- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS
CC UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COTYLEDON
CC DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR
CC EMBRYONAL TISSUES.
CC -!- PTM: GLYCOSYLATED.

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KW Glycosidase; Hydrolase; Glycoprotein; Multigene family.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1033 MW; 3331B8D051E04777 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 PP 5  
 ||  
 Db 3 PP 4

RESULT 52  
 AL19\_CARMA STANDARD; PRT; 10 AA.  
 AC P81822;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Carcinustatin 19.  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 OC Eubrachyura; Portunioidea; Portunidae; Carcinus.  
 OX NCBI\_TaxID=6759;  
 RN [1]

RP SEQUENCE.  
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
 RX MEDLINE=98121193; PubMed=9461295;  
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
 RA Thorpe A.;  
 RT "Isolation and identification of multiple neuropeptides of the  
 RT allatostatin superfamily in the shore crab Carcinus maenas.";  
 RL Eur. J. Biochem. 250:727-734 (1997).  
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 KW Neuropeptide family.  
 FT MOD\_RES 10 10  
 SQ SEQUENCE 10 AA; 1101 MW; 96687CDSAB369AB1 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 PT 6  
 ||  
 Db 2 PT 3

RESULT 53  
 BPP2\_BOTIN STANDARD; PRT; 10 AA.  
 AC P30422;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bradykinin-potentiating peptide S4,3,1 (i0C) (Angiotensin-converting  
 DE enzyme inhibitor).  
 OS Bothrops insularis (Island jararaca) (Queimada jararaca).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Bothrops.  
 OX NCBI\_TaxID=8723;  
 RN [1]

RP SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=90351557; PubMed=2386615;  
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;  
 RT "Primary structure and biological activity of bradykinin potentiating  
 RT peptides from Bothrops insularis snake venom.";  
 RL J. Protein Chem. 9:221-227 (1990).  
 CC -!- FUNCTION: This peptide both inhibits the activity of the

CC angiotensin-converting enzyme and enhances the action of  
 CC bradykinin by inhibiting the kinases that inactivate it.  
 CC It acts as an indirect hypotensive agent.  
 DR PIR; B37196; B37196.  
 KW Hypotensive agent; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1  
 SQ SEQUENCE 10 AA; 1213 MW; 30C53546C761F773 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 PP 5  
 ||  
 Db 9 PP 10

RESULT 54  
 BPP2\_BOTJA STANDARD; PRT; 10 AA.  
 AC P01022;  
 DT 21-JUN-1986 (Rel. 01, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bradykinin-potentiating peptide 10B (Angiotensin-converting enzyme  
 DE inhibitor V-6-II).  
 OS Bothrops jararaca (Jararaca).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Bothrops.  
 OX NCBI\_TaxID=8724;  
 RN [1]

RP SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=72118526; PubMed=4334402;  
 RA Ondetti M.A., Williams N.J., Sabo E.F., Pluscac J., Weaver E.R.,  
 RA Kocy O.;  
 RT "Angiotensin-converting enzyme inhibitors from the venom of Bothrops  
 RT jararaca. Isolation, elucidation of structure, and synthesis.";  
 RL Biochemistry 10:4033-4039 (1971).  
 CC -!- FUNCTION: This peptide both inhibits the activity of the  
 CC angiotensin-converting enzyme and enhances the action of  
 CC bradykinin by inhibiting the kinases that inactivate it.  
 CC It acts as an indirect hypotensive agent.  
 DR PIR; A01255; XAVI68.  
 KW Hypotensive agent; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1  
 SQ SEQUENCE 10 AA; 1232 MW; 30C53546C7741773 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 PP 5  
 ||  
 Db 9 PP 10

RESULT 55  
 BPP8\_BOTIN STANDARD; PRT; 10 AA.  
 AC P30426;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bradykinin-potentiating peptide S5,1 (Angiotensin-converting  
 DE enzyme inhibitor).  
 OS Bothrops insularis (Island jararaca) (Queimada jararaca).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Bothrops.  
 OX NCBI\_TaxID=8723;  
 RN [1]

```

RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; H37196; H37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 10 AA; 1173 MW; 2FF835545761F6D8 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
DB 9 PP 10

RESULT 56
BPP VIPAS
ID - BPP VIPAS STANDARD; PRT; 10 AA.
AC P31351;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide (Angiotensin-converting
DE enzyme inhibitor).
OS Vipera aspis (Aspic viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Vipera.
OX NCBI_TaxID=8706;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90382616; PubMed=2169439;
RA Komori Y., Sugihara H.;
RT "Characterization of a new inhibitor for angiotensin converting
RT enzyme from the venom of Vipera aspis aspis.";
RL Int. J. Biochem. 22:767-771(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; A60377; XASNPC.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 10 AA; 1062 MW; 3BA827C327686773 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
DB 9 PP 10

RESULT 57
BRK ONCMY
ID - BRK ONCMY STANDARD; PRT; 10 AA.
AC Q9PRZ1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lysyl-bradykinin-like.

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OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RX MEDLINE=94039817; PubMed=8224232;
RA Conlon J.M., Olson K.R.;
RT "Purification of a vasoactive peptide related to lysyl-bradykinin from
RT trout plasma.";
RL FEBS Lett. 334:75-78(1993).
CC -!- FUNCTION: SMOOTH MUSCLE CONTRACTION. PROBABLY PLAYS A ROLE FOR
CC THIS SYSTEM IN CARDIOVASCULAR REGULATION IN FISH.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Plasma.
CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
DR PIR; S39030; S39030.
KW Bradykinin; Vasodilator.
SQ SEQUENCE 10 AA; 1193 MW; 33C59075A3786777 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PL 3
DB 8 PL 9

RESULT 58
CATB_SHEEP
ID CATB_SHEEP STANDARD; PRT; 10 AA.
AC P83205;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Cathepsin B (EC 3.4.22.1) (Cathepsin B1) (Fragment).
GN CTSS.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RC TISSUE=Placenta;
RX MEDLINE=22506352; PubMed=12506352;
RA El Amir B., Remy B., Sousa N.M., Joris B., Ottiers N.G., Perenyi Z.,
RA Moko H.B., Beckers J.-F.M.P.;
RT "Isolation and partial characterization of three pregnancy-associated
RT glycoproteins from the ewe placenta.";
RL Mol. Reprod. Dev. 64:199-206(2003).
CC -!- FUNCTION: Thiol protease which is believed to participate in
CC intracellular degradation and turnover of proteins. Has also been
CC implicated in tumor invasion and metastasis.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of proteins with broad specificity
CC for peptide bonds. Preferentially cleaves -Arg-Arg-|-Xaa bonds in
CC small molecule substrates (thus differing from cathepsin L). In
CC addition to being an endopeptidase, shows peptidyl-dipeptidase
CC activity, liberating C-terminal dipeptides.
CC -!- SUBUNIT: Dimer of a heavy chain and a light chain cross-linked
CC by a disulfide bond (by similarity).
CC -!- SUBCELLULAR LOCATION: Lysosomal (by similarity).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
DR InterPro; IPR000169; SHprot acsite.
DR PROSITE; PS00640; THIOL_PROTEASE ASN; PARTIAL.
DR PROSITE; PS00139; THIOL_PROTEASE_CYS; PARTIAL.
DR PROSITE; PS00639; THIOL_PROTEASE_HIS; PARTIAL.
KW Hydrolase; Thiol protease; Lysosome.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1177 MW; 8795780DDAA9D5BA CRC64;

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Query Match 20.0%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LP 4  
||  
1 LP 2

Db

RESULT 59  
COXM RAT STANDARD; PRT; 10 AA.  
AC P80431;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Cytochrome c oxidase polypeptide VIIb, mitochondrial (EC 1.9.3.1)  
DE (Fragment).  
GN COX7B.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=Wistar; TISSUE=liver;  
RX MEDLINE=95324529; PubMed=7601105;  
RA Schaeffer H., Noack H., Halangk W., Brandt U., von Jagow G.;  
RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and  
RT amino-terminal sequences suggest identity of the fetal heart and the  
RT adult liver isoform."  
RL Eur. J. Biochem. 230:235-241(1995).  
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE  
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN  
CC MITOCHONDRIAL ELECTRON TRANSPORT.  
CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome  
CC c + 2 H(2)O.  
DR PIR; S65387; S65387.  
KW Oxidoreductase; Mitochondrion.  
FT NON TER 10  
SQ SEQUENCE 10 AA; 1210 MW; CFC70EB771A33326 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PT 6  
||  
7 PT 8

Db

RESULT 60  
COXQ RABIT STANDARD; PRT; 10 AA.  
ID COXQ RABIT  
AC P80336;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Cytochrome c oxidase polypeptide VIII-liver/heart (EC 1.9.3.1)  
DE (Fragment).  
GN COX8H.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Heart, and Liver;  
RA Freund R., Kadenbach B.;  
RL Submitted (MAR-1994) to the SWISS-PROT data bank.  
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE  
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN  
CC MITOCHONDRIAL ELECTRON TRANSPORT.

CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome  
CC c + 2 H(2)O.  
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIII FAMILY.  
KW Oxidoreductase; Mitochondrion.  
FT NON TER 10  
SQ SEQUENCE 10 AA; 1027 MW; 2C325CB40DC76338 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PT 6  
||  
9 PT 10

Db

RESULT 61  
COXQ SHEEP STANDARD; PRT; 10 AA.  
ID COXQ SHEEP  
AC P8037;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Cytochrome c oxidase polypeptide VIII-liver/heart (EC 1.9.3.1)  
DE (Fragment).  
OS Ovis aries (Sheep).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Caprinae; Ovis.  
OX NCBI\_TaxID=9940;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Heart, and Liver;  
RA Freund R., Kadenbach B.;  
RL Submitted (MAR-1994) to the SWISS-PROT data bank.  
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE  
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN  
CC MITOCHONDRIAL ELECTRON TRANSPORT.  
CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome  
CC c + 2 H(2)O.  
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIII FAMILY.  
KW Oxidoreductase; Mitochondrion.  
FT NON TER 10  
SQ SEQUENCE 10 AA; 1027 MW; C4E95CA33DC7633D CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PT 6  
||  
9 PT 10

Db

RESULT 62  
FAR6 PANRE STANDARD; PRT; 10 AA.  
ID FAR6 PANRE  
AC P82660;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE FMRamide-like neuropeptide PF6 (NGAPQPFVRF-amide).  
DE Panagrellus redivivus.  
OS Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
OC Eukaryota; Metazoa; Panagrolaimidae; Panagrellus.  
OX NCBI\_TaxID=6233;  
RN [1]  
RP SEQUENCE, FUNCTION, AND AMIDATION.  
RA Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,  
RA Maule A.G.;  
RT "Isolation, characterization and pharmacology of RMRamide-related  
RT peptides (FarPs) from free-living nematode, Panagrellus redivivus."  
RL Submitted (JUL-2000) to the SWISS-PROT data bank.

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CC -!- FUNCTION: MYOACTIVE.
CC -!- SIMILARITY: BELONGS TO THE FARP (FARFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 10 10.
SQ SEQUENCE 10 AA; 1132 MW; CH13EC9D776C76D CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QP 2
DB 5 QP 6

RESULT 63
GONL_ALLMI
ID GONL_ALLMI STANDARD; PRT; 10 AA.
AC P37041; P20407;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberin I (Gonadotropin-releasing hormone I) (GnRH-I) (LH-RH I)
DE (luliberin I).
OS Alligator mississippiensis (American alligator).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
OX NCBI_TaxID=8496;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=91352338; PubMed=1882082;
RA Lovejoy D.A., Fischer W.H., Parker D.B., McRory J.E., Park M.,
RA Lance V., Swanson P., Rivier J.E., Sherwood N.M.;
RT "Primary structure of two forms of gonadotropin-releasing hormone
from brains of the American alligator (Alligator mississippiensis).";
RL Regul. Pept. 33:105-116(1991).
CC -!- FUNCTION: Stimulates the secretion of gonadotropins.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the GnRH family.
CC PIR; A60066; RHAQ1.
DR InterPro; IPR002012; GnRH.
DR Pfam; PF00446; GnRH; 1.
DR PROSITE; PS00473; GnRH; 1.
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1172 MW; 284B23D7286B45A3 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QP 2
DB 8 QP 9

RESULT 64
GON3_ONCKE
ID GON3_ONCKE STANDARD; PRT; 10 AA.
AC P20367; P81751;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberin III (Gonadotropin-releasing hormone III) (GnRH-III) (LH-
DE RH III) (luliberin III).
CN GnRH3.
OS Oncorhynchus keta (Chum salmon), and
OS Clupea pallasii (Pacific herring).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;

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OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8018, 30724;
RN [1]
RP SEQUENCE.
RC SPECIES=O. keta;
RX MEDLINE=83195140; PubMed=6341999;
RA Sherwood N., Eiden L., Brownstein M., Spiess J., Rivier J., Vale W.;
RT "Characterization of a teleost gonadotropin-releasing hormone.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:2794-2798(1983).
RN [2]
RP SEQUENCE, AND FUNCTION.
RC SPECIES=C. pallasi; TISSUE=Brain, and Pituitary;
RX MEDLINE=20114351; PubMed=10650929;
RA Carlsfeld J., Powell J.F.F., Park M., Fischer W.H., Craig A.G.,
RA Chang J.P., Rivier J.E., Sherwood N.M.;
RT "Primary structure and function of three gonadotropin-releasing
hormones, including a novel form, from an ancient teleost, herring.";
RL Endocrinology 141:505-512(2000).
CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
the secretion of both luteinizing and follicle-stimulating
hormones.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the GnRH family.
CC PIR; A21114; A21114.
DR InterPro; IPR002012; GnRH.
DR Pfam; PF00446; GnRH; 1.
DR PROSITE; PS00473; GnRH; 1.
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1230 MW; 284B3233786B45A3 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LP 4
DB 8 LP 9

RESULT 65
GONL_SQUAC
ID GONL_SQUAC STANDARD; PRT; 10 AA.
AC P27429;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberin (Gonadotropin-releasing hormone) (GnRH) (LH-RH)
DE (luliberin).
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.
OX NCBI_TaxID=7797;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92335300; PubMed=1631133;
RA Lovejoy D.A., Fischer W.H., Ngamvongchon S., Craig A.G.,
RA Nahorniak C.S., Peter R.E., Rivier J.E., Sherwood N.M.;
RT "Distinct sequence of gonadotropin-releasing hormone (GnRH) in
dogfish brain provides insight into GnRH evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:6373-6377(1992).
CC -!- FUNCTION: STIMULATES THE SECRETION OF GONADOTROPINS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the GnRH family.
CC PIR; A46030; A46030.
DR InterPro; IPR002012; GnRH.
DR Pfam; PF00446; GnRH; 1.
DR PROSITE; PS00473; GnRH; 1.
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.

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SQ SEQUENCE 10 AA; 1204 MW; 284B32337871F5A3 CRC64;  
Query Match 20.0%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 3 LP 4  
Db 8 LP 9  
RESULT 66  
LABA\_JATMU  
ID LABA\_JATMU STANDARD; PRT; 10 AA.  
AC P13270;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Labaditin.  
OS Jatropa multifida (Physic nut).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Malpighiales; Euphorbiaceae; Jatropa.  
OX NCBI\_TaxID=3996;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Latex;  
RA Kosasi S., van der Sluis W.G., Boelens R., T'Hart L.A., Labadie R.P.;  
RT "Labaditin, a novel cyclic decapeptide from the latex of Jatropa  
multifida L. (Euphorbiaceae). Isolation and sequence determination  
by means of two-dimensional NMR.";  
RL FEBS Lett. 256:91-96(1989).  
CC -!- FUNCTION: LABADITIN IS AN ACTIVE PEPTIDE WHICH INHIBITS THE  
CLASSICAL PATHWAY OF COMPLEMENT ACTIVATION IN VITRO. ACTIVITY  
SEEMS TO BE BASED ON AN INTERACTION WITH C1.  
CC -!- PTM: This is a cyclic peptide.  
CC -!- DISEASE: LATEX OF THIS PLANT IS USED IN FOLKLORIC MEDICINE FOR  
TREATMENT OF INFECTED WOUNDS, SKIN INFECTIONS AND SCABIES.  
SQ SEQUENCE 10 AA; 1089 MW; D98AAD6362D1B362 CRC64;  
Query Match 20.0%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 6 TV 7  
Db 5 TV 6  
RESULT 67  
LPK2\_LOCMI  
ID LPK2\_LOCMI STANDARD; PRT; 10 AA.  
AC P41488;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Locustapyrokinin 2 (LOM-PK-2) (FXPRL-amide).  
OS Locusta migratoria (Migratory locust).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
OX NCBI\_TaxID=7004;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Brain;  
RX MEDLINE=94094539; PubMed=7903606;  
RA Schoofs L., Holman G.M., Nachman R., Proost P., van Damme J.,  
RA de Loof A.;  
RT "Isolation, identification and synthesis of locustapyrokinin II from  
Locusta migratoria, another member of the FXPRL-amide peptide  
family.";  
RL Comp. Biochem. Physiol. 106C:103-109(1993).  
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY (MYOTROPIC

CC -!- ACTIVITY).  
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
DR InterPro; IPR001484; Pyrokinin.  
DR PROSITE; PS00539; PYROKININ; 1.  
KW Neuropeptide; Amidation; Pyrokinin; Pyrrolidone carboxylic acid.  
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD RES 10 10 AMIDATION.  
SQ SEQUENCE 10 AA; 1145 MW; CFAF4271A9D1B772 CRC64;  
Query Match 20.0%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 5 PT 6  
Db 4 PT 5  
RESULT 68  
NS1\_MYCTU  
ID NS1\_MYCTU STANDARD; PRT; 10 AA.  
AC P81135;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE 30 kDa non-secretory protein 1 (Fragment).  
OS Mycobacterium tuberculosis.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
OX NCBI\_TaxID=1773;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=H37Rv;  
RA Prasad H.K., Annappurna P.S.;  
RL Submitted (DEC-1997) to the SWISS-PROT data bank.  
CC -!- CAUTION: We are unable to find this protein in the translation of  
the genome of strain H37Rv.  
FT NON\_TER 1 1  
FT NON\_TER 10 10  
SQ SEQUENCE 10 AA; 1042 MW; 8767FE6AB2C73771 CRC64;  
Query Match 20.0%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 PL 3  
Db 4 PL 5  
RESULT 69  
ODP2\_BOVIN  
ID ODP2\_BOVIN STANDARD; PRT; 10 AA.  
AC P11180;  
DT 01-JUL-1989 (Rel. 11, Created)  
DT 01-JUL-1989 (Rel. 11, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase  
complex (EC 2.3.1.12) (E2) (Fragment).  
GN DLAT.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=88024154; PubMed=3117054;  
RA Bradford A.P., Howell S., Aitken A., James L.A., Yeaman S.J.;  
RT "Primary structure around the lipooate-attachment site on the E2  
component of bovine heart pyruvate dehydrogenase complex.";  
RL Biochem. J. 245:919-922(1987).  
CC -!- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall



CC conversion of pyruvate to acetyl-CoA and CO(2). It contains  
 CC multiple copies of three enzymatic components: pyruvate  
 CC dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and  
 CC lipoamide dehydrogenase (E3).  
 CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide = CoA + S-  
 CC acetyldihydrolipoamide.  
 CC -!- COFACTOR: THE E2 COMPONENT CONTAINS TWO COVALENTLY-BOUND LIPOYL  
 CC LIPOYL.  
 CC -!- SUBUNIT: FORMS A 24-POLYPEPTIDE STRUCTURAL CORE WITH OCTAHEDRAL  
 CC SYMMETRY.  
 CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.  
 CC -!- SIMILARITY: BELONGS TO THE 2-OXOACID DEHYDROGENASE FAMILY.  
 CC -!- SIMILARITY: Contains 2 lipoyl-binding domains.  
 DR INTERPRO: IPR003016; LIPOYL.  
 DR PROSITE: PS00189; LIPOYL; PARTIAL.  
 KW Glycolysis; Transferase; Acyltransferase; Repeat; Mitochondrion;  
 KW Lipoyl 1 1 LIPOYL.  
 FT NON\_TER 1 5  
 FT BINDING 5 5 LIPOYL.  
 FT NON\_TER 10 10  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1066 MW; 889BECDD1ADD33AB1 CRC64;  
 Query Match 20.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 TV 7  
 ||  
 Db 7 TV 8  
 ||  
 RESULT 70  
 ID\_FVK LOCM1 STANDARD; PRT; 10 AA.  
 AC P83382;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Periviscerokinin (Iom-PVK-1).  
 OS Locusta migratoria (Migratory locust).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
 CC Acridoidea; Acrididae; Oedipodinae; Locusta.  
 CC NCBI\_TaxID=7004;  
 [1]  
 RN SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
 RP TISSUE=Abdominal perisymphathetic organs;  
 RX MEDLINE=21896327; PubMed=11897380;  
 RA Predel R., Gaede G.;  
 RT "Identification of the abundant neuropeptide from abdominal  
 RT perisymphathetic organs of locusts.";  
 RL Peptides 23:621-627(2002).  
 CC -!- FUNCTION: Myotropic peptide; increases the frequency of  
 CC contraction of the heart and stimulates amplitude and tonus of the  
 CC foregut.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- MASS SPECTROMETRY: MW=1104.5; METHOD=MALDI.  
 DR GO: GO:0005576; C:extracellular; IDA.  
 DR GO: GO:0005184; P:neuropeptide hormone activity; IDA.  
 DR GO: GO:0007218; P:neuropeptide signaling pathway; IDA.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 10 10  
 FT MOD\_RES 10 10  
 SQ SEQUENCE 10 AA; 1105 MW; 39811269D6D9C728 CRC64;  
 Query Match 20.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 9 FP 10  
 ||  
 Db 7 FP 8  
 ||

RESULT 71  
 Q2OB COMTE STANDARD; PRT; 10 AA.  
 ID P80465;  
 AC 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Quinolone 2-oxoreductase, beta chain (EC 1.3.99.17) (Fragment).  
 OS Comamonas testosteroni (Pseudomonas testosteroni).  
 CC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 CC Comamonadaceae; Comamonas.  
 CC NCBI\_TaxID=285;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=63;  
 RX MEDLINE=96035889; PubMed=7556204;  
 RA Schach S., Tshisuaka B., Fetzner S., Lingens F.;  
 RT "Quinolone 2-oxoreductase and 2-oxo-1,2-dihydroquinoline 5,6-  
 RT dioxygenase from Comamonas testosteroni 63. The first two enzymes in  
 RT quinoline and 3-methylquinoline degradation.";  
 RL Eur. J. Biochem. 232:536-544(1995).  
 CC -!- FUNCTION: CONVERTS (3-METHYL-)-QUINOLINE TO (3-METHYL-)-2-OXO-  
 CC 1,2-DIHYDROQUINOLINE.  
 CC -!- CATALYTIC ACTIVITY: Quinolone + acceptor + H(2)O = isoquinolin-  
 CC 1(2H)-one + reduced acceptor.  
 CC -!- COFACTOR: FAD, MOLYBDENUM AND IRON-SULFUR.  
 CC -!- PATHWAY: Degradation of quinoline and (3-methyl-)-quinoline; first  
 CC step.  
 CC -!- SUBUNIT: HETEROHEXAMER OF TWO ALPHA CHAINS, TWO BETA CHAINS, AND  
 CC TWO GAMMA CHAINS (PROBABLE).  
 KW Oxidoreductase; Flavoprotein; FAD; Molybdenum.  
 FT NON\_TER 10 10  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1241 MW; C2E2C25DD9CDC769 CRC64;  
 Query Match 20.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 9 FP 10  
 ||  
 Db 3 FP 4  
 ||  
 RESULT 72  
 ID SLAP\_BACTG STANDARD; PRT; 10 AA.  
 AC P49325;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE S-layer protein (Surface layer protein) (Fragment).  
 OS Bacillus thuringiensis (subsp. galleriae).  
 CC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.  
 CC NCBI\_TaxID=29338;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=NRRL 4045; PubMed=2592346;  
 RX MEDLINE=90078111; PubMed=2592346;  
 RA Lucke M.D., Beveridge T.J.;  
 RT "Characterization of a dynamic S layer on Bacillus thuringiensis.";  
 RL J. Bacteriol. 171:6656-6667(1989).  
 CC -!- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY  
 CC OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA.  
 CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A  
 CC S-LAYER WITH OBLIQUE (P2) SYMMETRY.  
 DR PIR; A60476; A60476.  
 KW Cell wall; S-layer.  
 FT NON\_TER 10 10  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1080 MW; 57AECACAB769D1A3 CRC64;  
 Query Match 20.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PP 10  
 ||  
 5 PP 6

Db

RESULT 73

TEMK\_RANTE STANDARD; PRT; 10 AA.

AC P56923;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Tempoin K.  
 OS Rana temporaria (European common frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
 OX NCBI\_TaxID=8407;  
 RN [1]  
 RP SEQUENCE.

RC TISSUE=Skin secretion;  
 RX MEDLINE=97175050; PubMed=9022710;  
 RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,  
 RA Barra D.;  
 RT "Temporins, antimicrobial peptides from the European red frog Rana  
 RT temporaria.";  
 RL Eur. J. Biochem. 242:788-792(1996).  
 CC -!- FUNCTION: Has antibacterial activity against Gram-positive  
 CC bacteria.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the brevinin family.  
 KW Amphibian defense peptide; Antibiotic; Amidation.  
 FT MOD RES 10  
 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1123 MW; 390549B337272457 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred.No. 7.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LP 4  
 ||  
 2 LP 3

Db

RESULT 74

TKL2\_LOCM1 STANDARD; PRT; 10 AA.

AC P16224;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Locustatachykinin II (TK-II).  
 OS Locusta migratoria (Migratory locust).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
 OX NCBI\_TaxID=7004;  
 RN [1]  
 RP SEQUENCE.

RC TISSUE=Brain;  
 RX MEDLINE=90184489; PubMed=2311766;  
 RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;  
 RT "Locustatachykinin I and II, two novel insect neuropeptides with  
 RT homology to peptides of the vertebrate tachykinin family.";  
 RL FEBS Lett. 261:397-401(1990).  
 CC -!- FUNCTION: MYOACTIVE PEPTIDE. STIMULATES THE CONTRACTION OF THE  
 CC OVIDUCT AND FOREGUT.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.  
 KW Tachykinin; Neuropeptide; Amidation.  
 FT MOD RES 10  
 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1066 MW; 5D52CD6B59C865B7 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred.No. 7.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PL 3  
 ||  
 2 PL 3

Db

RESULT 75

TMOF\_AEDAE STANDARD; PRT; 10 AA.

AC P19425;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE Trypsin-modulating oostatic factor (TMOF) (COOH).  
 OS Aedes aegypti (Yellowfever mosquito).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.  
 OX NCBI\_TaxID=7159;  
 RN [1]  
 RP SEQUENCE.

RC STRAIN=Vero beach; TISSUE=Ovary;  
 RX MEDLINE=90367888; PubMed=2394318;  
 RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;  
 RT "Mosquito oostatic factor: a novel decapeptide modulating  
 RT trypsin-like enzyme biosynthesis in the midgut.";  
 RL FASEB J. 4:3015-3020(1990).  
 RN [2]  
 RP SEQUENCE.

RC STRAIN=Vero beach; TISSUE=Ovary;  
 RX MEDLINE=93357794; PubMed=8353526;  
 RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;  
 RT "Mass spectrometry and characterization of Aedes aegypti trypsin  
 RT modulating oostatic factor (TMOF) and its analogs.";  
 RL Insect Biochem. Mol. Biol. 23:703-712(1993).  
 CC -!- FUNCTION: HAS AN OOSTATIC ACTIVITY. INHIBITS TRYPSIN BIOSYNTHESIS  
 CC IN THE MIDGUT WHICH INDIRECTLY REDUCES THE VITELLOGENIN  
 CC CONCENTRATION IN THE HEMOLYPH RESULTING IN INHIBITION OF OOCYTE  
 CC DEVELOPMENT.  
 CC -!- DEVELOPMENTAL STAGE: SYNTHESIZED AND RELEASED FROM FOLLICULAR  
 CC EPITHELIUM 18-24 HRS AFTER A BLOOD MEAL. SYNTHESIS PEAKS AT  
 CC 36 HRS AND STOPS AT 56 HRS.  
 DR PIR; A36454; A36454.  
 KW Hormone.  
 FT DOMAIN 3 10 POLY-PRO.  
 FT VARIANT 1 2 YD -> DY (IN TMFO(B)).  
 SQ SEQUENCE 10 AA; 1047 MW; 236D0A777776DC7 CRC64;

Query Match 20.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred.No. 7.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PP 5  
 ||  
 5 PP 6

Db

Search completed: November 25, 2003, 19:28:23  
 Job time : 3.61794 secs

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:25:50 ; Search time 18.7791 Seconds  
(without alignments)  
137.415 Million cell updates/sec

Title: US-09-641-801-25

Perfect score: 10

Sequence: 1 QPLPPTWMP 10

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

1: sp\_archea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mbc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp Vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	4	40.0	12	2 Q8KZ86	Q8kz86 acinetobact
2	4	40.0	12	4 Q9BZ49	Q9bz49 homo sapien
3	4	40.0	13	2 Q9L8K1	Q9l8k1 enterococcu
4	4	40.0	13	4 Q14182	Q14182 homo sapien
5	4	40.0	15	10 Q40562	Q40562 nicotiana t
6	4	40.0	15	10 Q40563	Q40563 nicotiana t
7	4	40.0	18	12 Q84129	Q84129 influenzavi
8	4	40.0	19	2 Q9RBV1	Q9rbv1 pseudomonas
9	4	40.0	20	4 Q9UCAB	Q9uca8 homo sapien
10	4	40.0	20	10 Q9S8A8	Q9sca8 scetale cere
11	4	40.0	20	13 Q9PRN3	Q9prn3 petromyzon
12	3	30.0	9	2 Q9P8K3	Q9p8k3 anabaena sp
13	3	30.0	9	5 Q9TWV0	Q9twv0 anthopleura
14	3	30.0	9	10 Q9S8J8	Q9s8j8 oryza sativ
15	3	30.0	9	16 Q935G1	Q935g1 salmonella
16	3	30.0	10	2 Q9R5T2	Q9rst2 acetobacter

17	3	30.0	10	4 Q14096	Q14096 homo sapien
18	3	30.0	10	11 Q9QVF7	Q9qvf7 rattus sp.
19	3	30.0	10	11 Q8VHM9	Q8vhn9 mus musculus
20	3	30.0	10	12 Q8JV78	Q8jv78 polyomaviru
21	3	30.0	10	13 Q90ZV8	Q90zv8 psittacus e
22	3	30.0	11	4 Q60761	Q60761 homo sapien
23	3	30.0	11	4 Q9UCR1	Q9ucr1 homo sapien
24	3	30.0	11	6 Q9GL48	Q9gl48 sus scrofa
25	3	30.0	11	10 Q9S8Z9	Q9s8z9 psophocarpu
26	3	30.0	12	4 Q9P116	Q9p116 homo sapien
27	3	30.0	12	4 Q9NTQ2	Q9ntq2 homo sapien
28	3	30.0	12	6 Q9TRU1	Q9tru1 bos taurus
29	3	30.0	12	10 P82329	P82329 pisum sativ
30	3	30.0	13	4 Q14890	Q14890 homo sapien
31	3	30.0	13	4 Q9UNV6	Q9unv6 homo sapien
32	3	30.0	13	6 Q9TRW6	Q9trw6 bos taurus
33	3	30.0	13	10 Q42373	Q42373 solanum tub
34	3	30.0	13	11 Q88176	Q88176 mus musculus
35	3	30.0	14	8 Q9T2K7	Q9t2k7 chlamydomon
36	3	30.0	14	10 P82326	P82326 pisum sativ
37	3	30.0	14	11 Q70599	Q70599 rattus norv
38	3	30.0	14	16 Q9KE26	Q9ke26 bacillus ha
39	3	30.0	15	2 Q9R5D5	Q9r5d5 chromatium
40	3	30.0	15	6 Q9TR62	Q9tr62 oryctolaquus
41	3	30.0	15	11 Q9QV25	Q9qv25 rattus sp.
42	3	30.0	15	12 Q69353	Q69353 herpes simp
43	3	30.0	16	2 Q9R5K7	Q9r5k7 streptomyce
44	3	30.0	16	4 Q9NNZ2	Q9nnz2 homo sapien
45	3	30.0	16	5 Q18378	Q18378 drosophila
46	3	30.0	16	8 P92732	P92732 fejeriarya
47	3	30.0	17	2 Q8VME2	Q8vme2 pseudomonas
48	3	30.0	17	2 P97135	P97135 mycobacteri
49	3	30.0	17	4 Q15276	Q15276 homo sapien
50	3	30.0	17	4 Q96P96	Q96p96 homo sapien
51	3	30.0	17	6 Q9TRU8	Q9tru8 bos taurus
52	3	30.0	17	10 P83061	P83061 spinacia ol
53	3	30.0	17	12 Q8B4C4	Q8b4c4 hepatitis b
54	3	30.0	18	2 Q9R5U2	Q9r5u2 pseudomonas
55	3	30.0	18	2 Q9R5F9	Q9r5f9 aicalignes
56	3	30.0	18	2 Q9R4V9	Q9r4v9 campylobact
57	3	30.0	18	2 Q9EYW5	Q9eyw5 erwiania ste
58	3	30.0	18	2 Q9R4C6	Q9r4c6 agrobacteri
59	3	30.0	18	4 Q96F98	Q96f98 homo sapien
60	3	30.0	18	4 Q16244	Q16244 homo sapien
61	3	30.0	18	4 Q8NF84	Q8nfb4 homo sapien
62	3	30.0	18	10 Q9S915	Q9s915 triticum tu
63	3	30.0	19	2 Q9K4X0	Q9k4x0 planktothri
64	3	30.0	19	4 Q9UC80	Q9uc80 homo sapien
65	3	30.0	19	4 Q8NFL2	Q8nfl2 homo sapien
66	3	30.0	19	4 Q9UCX6	Q9uck6 homo sapien
67	3	30.0	19	8 Q31687	Q31687 artemia par
68	3	30.0	19	8 Q9GI97	Q9gi97 sargassum p
69	3	30.0	19	10 Q9S8F5	Q9s8f5 beta vulgar
70	3	30.0	19	12 Q69099	Q69099 herpes simp
71	3	30.0	19	13 Q9PRT0	Q9prt0 gallus gall
72	3	30.0	19	13 Q9PRN4	Q9prn4 petromyzon
73	3	30.0	19	15 Q90Rf8	Q90rf8 human immu
74	3	30.0	19	15 Q905E8	Q905e8 human immu
75	3	30.0	20	2 Q9R4M9	Q9r4m9 pseudomonas
76	3	30.0	20	2 Q931I1	Q931i1 vibrio harv
77	3	30.0	20	2 Q53370	Q53370 escherichia
78	3	30.0	20	2 Q50180	Q50180 pseudomonas
79	3	30.0	20	2 Q46499	Q46499 desulfovibr
80	3	30.0	20	2 Q9R5E8	Q9r5e8 bacillus sp
81	3	30.0	20	4 Q96T45	Q96t45 homo sapien
82	3	30.0	20	4 Q9UCB7	Q9ucb7 homo sapien
83	3	30.0	20	4 Q9UBC8	Q9ubc8 homo sapien
84	3	30.0	20	5 Q25281	Q25281 leishmania
85	3	30.0	20	7 Q8WLP7	Q8wlp7 macaca mula
86	3	30.0	20	10 Q9S8H1	Q9s8h1 hordeum vul
87	3	30.0	20	11 Q9QW31	Q9qw31 rattus sp.
88	3	30.0	20	11 Q9QVQ0	Q9qvq0 rattus sp.
89	2	20.0	5	13 P83308	P83308 gallus gall

90 2 20.0 7 2 P70804  
 91 2 20.0 7 2 O50556  
 92 2 20.0 7 2 Q54248  
 93 2 20.0 7 2 Q34028  
 94 2 20.0 7 8 P92214  
 95 2 20.0 7 8 P92393  
 96 2 20.0 7 8 P92403  
 97 2 20.0 7 8 P92427  
 98 2 20.0 7 8 P92430  
 99 2 20.0 7 8 P92221  
 100 2 20.0 7 8 P92425

## ALIGNMENTS

RESULT 1  
 Q8KZ86 PRELIMINARY; PRT; 12 AA.  
 AC Q8KZ86;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Class I integrin DNA integrase (Fragment).  
 GN INT1L.  
 OS Acinetobacter baumannii.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Moraxellaceae; Acinetobacter.  
 OX NCBI\_TaxID=470;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=204A;  
 RA Dolzani L., Gombac F., Lagatolla C., Riccio M.L., Rossolini G.M.,  
 RA Tonin E., Monti-Bragadin C.;  
 RT "Carriage of class I and II integrons in Italian clinical isolates of  
 RT Acinetobacter baumannii";  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ313334; CAC85941.1; -.  
 FT NON TER 12  
 SQ SEQUENCE 12 AA; 1296 MW; 90426B8F5E376DC1 CRC64;

Query Match 40.0%; Score 4; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5  
 DB 7 PLPP 10

RESULT 2  
 Q9BZ49 PRELIMINARY; PRT; 12 AA.  
 AC Q9BZ49;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE Glycophorin C (Fragment).  
 GN Homo sapiens (Human).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Patel S.S., Mehlotra R.K., Kastens W., Mgone C.S., Kazura J.W.,  
 RA Zimmerman P.A.;  
 RT "The association of the glycophorin C exon 3 deletion with  
 RT ovalocytosis and malaria susceptibility in the Wosera, Papua New  
 RT Guinea";  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF342984; AAK01459.1; -.  
 FT NON TER 1  
 FT NON TER 12

SQ SEQUENCE 12 AA; 1361 MW; 2A07044DB8377378 CRC64;  
 Query Match 40.0%; Score 4; DB 4; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5  
 DB 7 PLPP 10

RESULT 3  
 Q9L8K1 PRELIMINARY; PRT; 13 AA.  
 AC Q9L8K1;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE VANS (Fragment).  
 GN VANSB.  
 OS Enterococcus faecalis (Streptococcus faecalis).  
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.  
 OX NCBI\_TaxID=1351;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BM4281;  
 RX MEDLINE=20307504; PubMed=10846225;  
 RA Dahl K.H., Lundblad E.W., Roekenes T.P., Olsvik O., Sundsfjord A.;  
 RT "Genetic linkage of the vanB2 gene cluster to Tn5382 in vancomycin  
 RT resistant enterococci and characterization of two novel insertion  
 RT sequences."; 146:1469-1479(2000).  
 RL Microbiology  
 DR EMBL; AF201896; AAF73374.1; -.  
 FT NON TER 1  
 SQ SEQUENCE 13 AA; 1502 MW; 8D0E282189F9672A CRC64;

Query Match 40.0%; Score 4; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPPT 6  
 DB 7 LPPT 10

RESULT 4  
 Q14182 PRELIMINARY; PRT; 13 AA.  
 AC Q14182;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)  
 DE Deoxynucleotidyltransferase (Fragment).  
 GN DNTT.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87213162; PubMed=3579900;  
 RA Koilwal O., Kaneda T., Morishita R.;  
 RT "Analysis of human terminal deoxynucleotidyl transferase cDNA  
 RT expressible in mammalian cells";  
 RL Biochem. Biophys. Res. Commun. 144:185-190(1987).  
 DR EMBL; M26144; AAA74588.1; -.  
 GN Transferase.  
 FT NON TER 13  
 FT NON TER 13  
 SQ SEQUENCE 13 AA; 1442 MW; 25B7D365F34FC408 CRC64;

Query Match 40.0%; Score 4; DB 4; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 QPLP 4
Db      8 QPLP 11

RESULT 5
Q40562
ID Q40562 PRELIMINARY; PRT; 15 AA.
AC Q40562;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Small ras-related protein (fragment).
GN RAN-A2.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SR1;
RX MEDLINE=95078947; PubMed=7987414;
RA Merkle T., Haizel T., Matsumoto T., Harter K., Dallmann G., Nagy F.;
RT "Phenotype of the fission yeast cell cycle regulatory mutant pimi-46
RT is suppressed by a tobacco cDNA encoding a small, Ran-like GTP-binding
RT protein."
RL Plant J. 6:555-565(1994).
DR EMBL; L16786; AAA73565.1; -.
KW GTP-binding.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1707 MW; 8AB89F924EA30CAF CRC64;

Query Match 40.0%; Score 4; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QPLP 4
Db      3 QPLP 6

RESULT 6
Q40563
ID Q40563 PRELIMINARY; PRT; 15 AA.
AC Q40563;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Small ras-related protein (fragment).
GN RAN-B2.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SR1;
RX MEDLINE=95078947; PubMed=7987414;
RA Merkle T., Haizel T., Matsumoto T., Harter K., Dallmann G., Nagy F.;
RT "Phenotype of the fission yeast cell cycle regulatory mutant pimi-46
RT is suppressed by a tobacco cDNA encoding a small, Ran-like GTP-binding
RT protein."
RL Plant J. 6:555-565(1994).
DR EMBL; L16788; AAA73565.1; -.
KW GTP-binding.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1604 MW; 9A57F48F1FFFFFAF CRC64;

Query Match 40.0%; Score 4; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;

QY      1 QPLP 4
Db      8 QPLP 11

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QPLP 4
Db      4 QPLP 7

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7
Q84129
ID Q84129 PRELIMINARY; PRT; 18 AA.
AC Q84129;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Influenza A/Swine/Wisconsin/OM/2 (H1N1), non-structural protein (Seg
DE 8), COOH terminus of NS1 (fragment).
OS Influenzavirus A.
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses.
OX NCBI_TaxID=197911;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83303830; PubMed=6612993;
RA Parvin J.D., Young J.F., Palese P.;
RT "nonsense mutations affecting the lengths of the ns1 nonstructural
RT proteins of influenza A virus isolates."
RL Virology 128:512-517(1983).
DR EMBL; K00959; AAA43541.1; -.
DR InterPro; IPR000256; Flu_NS1.
DR Pfam; PF00600; Flu_NS1; I.
FT NON_TER 1
SQ SEQUENCE 18 AA; 2105 MW; 87174BD420FFEBEF CRC64;

Query Match 40.0%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PLPP 5
Db      12 PLPP 15

RESULT 8
Q9REV1
ID Q9REV1 PRELIMINARY; PRT; 19 AA.
AC Q9REV1;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Integrase (fragment).
OS Pseudomonas sp. R9.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=101164;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R9; TRANSPOSON=Tn1404;
RX MEDLINE=20011227; PubMed=10543801;
RA Schnabel E.L., Jones A.L.;
RT "Distribution of tetracycline resistance genes and transposons among
RT phyloplane bacteria in Michigan apple orchards."
RL Appl. Environ. Microbiol. 65:4898-4907(1999).
DR EMBL; AF157798; AAD47998.1; -.
FT NON_TER 19
SQ SEQUENCE 19 AA; 2065 MW; 19EF26DDCA6290F0 CRC64;

Query Match 40.0%; Score 4; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PLPP 5
Db      7 PLPP 10

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RESULT 9
Q9UCA8
ID Q9UCA8 PRELIMINARY; PRT; 20 AA.
AC Q9UCA8;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE Tumor-derived adhesion factor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=94161713; PubMed=8117260;
RA Akaogi K., Okabe Y., Funahashi K., Yoshitake Y., Nishikawa K.,
RA Yasumitsu H., Umeda M., Miyazaki K.;
RT "Cell adhesion activity of a 30-kDa major secreted protein from human
RT bladder carcinoma cells.";
RL Biochem. Biophys. Res. Commun. 198;1046-1053(1994).
SQ SEQUENCE 20 AA; 1979 MW; EF6F9DC6DCA0AE8D CRC64;

Query Match 40.0%; Score 4; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
Db 16 PLPP 19

RESULT 10
Q9S8A8
ID Q9S8A8 PRELIMINARY; PRT; 20 AA.
AC Q9S8A8;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE Gamma-35 SECALIN isoform P9-12 (COELIAC immunoreactive protein)
DE (Fragment).
OS Secale cereale (Rye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Secale.
OX NCBI_TaxID=4550;
RN [1]
RP SEQUENCE.
RX MEDLINE=96283789; PubMed=8679669;
RA Rocher A., Calero M., Soriano F., Mendez E.;
RA "Identification of major rye secalins as coeliac immunoreactive
RT proteins.";
RL Biochim. Biophys. Acta 1295;13-22(1996).
SQ SEQUENCE 20 AA; 2249 MW; 96D3DA4098B5C80 CRC64;

Query Match 40.0%; Score 4; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPLP 4
Db 16 QPLP 19

RESULT 11
Q9PRN3
ID Q9PRN3 PRELIMINARY; PRT; 20 AA.
AC Q9PRN3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE Melanotropin MSH-B.
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OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hypercoartia;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
OX NCBI_TaxID=7757;
RN [1]
RP SEQUENCE.
RX MEDLINE=96122167; PubMed=8537171;
RA Takahashi A., Amemiya Y., Nozaki M., Sower S.A., Joss J., Gorbman A.,
RA Kawauchi H.;
RT "Isolation and characterization of melanotropins from lamprey
RT pituitary glands.";
RL Int. J. Pept. Protein Res. 46;197-204(1995).
SQ SEQUENCE 20 AA; 2403 MW; AC4DAD67CC69AB0D CRC64;

Query Match 40.0%; Score 4; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPLP 4
Db 17 QPLP 20

RESULT 12
P83157
ID P83157 PRELIMINARY; PRT; 9 AA.
AC P83157;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Superoxide dismutase [Fe] (EC 1.15.1.1) (fragment).
OS Anabaena sp. (strain L31).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OX NCBI_TaxID=29412;
RN [1]
RP SEQUENCE.
RA Apte S.K., Uhlemann E., Schmid R., Altendorf K.;
RL Submitted (OCT-2001) to the SWISS-PROT data bank.
CC -!- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
CC CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS.
CC -!- CATALYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) = O(2) + H(2)O(2).
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
CC FAMILY.
CC InterPro: IPR001189; SODismutase.
DR PROSITE: PS00088; SOD MN; PARTIAL.
KW Oxidoreductase; Iron; Metal-binding.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1063 MW; C54267376B06C2C9 CRC64;

Query Match 30.0%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4
Db 6 PLP 8

RESULT 13
Q9TWV0
ID Q9TWV0 PRELIMINARY; PRT; 9 AA.
AC Q9TWV0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE Antho-RPAMIDE-NEUROPEPTIDE.
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthaeae; Actiniidae; Anthopleura.
OX NCBI_TaxID=6110;
RN [1]
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PP SEQUENCE.
RX MEDLINE=93126143; PubMed=1480510;
RA Carstensen K., Rinehart K.L., McFarlane I.D., Grimmelikhuijzen C.J.;
RT "Isolation of Leu-Pro-Gly-Pro-Leu-Pro-Arg-Pro-NH2 (Antho-Ramide),
RT an N-terminally protected, biologically active neuropeptide from sea
RT anemones.";
RL Peptides 13:851-857(1992).
SQ SEQUENCE 9 AA; 943 MW; 2908176737686777 CRC64;

Query Match 30.0%; Score 3; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LPP 5
Db 1 LPP 3

RESULT 14
Q9S8J8 PRELIMINARY; PRT; 9 AA.
AC Q9S8J8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE ORYZATENSIN=BIOACTIVE peptide.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OC NCBI_TaxID=4530;
OX [1]
RN [1]
RP SEQUENCE.
RX MEDLINE=95102521; PubMed=7804141;
RA Takahashi M., Moriguchi S., Yoshikawa M., Sasaki R.;
RT "Isolation and characterization of oxytensin: a novel bioactive
RT peptide with ileum-contracting and immunomodulating activities derived
RT from rice albumin.";
RL Biochem. Mol. Biol. Int. 33:1151-1158(1994).
DR Gramene; Q9S8J8; -.
SQ SEQUENCE 9 AA; 1093 MW; 0E8C67377B56877B CRC64;

Query Match 30.0%; Score 3; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLP 4
Db 6 PLP 8

RESULT 15
Q935G1 PRELIMINARY; PRT; 9 AA.
AC Q935G1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Putative membrane protein (Fragment).
GN HCM1_01C.
OS Salmonella typhi.
OG Plasmid pHCM1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OC NCBI_TaxID=601;
OX [1]
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,

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RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrall B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
DR EMBL; AL513383; CAD09867.1; -.
KW Plasmid; Complete proteome.
FT NON_TER 9
SQ SEQUENCE 9 AA; 904 MW; 5FCDCT7776D86767 CRC64;

Query Match 30.0%; Score 3; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLP 4
Db 1 PLP 3

RESULT 16
Q9R5T2 PRELIMINARY; PRT; 10 AA.
AC Q9R5T2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE NADP-linked glucose-6-phosphate dehydrogenase (Fragment).
OS Acetobacter hansenii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Acetobacteraceae; Gluconacetobacter.
OC NCBI_TaxID=436;
OX [1]
RN [1]
RP SEQUENCE.
RX MEDLINE=92027789; PubMed=1929428;
RA Levy H.R., Cook C.;
RT "Purification and properties of NADP-linked glucose-6-phosphate
RT dehydrogenase from Acetobacter hansenii (Acetobacter xylinum).";
RL Arch. Biochem. Biophys. 291:161-167(1991).
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1111 MW; 5D91D4AAB2D77767 CRC64;

Query Match 30.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LPP 5
Db 3 LPP 5

RESULT 17
Q14096 PRELIMINARY; PRT; 10 AA.
AC Q14096;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CYP2B6 gene cryptic exon 3A of cytochrome P4501B6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
OX [1]
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90174922; PubMed=2308928;
RA Miles J.S., McLaren A.W., Gonzalez F.J., Wolf C.R.;
RT "Alternative splicing in the human cytochrome P4501B6 gene: use of a
RT cryptic exon within intron 3 and splice acceptor site within exon 4.";
RL Nucleic Acids Res. 18:189-189(1990).
DR EMBL; X16864; CAA34754.1; -.

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SQ SEQUENCE 10 AA; 895 MW; 4181B9D87DC77767 CRC64;  
 Query Match 30.0%; Score 3; DB 4; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 LPP 5  
 DB 3 LPP 5  
 RESULT 18  
 Q9QVF7 PRELIMINARY; PRT; 10 AA.  
 ID Q9QVF7  
 AC Q9QVF7  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Beta 2-glycoprotein I, beta 2-GPI (Fragment).  
 OS Rattus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10118;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92135065; PubMed=1777418;  
 RA Matsuura E., Igarashi M., Igarashi Y., Nagae H., Ichikawa K.,  
 RA Yasuda T., Koike T.;  
 RT "Molecular definition of human beta 2-glycoprotein I (beta 2-GPI) by  
 RT cDNA cloning and inter-species differences of beta 2-GPI in  
 RT alternation of anticardiolipin binding."  
 RL Int. Immunol. 3:1217-1221(1991).  
 FT NON\_TER 1 1  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1100 MW; 945681B767376EAL CRC64;  
 Query Match 30.0%; Score 3; DB 11; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 PLP 4  
 DB 5 PLP 7  
 RESULT 19  
 Q8VHM9 PRELIMINARY; PRT; 10 AA.  
 ID Q8VHM9  
 AC Q8VHM9  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Interferon receptor 2a' (Fragment).  
 GN IFNAR2  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6;  
 RA Hardy M.P., Hertzog P.J., Owczarek C.M.;  
 RT "The genomic structure and expression patterns of the gene encoding  
 RT the second chain of the murine interleukin 10 receptor, IL-10R2."  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6;  
 RA Hardy M.P., Hertzog P.J., Owczarek C.M.;  
 RT "The organization, transcriptional regulation and chromosomal  
 RT localization of the locus encoding the gene for the murine type I  
 RT interferon receptor, Ifnar2."  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF440786; AAL40944.1; --  
 KW Receptor.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 10 AA; 1139 MW; 322A36A72449C737 CRC64;  
 Query Match 30.0%; Score 3; DB 11; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 LPP 5  
 DB 1 LPP 3  
 RESULT 20  
 Q8JV78 PRELIMINARY; PRT; 10 AA.  
 ID Q8JV78  
 AC Q8JV78  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Large T antigen (Fragment).  
 OS Polyomavirus JC.  
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.  
 OX NCBI\_TaxID=10632;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=USAI;  
 RX MEDLINE=21465052; PubMed=11581397;  
 RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,  
 RA Girones R.;  
 RT "Potential transmission of human polyomaviruses through the  
 RT gastrointestinal tract after exposure to virions or viral DNA."  
 RL J. Virol. 75:10290-10299(2001).  
 DR EMBL; AF303946; AAM97796.1; --  
 FT NON\_TER 1 1  
 SQ SEQUENCE 10 AA; 1183 MW; 4CD6A96731A32763 CRC64;  
 Query Match 30.0%; Score 3; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 LPP 5  
 DB 7 LPP 9  
 RESULT 21  
 Q90ZV8 PRELIMINARY; PRT; 10 AA.  
 ID Q90ZV8  
 AC Q90ZV8  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Adenylate kinase (Fragment).  
 OS Psittacus erithacus (grey parrot).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Psittaciformes; Psittacidae; Psittacus.  
 OX NCBI\_TaxID=57247;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Shapiro L.H., Dumbacher J.P.;  
 RT "Adenylate kinase intron 5: a new nuclear locus for avian  
 RT systematics."  
 RL Auk 118:248-255(2001).  
 DR EMBL; AF307895; AAK43534.1; --  
 KW Kinase.  
 FT NON\_TER 1 1  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1099 MW; 22847A272731B777 CRC64;  
 Query Match 30.0%; Score 3; DB 13; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;



Matches: 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPT 6  
|||  
Db 3 PPT 5

## RESULT 22

O60761 ID O60761 PRELIMINARY; PRT; 11 AA.  
AC O60761;  
DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE NPT-1 protein (Fragment).  
GN NPT-1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98207718; PubMed=9545579;  
RA Taketani Y., Miyamoto K., Chikamori M., Tanaka K., Yamamoto H.,  
RA Tatsuni S., Morita K., Takeda E.  
RT "Characterization of the 5' flanking region of the human NPT-1  
RT Na+/phosphate cotransporter gene.";  
RL Biochim. Biophys. Acta 1396:267-272(1998).  
DR EMBL; D83236; BAA25645.1; -.  
FT NON TER 11  
SQ SEQUENCE 11 AA; 1358 MW; 884E2D4E6734044A CRC64;

Query Match 30.0%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LPP 5  
|||  
Db 7 LPP 9

## RESULT 23

Q9UCR1 ID Q9UCR1 PRELIMINARY; PRT; 11 AA.  
AC Q9UCR1;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE AUTOTAXIN (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92129337; PubMed=1733949;  
RA Stracke M.L., Krutzsch H.C., Unsworth E.J., Arestad A., Cioce V.,  
RA Schiffmann E., Liotta L.A.;  
RT "Identification, purification, and partial sequence analysis of  
RT autotaxin, a novel motility-stimulating protein.";  
RL J. Biol. Chem. 267:2524-2529(1992).  
FT NON TER 11  
FT NON TER 11  
SQ SEQUENCE 11 AA; 1171 MW; 2723615AA0437737 CRC64;

Query Match 30.0%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPL 3  
|||  
Db 3 QPL 5

## RESULT 24

Q9GL48 ID Q9GL48 PRELIMINARY; PRT; 11 AA.  
AC Q9GL48;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE G protein-coupled receptor (Fragment).  
OS Sus scrofa (pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Nagasaka T., Bouliday G., Coupel S., Coulon F., Tesson L.,  
RA Heslan J.-M., Soullou J.-P., Charreau B.;  
RT "Alternative double screening for differentially expressed genes by  
RT modified RNA differential display and semi-quantitative Reverse  
RT Northern blot.";  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF319662; AAG33870.1; -.  
KW Receptor.  
FT NON TER 1  
SQ SEQUENCE 11 AA; 1298 MW; 822261F10861BB41 CRC64;

Query Match 30.0%; Score 3; DB 6; Length 11;  
Best Local Similarity 100.0%; Pred. No. 5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPT 6  
|||  
Db 2 PPT 4

## RESULT 25

Q9S8Z9 ID Q9S8Z9 PRELIMINARY; PRT; 11 AA.  
AC Q9S8Z9;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE M1 peptide (Fragment).  
OS Psophocarpus tetragonolobus (Goa bean) (Asparagus bean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
OC Psophocarpus.  
OX NCBI\_TaxID=3891;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92232221; PubMed=1368037;  
RA Hirano H., Kagawa H., Okubo K.;  
RL Phytochemistry 31:731-735(1992).  
FT NON TER 1  
FT NON TER 11  
SQ SEQUENCE 11 AA; 1120 MW; 8391BABCDD77772D1 CRC64;

Query Match 30.0%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PTV 7  
|||  
Db 3 PTV 5

## RESULT 26

Q9P116 ID Q9P116 PRELIMINARY; PRT; 12 AA.  
AC Q9P116;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Apolipoprotein E receptor 2 (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Korschinek I., Gharehbaghi-Schnell E., Lang I., Binder R.B.;  
RT "Expression of Apolipoprotein E Receptor 2 in atherosclerosis."  
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; APL29170; AAF66440.1; -.  
KW Lipoprotein; Receptor.  
FT NON\_TER 1  
FT NON\_TER 12  
FT NON\_TER 12  
SQ SEQUENCE 12 AA; 1467 MW; 4E89354104044877 CRC64;  
  
Query Match 30.0%; Score 3; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 PPT 6  
DB 1 PPT 3  
  
RESULT 27  
Q9NTQ2 PRELIMINARY; PRT; 12 AA.  
AC Q9NTQ2;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DE 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
DE D3402L9.1 (Mu opiate receptor (MOR1)) (Fragment).  
GN D3402L9.1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Phillimore B.;  
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; ALI32774; CAB76846.1; -.  
KW Receptor.  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 12 AA; 1296 MW; 68479422BDAB1DDB CRC64;  
  
Query Match 30.0%; Score 3; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 PLP 4  
DB 10 PLP 12  
  
RESULT 28  
Q9TRUI PRELIMINARY; PRT; 12 AA.  
AC Q9TRUI;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE 43 kDa CYANOGEN bromide fragment PEAK 7 (Fragment).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92132498; PubMed=1734497;

RA Veiby O.P., Sletten K., Husby G., Nordstoga K.;  
RT "Amino acid sequence analyses of non-AA proteins from amyloid fibrils of bovine kidney."  
RL Scand. J. Immunol. 35:63-69(1992).  
FT NON\_TER 1  
FT NON\_TER 12  
FT NON\_TER 12  
SQ SEQUENCE 12 AA; 1257 MW; OD5C94FDE9B76AA4 CRC64;  
  
Query Match 30.0%; Score 3; DB 6; Length 12;  
Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 PTV 7  
DB 7 PTV 9  
  
RESULT 29  
P82329 PRELIMINARY; PRT; 12 AA.  
AC P82329;  
DT 01-JUN-2000 (TrEMBLrel. 14, Created)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
DE Unknown protein from 2D-page of thylakoid lumen (SPOT11) (Fragment).  
OS Pisum sativum (Garden pea).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.  
OX NCBI\_TaxID=3888;  
RN [1]  
RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.  
RC STRAIN=cv. DE GRACE; TISSUE=LEAF;  
RX MEDLINE=20181728; PubMed=10715320;  
RA Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F., Adamaka I., van Wijk K.J.;  
RT "Proteomics of the chloroplast: systematic identification and targeting analysis of lumenal and peripheral thylakoid proteins."  
RL Plant Cell 12:319-341(2000).  
CC -|- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN.  
CC -|- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.  
CC -|- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 6.5, ITS MW IS: 24.1 KDA.  
KW Chloroplast; Thylakoid membrane.  
FT NON\_TER 12  
FT NON\_TER 12  
SQ SEQUENCE 12 AA; 1244 MW; CBE0AD74B3D5B862 CRC64;  
  
Query Match 30.0%; Score 3; DB 10; Length 12;  
Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 LPP 5  
DB 9 LPP 11  
  
RESULT 30  
Q14890 PRELIMINARY; PRT; 13 AA.  
AC Q14890;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Mucin (Fragment).  
GN MUC5AC.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Tracheobronchial mucosa;  
RX Guyonnet-Duperat V., Audie J., Debailleul V., Laine A., Buisine M.,

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RA Zouitina-Gallieque S., Pigny P., Degand P., Aubert J., Porchet N.;
RT "Characterization of the human mucin gene MUC5AC: a consensus
RT cysteine-rich domain for 11p15 mucin genes.";
RL Biochem. J. 0:0-0(1994).
DR EMBL; Z34280; CAA84034.1; -.
FT NON_TER 1 1
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1580 MW; 535DF5A5183B7767 CRC64;

Query Match 30.0%; Score 3; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
DB 6 LPP 8

RESULT 31
Q9UNV6 PRELIMINARY; PRT; 13 AA.
AC Q9UNV6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Inosine monophosphatase 2 (Fragment).
GN IMPA2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RX MEDLINE=97463449; PubMed=9322233;
RA Yoshikawa T., Turner G., Esterling L.E., Sanders A.R.,
RA Detera-Wadleigh S.D.;
RT "A novel human myo-inositol monophosphatase gene, IMP.18p, maps to a
RT susceptibility region for bipolar disorder.";
RL Mol. Psychiatry 2:393-397(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20284187;
RA Yoshikawa T., Padigar M., Karkera J.D., Sharma M., Berrettini W.H.,
RA Esterling L.E., Detera-Wadleigh S.D.;
RT "Genomic structure and novel variants of myo-inositol monophosphatase
RT 2.";
RL Mol. Psychiatry 5:165-171(2000).
DR EMBL; AF085628; RAD22141.1; -.
DR EMBL; AF085627; RAD22141.1; JOINED.
FT NON_TER 1 1
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1491 MW; E8154075786DD401 CRC64;

Query Match 30.0%; Score 3; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PTV 7
DB 9 PTV 11

RESULT 32
Q9TRW6 PRELIMINARY; PRT; 13 AA.
AC Q9TRW6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 25 kDa protein P25, peptide F3 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

RA Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=91372400; PubMed=1909972;
RA Takahashi M., Tomizawa K., Ishiguro K., Sato K., Omori A., Sato S.,
RA Shiratsuchi A., Uchida T., Imahori K.;
RT "A novel brain-specific 25 kDa protein (p25) is phosphorylated by a
RT Ser/Thr-Pro Kinase (fPK II) from tau protein kinase fractions.";
RL FEBS Lett. 289:37-43(1991).
FT NON_TER 1 1
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1375 MW; 2C2822494805D1B7 CRC64;

Query Match 30.0%; Score 3; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PTV 7
DB 6 PTV 8

RESULT 33
Q42373 PRELIMINARY; PRT; 13 AA.
AC Q42373;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Patatin class I (Fragment).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]_TaxID=4113;
RP SEQUENCE FROM N.A.
RX MEDLINE=86226014; PubMed=3371664;
RA Mignery G.A., Pikaard C.S., Park W.D.;
RT "Molecular characterization of the patatin multigene family of
RT potato.";
RL Gene 62:27-44(1988).
DR EMBL; M18882; AAA33830.1; -.
DR EMBL; M18881; AAA33829.1; -.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1456 MW; 916595F37A6E29D5 CRC64;

Query Match 30.0%; Score 3; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TVM 8
DB 11 TVM 13

RESULT 34
O88176 PRELIMINARY; PRT; 13 AA.
AC O88176;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Neural cell adhesion molecule (Fragment).
GN NCAM1 OR NCAM
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=Balb-c; TISSUE=Liver;

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RX MEDLINE=98250618; PubMed=9582442;  
RA Kawahigashi H., Harada Y., Asano A., Nakamura M.;  
RT "A cis-acting regulatory element that affects the alternative splicing  
of a muscle-specific exon in the mouse NCAM gene.";  
RL Blochim. Biophys. Acta 1397:305-315(1998).  
DR EMBL; AB001873; BAA31275.1; -.  
DR MGD; MGI:97281; Ncam1.  
FT NON\_TER 1 1  
FT NON\_TER 13 13  
SQ SEQUENCE 13 AA; 1496 MW; CC6098B54C72D732 CRC64;  
Query Match 30.0%; Score 3; DB 11; Length 13;  
Best Local Similarity 100.0%; Pred. No. 5.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 PLP 4  
Db 3 PLP 5  
RESULT 35  
Q9T2K7 PRELIMINARY; PRT; 14 AA.  
AC Q9T2K7;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE 18-kDa chloroplast DNA-binding iron-sulfur protein (Fragment).  
OS Chlamydomonas reinhardtii.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;  
OC Chlamydomonadaceae; Chlamydomonas.  
OX NCBI\_TaxID=3055;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92404720; PubMed=2562513;  
RA Wu M., Nie Z.-Q., Yang J.;  
RT "The 18-kD protein that binds to the chloroplast DNA replicative  
RT origin is an iron-sulfur protein related to a subunit of NADH  
RT dehydrogenase.";  
RL Plant Cell 1:551-557(1989).  
SQ SEQUENCE 14 AA; 1698 MW; 7799E02B12C200CB CRC64;  
Query Match 30.0%; Score 3; DB 8; Length 14;  
Best Local Similarity 100.0%; Pred. No. 6.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 MFP 10  
Db 1 MFP 3  
RESULT 36  
P82326 PRELIMINARY; PRT; 14 AA.  
AC P82326;  
DT 01-JUN-2000 (TrEMBLrel. 14, Created)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
DE Unknown protein from 2D-page of thylakoid lumen (SPOT107) (Fragment).  
OS Pisum sativum (Garden pea).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.  
OX NCBI\_TaxID=3388;  
RN [1]  
RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.  
RC STRAIN=cv. DE GRACE; TISSUE=LEAF;  
RX MEDLINE=20181728; PubMed=10715320;  
RA Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,  
RA Adamska I., van Wijk K.J.;  
RT "Proteomics of the chloroplast: systematic identification and  
RT targeting analysis of luminal and peripheral thylakoid proteins.";

RL Plant Cell 12:319-341(2000).  
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN.  
CC -!- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.  
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 6.0, ITS MW IS: 18.3 KDA.  
KW Chloroplast; Thylakoid membrane.  
FT NON\_TER 14 14  
FT NON\_TER 14 14  
SQ SEQUENCE 14 AA; 1580 MW; 314A6CB514E1B237 CRC64;  
Query Match 30.0%; Score 3; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 6.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 LPP 5  
Db 5 LPP 7  
RESULT 37  
O70599 PRELIMINARY; PRT; 14 AA.  
AC O70599;  
DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Thymidine kinase (EC 2.7.1.21) (Fragment).  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley;  
RA Sauer M.;  
RL Thesis (1999), University of Vienna, Inst. of Molecular Biology.  
DR EMBL; AJ006455; CAA07030.1; -.  
KW Kinase; Transferase.  
FT NON\_TER 14 14  
FT NON\_TER 14 14  
SQ SEQUENCE 14 AA; 1579 MW; 294979C45CB2E8B7 CRC64;  
Query Match 30.0%; Score 3; DB 11; Length 14;  
Best Local Similarity 100.0%; Pred. No. 6.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 PTV 7  
Db 7 PTV 9  
RESULT 38  
Q9KE26 PRELIMINARY; PRT; 14 AA.  
AC Q9KE26;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Hypothetical protein BH1032.  
GN BH1032.  
OS Bacillus halodurans.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=86665;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C-125 / JCM 9153;  
RX MEDLINE=20512582; PubMed=11058132;  
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,  
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,  
RA Horikoshi K.;  
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus  
RT halodurans and genomic sequence comparison with Bacillus subtilis.";  
RL Nucleic Acids Res. 28:4317-4331(2000).  
DR EMBL; AP001510; BAB04751.1; -.  
KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 14 AA; 1697 MW; A9A302145A7AE8A6 CRC64;

Query Match 30.0%; Score 3; DB 16; Length 14;  
Best Local Similarity 100.0%; Pred. No. 6.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TVM 8  
|||  
Db 8 TVM 10

RESULT 39

Q9R5D5 PRELIMINARY; PRT; 15 AA.

ID Q9R5D5  
AC Q9R5D5;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE POLY(3-HYDROXYBUTYRIC acid) granule-associated 40 kDa protein (Fragment).  
OS Chromatium vinosum.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Chromatiales;  
OC Chromatiaceae; Allochrochromatium.  
OX NCBI\_TaxID=1049;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=93146381; PubMed=1490603;  
RA Liebergessel M., Schmidt B., Steinbuechel A.;  
RT "Isolation and identification of granule-associated proteins relevant for poly(3-hydroxyalkanoic acid) biosynthesis in Chromatium vinosum D.";  
RT D.";  
RT FEMS Microbiol. Lett. 78:227-232(1992).  
RL  
SQ SEQUENCE 15 AA; 1834 MW; 215B7FCFCF65B88E CRC64;

Query Match 30.0%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 MFP 10  
|||  
Db 1 MFP 3

RESULT 40

Q9TR62 PRELIMINARY; PRT; 15 AA.

ID Q9TR62  
AC Q9TR62;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE Apolipoprotein A-IV (Fragment).  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=95329112; PubMed=7605356;  
RA Mezdoor H., Yamamura T., Nomura S., Yamamoto A.;  
RT "Genetic but not diet-induced hypercholesterolemia causes low apolipoprotein A-IV level in rabbit sera.";  
RL Atherosclerosis 113:171-178(1995).  
SQ SEQUENCE 15 AA; 1761 MW; DE115BB7351F0ABC CRC64;

Query Match 30.0%; Score 3; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TVM 8  
|||  
Db 9 TVM 11

RESULT 41

Q9QV25 PRELIMINARY; PRT; 15 AA.

ID Q9QV25  
AC Q9QV25;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Sigma receptor cyclophilin-like component (Fragment).  
OS Rattus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10118;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=94322640; PubMed=8046989;  
RA Schuster D.I., Ehrlich G.K., Murphy R.B.;  
RT "Purification and partial amino acid sequence of a 28 kDa cyclophilin-like component of the rat liver sigma receptor.";  
RL Life Sci. 55:151-151(1994).  
SQ SEQUENCE 15 AA; 1622 MW; 95E384B4EC8D14D4 CRC64;

Query Match 30.0%; Score 3; DB 11; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PTV 7  
|||  
Db 3 PTV 5

RESULT 42

Q69353 PRELIMINARY; PRT; 15 AA.

ID Q69353  
AC Q69353;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE HSV-2 (333) N terminus of 17.8 kDa protein gene (0.642 mu) (Fragment).  
OS Herpes simplex virus (type 2).  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Alphaherpesvirinae; Simplexvirus.  
OX NCBI\_TaxID=10310;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85033906; PubMed=6092683;  
RA Draper K.G., Frink R.J., Devi G.B., Swain M., Galloway D.,  
RA Wagner E.K.;  
RT "Herpes simplex virus types 1 and 2 homology in the region between 0.58 and 0.68 map units.";  
RL J. Virol. 52:615-623(1984).  
DR EMBL; K03360; AAA45840.1; -.  
FT NON TER 15  
SQ SEQUENCE 15 AA; 1603 MW; 20B04D60BA4507FE CRC64;

Query Match 30.0%; Score 3; DB 12; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPL 3  
|||  
Db 11 QPL 13

RESULT 43

Q9R5K7 PRELIMINARY; PRT; 16 AA.

ID Q9R5K7  
AC Q9R5K7;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE 23.4-kDa chitinase (Fragment).  
OS Streptomyces olivaceoviridis (Streptomyces corchorusii).

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomycineae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=1921;  
 RN [1]\_SEQUENCE.  
 RP SEQUENCE.  
 RX MEDLINE=92276319; PubMed=1592803;  
 RA Romaguera A., Menge U., Breves R., Diekmann H.;  
 RT "Chitinases of Streptomyces olivaceoviridis and significance of  
 RT processing for multiplicity.";  
 RL J. Bacteriol. 174:3450-3454(1992).  
 FT NON\_TER 1  
 FT NON\_TER 16  
 SQ SEQUENCE 16 AA; 2014 MW; 0F732A24DC14CE01 CRC64;  
 Query Match 30.0%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 MFP 10  
 Db |||  
 6 MFP 8  
 RESULT 44  
 Q9NNZ2 PRELIMINARY; PRT; 16 AA.  
 ID Q9NNZ2  
 AC Q9NNZ2  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
 DE Integrin alpha-2 subunit (Fragment).  
 GN ITGA2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98421383; PubMed=9746778;  
 RA Kritzik M., Savage B., Nugent D.J., Santoso S., Ruggeri Z.M.,  
 RA Kunitzki T.J.;  
 RT "Nucleotide polymorphisms in the alpha2 gene define multiple alleles  
 RT that are associated with differences in platelet alpha2 beta1  
 RT density.";  
 RL Blood 92:2382-2388(1998).  
 DR EMBL: AF062039; AAF77577.1; -.  
 FT NON\_TER 16  
 FT NON\_TER 16  
 SQ SEQUENCE 16 AA; 1635 MW; F6A5FC64F83370A9 CRC64;  
 Query Match 30.0%; Score 3; DB 4; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 PLP 4  
 Db |||  
 10 PLP 12  
 RESULT 45  
 O18378 PRELIMINARY; PRT; 16 AA.  
 ID O18378  
 AC O18378  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE Hypothetical 1.5 kDa protein in ANON-37CS 5'REGION (ORF3).  
 GN ANON-37CC.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Great A., Lamberton L., Williams P.A., Thomas C.M.;

RP SEQUENCE FROM N.A.  
 RX MEDLINE=88038375; PubMed=3478553;  
 RA Eveleth D.D., Marsh J.L.;  
 RT "Overlapping transcription units in Drosophila: sequence and structure  
 RT of the Cs gene.";  
 RL Mol. Gen. Genet. 209:290-298(1987).  
 DR EMBL: X05991; CAA29407.1; -.  
 DR Flybase; FBgn0026744; anon-37Cc.  
 KW Hypothetical protein.  
 SQ SEQUENCE 16 AA; 1543 MW; F6F881ED5A799277 CRC64;  
 Query Match 30.0%; Score 3; DB 5; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 PTV 7  
 Db |||  
 13 PTV 15  
 RESULT 46  
 P92732 PRELIMINARY; PRT; 16 AA.  
 ID P92732  
 AC P92732  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE NADH dehydrogenase subunit II (Fragment).  
 GN ND2.  
 OS Fejervarya limnocharis (Bole's wart frog).  
 OC Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae;  
 OC Fejervarya.  
 OX NCBI\_TaxID=110108;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97153826; PubMed=9000757;  
 RA Macey J.R., Larson A., Ananjeva N.B., Fang Z., Papenfuss T.J.;  
 RT "Two novel gene orders and the role of light-strand replication in  
 RT rearrangement of the vertebrate mitochondrial genome.";  
 RL Mol. Biol. Evol. 14:91-104(1997).  
 DR EMBL: U71324; AAB48287.1; -.  
 KW Mitochondrion.  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 16 AA; 1860 MW; DD1C1017F8B19DEE CRC64;  
 Query Match 30.0%; Score 3; DB 8; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 MFP 10  
 Db |||  
 5 MFP 7  
 RESULT 47  
 Q8VME2 PRELIMINARY; PRT; 17 AA.  
 ID Q8VME2  
 AC Q8VME2  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE PARC protein (Fragment).  
 GN PARC.  
 OS Pseudomonas putida.  
 OC Plasmid pWWO.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxID=303;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Great A., Lamberton L., Williams P.A., Thomas C.M.;

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RT "Complete nucleotide sequence of lncP-9 plasmid pW0.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ344068; CAC86875.1; -.
KW Plasmid.
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1903 MW; A58E0B85C365A999 CRC64;

Query Match 30.0%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPL 3
DB 14 QPL 16

RESULT 48
P97135 PRELIMINARY; PRT; 17 AA.
AC P97135;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GyxA protein (Fragment).
GN GYXA.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN:H37Ra;
RX MEDLINE=95072534; PubMed=7981652;
RA Madhusudan K., Ramesh V., Nagaraja V.;
RT "Molecular cloning of gyrA and gyrB genes of Mycobacterium
RT tuberculosis: analysis of nucleotide sequence.";
RL Biochem. Mol. Biol. Int. 33:651-660 (1994).
DR EMBL; X78888; CAA55487.1; -.
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1916 MW; EF0B750A36E365AE CRC64;

Query Match 30.0%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
DB 6 LPP 8

RESULT 49
O15276 PRELIMINARY; PRT; 17 AA.
AC O15276;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Mitochondrial translation elongation factor EF-Tu (Fragment).
GN TUFM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Jacobs H.T., Smurthwaite L., Koshy R.;
RT "Human genomic sequences encoding mitochondrial elongation factor EF-
RT Tu: Evidence for post-endosymbiotic intron insertion.";
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y11797; CAA72493.1; -.
KW Elongation factor.
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1763 MW; BE06BF41F3A2BF94 CRC64;

Query Match 30.0%; Score 3; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4
DB 14 PLP 16

RESULT 50
Q96P96 PRELIMINARY; PRT; 17 AA.
AC Q96P96;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NHP2-like protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kang H.S., Park Y.J., Jung H.M., Jun D.Y., Huh T.L., Kim Y.H.;
RT "Characterization of TPA-responsive genes in U937 cells using ordered
RT differential display PCR.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF401217; AAL02173.1; -.
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1948 MW; AB699819BD70BCEF CRC64;

Query Match 30.0%; Score 3; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4
DB 14 PLP 16

RESULT 51
Q9TRU8 PRELIMINARY; PRT; 17 AA.
AC Q9TRU8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Leukemia inhibitory factor, LIF=INHIBITOR of aortic endothelial cell
DE growth (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=92115728; PubMed=1370585;
RA Ferrara N., Miner J., Henzel W.J.;
RT "Pituitary follicular cells secrete an inhibitor of aortic endothelial
RT cell growth: identification as leukemia inhibitory factor.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:698-702 (1992).
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1763 MW; BE06BF41F3A2BF94 CRC64;

Query Match 30.0%; Score 3; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4
DB 14 PLP 16

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Db          2 PTP 4

RESULT 52
P83061
ID P83061 PRELIMINARY; PRT; 17 AA.
AC P83061;
DT 01-OCT-2001 (TREMBlrel. 18, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Putative FK506-binding protein (FKBP) (peptidyl-prolyl cis-trans
DE isomerase) (PPIase) (EC 5.2.1.8) (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllaceae; Chenopodiaceae; Spinacia.
OC NCBI_TaxID=3562;
RN [1]
RP SEQUENCE, AND SUBCELLULAR LOCATION.
RA Schubert M., Peterson U., Funk C., Haas B., Schroeder W.P.,
RA Kieselbach T.;
RL Submitted (JUL-2001) to the SWISS-PROT data bank.
CC -!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS (BY
CC SIMILARITY).
CC -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPEPTIDES.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST; WITHIN THE THYLAKOID LUMEN.
CC -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
DR InterPro; IPR001179; FKBP_PPIase.
KW Isomerase; Rotamase; Chloroplast.
FT NON_TER 17
SQ SEQUENCE 17 AA; 1771 MW; E2013F998EFBF908 CRC64;

Query Match 30.0%; Score 3; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
Db 3 LPP 5

RESULT 53
Q8B4C4
ID Q8B4C4 PRELIMINARY; PRT; 17 AA.
AC Q8B4C4;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Precore.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OC NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RA Vaishali C., Acharya S.K., Panda S.K.;
RT "Cryptic Hepatitis B virus infection: analysis of the complete genomic
RT sequence of HBV from nine patients with seronegative viral
RT hepatitis."
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY161158; AA012630.1; -.
SQ SEQUENCE 17 AA; 1908 MW; 0B63A9BF82802588 CRC64;

Query Match 30.0%; Score 3; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PTV 7
Db 15 PTV 17

RESULT 54
Q9RSU2
ID Q9RSU2 PRELIMINARY; PRT; 18 AA.
AC Q9RSU2;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE 2-amino-benzoate-CoA LIGASE=E3 (Fragment).
OS Pseudomonas.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae.
OC NCBI_TaxID=286;
RN [1]
RP SEQUENCE.
RX MEDLINE=91358327; PubMed=1885526;
RA Altenschmidt U., Oswald B., Fuchs G.;
RT "Purification and characterization of benzoate-coenzyme A ligase and
RT 2-aminobenzoate-coenzyme A ligases from a denitrifying Pseudomonas
RT sp."
RL J. Bacteriol. 173:5494-5501 (1991).
FT NON_TER 18
FT NON_TER 18
SQ SEQUENCE 18 AA; 2061 MW; C43F8799692771EF CRC64;

Query Match 30.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
Db 12 LPP 14

RESULT 55
Q9RSF9
ID Q9RSF9 PRELIMINARY; PRT; 18 AA.
AC Q9RSF9;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Arsenite oxidase, AOI (Fragment).
OS Alcaligenes faecalis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Alcaligenes.
OC NCBI_TaxID=511;
RN [1]
RP SEQUENCE.
RX MEDLINE=93054722; PubMed=1331097;
RA Anderson G.L., Williams J., Hille R.;
RT "The purification and characterization of arsenite oxidase from
RT Alcaligenes faecalis, a molybdenum-containing hydroxylase."
RL J. Biol. Chem. 267:23674-23682 (1992).
FT NON_TER 18
FT NON_TER 18
SQ SEQUENCE 18 AA; 1938 MW; 4EDDC418B71A4574 CRC64;

Query Match 30.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
Db 9 LPP 11

RESULT 56
Q9R4V9
ID Q9R4V9 PRELIMINARY; PRT; 18 AA.
AC Q9R4V9;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE 10 kDa heat shock- and alkaline PH-induced protein (Fragment).
OS Campylobacter jejuni.
```



OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;  
OC Campylobacteraceae; Campylobacter.  
OX NCBI\_TaxID=197;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=95012609; PubMed=7927682;  
RA Wu Y.-L., Lee L.H., Rollins D.M., Ching W.M.;  
RT "Heat shock- and alkaline pH-induced proteins of Campylobacter jejuni;  
RT characterization and immunological properties.";  
RL Infect. Immun. 62:4256-4260(1994).  
SQ SEQUENCE 18 AA; 2056 MW; 9E4FED7B84DA76C4 CRC64;

Query Match 30.0%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPL 3  
Db 4 QPL 6

RESULT 57  
Q9EYW5 PRELIMINARY; PRT; 18 AA.  
AC Q9EYW5;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE RepB.  
GN REPB.  
OS Erwinia stewartii.  
OG Plasmid pSW800.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Pantoea.  
OX NCBI\_TaxID=66271;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Wu C.-Y., Liu S.-T.;  
RT "Erwinia stewartii plasmid pSW800 basic replicon, repA and repB  
RT genes.";  
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF310258; AAG4776.1; -.  
KW Plasmid.  
SQ SEQUENCE 18 AA; 1952 MW; C8FD2873F9CAC66C CRC64;

Query Match 30.0%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPL 3  
Db 6 QPL 8

RESULT 58  
Q9R4C6 PRELIMINARY; PRT; 18 AA.  
AC Q9R4C6;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Protocatechuate 3,4-dioxygenase type I alpha subunit (EC 1.13.11.3)  
DE (Fragment).  
OS Agrobacterium tumefaciens.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Rhizobiaceae; Rhizobium.  
OX NCBI\_TaxID=358;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=96337865; PubMed=8772173;  
RA Hammer A., Stolz A., Knackmuss H.;  
RT "Purification and characterization of a novel type of protocatechuate  
RT 3,4-dioxygenase with the ability to oxidize 4-sulfocatechol.";

RL Arch. Microbiol. 166:92-100(1996).  
SQ SEQUENCE 18 AA; 2152 MW; BFC56CABD4376D84 CRC64;

Query Match 30.0%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPL 3  
Db 2 QPL 4

RESULT 59  
Q96F98 PRELIMINARY; PRT; 18 AA.  
AC Q96F98;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Hypothetical protein (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC011455; AAH11455.1; -.  
KW Hypothetical protein.  
FT NON\_TER 1  
SQ SEQUENCE 18 AA; 2114 MW; 3A6C3E2BF620B9CD CRC64;

Query Match 30.0%; Score 3; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPT 6  
Db 9 PPT 11

RESULT 60  
Q16244 PRELIMINARY; PRT; 18 AA.  
AC Q16244;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)  
DE STS protein (Fragment).  
GN STS.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95038775; PubMed=7951263;  
RA Yen P.H., Ferrero G.B., Chinault A.C., Mohandas T., Ballabio A.;  
RT "Characterization of the deletion breakpoints in a patient with  
RT steroid sulfatase deficiency.";  
RL Hum. Mutat. 4:76-78(1994).  
DR EMBL; S74383; AAD14153.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 18 AA; 1958 MW; 3B3072711330CCFA CRC64;

Query Match 30.0%; Score 3; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PTP 4  
Db 11

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Db          2 PLP 4

RESULT 61
Q8NFB4
ID Q8NFB4 PRELIMINARY; PRT; 18 AA.
AC Q8NFB4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Mutant enamelin (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kida M., Ariga T.;
RT "Autosomal-dominant hypoplastic form of amelogenesis imperfecta caused
RT by an enamelin gene mutation at exon-intron boundary.";
RL J. Dent. Res. 0:0-0(2002).
DR EMBL; AF530444; AAM97323.1; -.
FT NON_TER 1 18
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 1893 MW; 492D2B2E3B8B512 CRC64;

Query Match 30.0%; Score 3; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
Db 2 LPP 4

RESULT 62
Q8S915
ID Q8S915 PRELIMINARY; PRT; 18 AA.
AC Q8S915;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE TETRAERIC alpha-amylase inhibitor 16 kDa subunit, CM16*
DE (Fragment).
OS Triticum turgidum (Poulard wheat) (Rivet wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4571;
RN [1]
RP SEQUENCE.
RX MEDLINE=92143804; PubMed=1736890;
RA Sanchez-Monge R., Gomez L., Barber D., Lopez-Otin C., Armentia A.,
RA Salcedo G.;
RT "Wheat and barley allergens associated with baker's asthma.
RT Glycosylated subunits of the alpha-amylase-inhibitor family have
RT enhanced IGE-binding capacity.";
RL Biochem. J. 281:401-405(1992).
FT NON_TER 1 18
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 1988 MW; 681835D1F68C30F8 CRC64;

Query Match 30.0%; Score 3; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4
Db 16 PLP 18

RESULT 63
Q9K4X0
ID Q9K4X0 PRELIMINARY; PRT; 19 AA.
AC Q9K4X0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GvPC-28 protein (Fragment).
DE GvPC-28.
GN Planktothrix agardhii.
OS Bacteria; Cyanobacteria; Oscillatoriales; Planktothrix.
OX NCBI_TaxID=54305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CYA 137;
RC MEDLINE=20391846; PubMed=10931905;
RA Beard S.J., Davis P.A., Iglesias-Rodriguez D., Skulberg O.M.,
RA Walsby A.E.;
RT "Gas vesicle genes in Planktothrix spp. from Nordic lakes: strains
RT with weak gas vesicles possess a longer variant of gvpC.";
RL Microbiology 146:2009-2018(2000).
DR EMBL; AJ253133; CAB59522.1; -.
FT NON_TER 1 1
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 1944 MW; 647F169473797D19 CRC64;

Query Match 30.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PTV 7
Db 2 PTV 4

RESULT 64
Q9UC80
ID Q9UC80 PRELIMINARY; PRT; 19 AA.
AC Q9UC80;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE 21.5 kDa stone matrix protein (RC 1.15.1.1) (Superoxide dismutase
DE [Mn/Fe]) (Fragment).
DE (Mn/Fe).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=95215817; PubMed=7701298;
RA Binette J.P., Binette M.B.;
RT "Sequencing of proteins extracted from stones.";
RL Scanning Microsc. 8:233-239(1994).
CC -1- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
CC CELLS AND WHICH ARE TOXIC TO BIOLOGICAL SYSTEMS (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 2 SUPEROXIDE + 2 H(+) = O(2) + H(2)O(2).
CC -1- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
CC FAMILY.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sodfe; 1.
KW Oxidoreductase.
SQ SEQUENCE 19 AA; 2116 MW; A0D0DAE848EE7894 CRC64;

Query Match 30.0%; Score 3; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LPP 5
Db 4 LPP 6

RESULT 65
Q8NFL2
ID Q8NFL2 PRELIMINARY; PRT; 19 AA.

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AC Q8NPL2;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Prolyl isomerase (Fragment).  
 GN PIN1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]\_TaxID=9606;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22095969; PubMed=12101225;  
 RA Ryo A., Liou Y.C., Wulf G., Nakamura M., Lee S.W., Lu K.P.;  
 RT "PIN1 Is an E2F Target Gene Essential for Neu/Ras-Induced  
 RT Transformation of Mammary Epithelial Cells."  
 RL Mol. Cell. Biol. 22:5281-5295(2002).  
 DR EMBL; AF501321; AAM81970.1; -.  
 KW Isomerase.  
 FT NON TER 19 19  
 SQ SEQUENCE 19 AA; 2235 MW; 1C4FC381C8A0F17F CRC64;  
 Query Match 30.0%; Score 3; DB 4; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 7.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 LPP 5  
 Db |||  
 7 LPP 9  
 ID Q9UCK6 PRELIMINARY; PRT; 19 AA.  
 AC Q9UCK6;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
 DE Aspartylglucosaminidase beta 1 subunit (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]\_TaxID=9606;  
 RP SEQUENCE.  
 RX MEDLINE=93111925; PubMed=1281977;  
 RA Rip J.W., Coulter-Mackie M.B., Rupa C.A., Gordon B.A.;  
 RT "Purification and structure of human liver aspartylglucosaminidase."  
 RL Biochem. J. 288:1005-1010(1992).  
 DR HSP; P20933; 1APV.  
 SQ SEQUENCE 19 AA; 2127 MW; BC2F148525610300 CRC64;  
 Query Match 30.0%; Score 3; DB 4; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 7.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 LPP 4  
 Db |||  
 2 LPP 4  
 ID Q31687 PRELIMINARY; PRT; 19 AA.  
 AC Q31687;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE ATPase subunit 8 (Fragment).  
 GN ATP8.  
 OS Artemia parthenogenetica.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Branchiopoda; Anostraca;

OC Artemiidae; Artemia.  
 OX NCBI\_TaxID=6663;  
 RN [1]\_TaxID=6663;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=La Mata;  
 RX MEDLINE=94223692; PubMed=8169960;  
 RA Perez M.L., Valverde J.R., Batuecas B., Amat F., Marco R., Garesse R.;  
 RT "Speciation in the artemia genus: mitochondrial DNA analysis of  
 RT bisexual and parthenogenetic brine shrimps."  
 RL J. Mol. Evol. 38:156-168(1994).  
 DR EMBL; X67263; CAA47685.1; -.  
 KW Mitochondrion.  
 FT NON TER 1 1  
 FT NON TER 19 19  
 SQ SEQUENCE 19 AA; 2246 MW; 41922AD313E087E3 CRC64;  
 Query Match 30.0%; Score 3; DB 8; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 7.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 LPP 4  
 Db |||  
 6 LPP 8  
 ID Q9GI97 PRELIMINARY; PRT; 19 AA.  
 AC Q9GI97;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit  
 DE (Fragment).  
 OS Sargassum polycystum.  
 GN RBCL.  
 OG Chloroplast.  
 OC Eukaryota; stramenopiles; Phaeophyceae; Fucales; Sargassaceae;  
 OC Sargassum.  
 OX NCBI\_TaxID=127578;  
 RN [1]\_TaxID=127578;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=nepl27;  
 RA Phillips N.E.;  
 RT "Molecular phylogenetic analysis of the pan-pacific genus Sargassum  
 RT (Fucales, Phaeophyceae)."  
 RL Thesis (1998), University of Hawaii.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=nepl27;  
 RA Phillips N.E., Smith C.M., Morden C.W.;  
 RT "Testing the systematics of the genus Sargassum (Fucales,  
 RT Phaeophyceae) with the Rubisco operon."  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF244344; AAF98113.1; -.  
 KW Chloroplast.  
 FT NON TER 1 1  
 SQ SEQUENCE 19 AA; 2108 MW; A02FD2E6DD68A57 CRC64;  
 Query Match 30.0%; Score 3; DB 8; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 7.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 PPT 6  
 Db |||  
 4 PPT 6  
 ID Q9S8F5 PRELIMINARY; PRT; 19 AA.  
 AC Q9S8F5;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)

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DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE PMP=31 kDa plasma membrane intrinsic protein (Fragment).
OC Beta vulgaris (Sugar beet).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Beta.
OX NCBI_TaxID=161934;
[1]
RN SEQUENCE.
RP MEDLINE=95303965; PubMed=7784509;
RA Qi X., Tai C.Y., Wasserman B.P.;
RA "Plasma membrane intrinsic proteins of Beta vulgaris L.";
RL Plant Physiol. 108:387-392(1995).
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2102 MW; 5BF1773684FF8D84 CRC64;

Query Match 30.0%; Score 3; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPL 3
Db 10 QPL 12

RESULT 70
Q69099
ID Q69099 PRELIMINARY; PRT; 19 AA.
AC Q69099;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Protein 32 (Fragment).
OS Herpes simplex virus (type 2).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10310;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=90156509; PubMed=2154597;
RA Yei S., Chowdhury S.I., Bhat B.M., Conley A.J., Wold W.S.,
RA Batterson W.;
RA "Identification and characterization of the Herpes simplex virus type
RT 2 gene encoding the essential capsid protein ICP32/VP19c.";
RL J. Virol. 64:1124-1134(1990).
DR EMBL; M33905; AAA45846.1; -.
FT NON_TER 19
FT NON_TER 19
SQ SEQUENCE 19 AA; 2058 MW; 47125921CA53FA35 CRC64;

Query Match 30.0%; Score 3; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLP 4
Db 5 PLP 7

RESULT 71
Q9PRT0
ID Q9PRT0 PRELIMINARY; PRT; 19 AA.
AC Q9PRT0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE 23A7 antigen (Fragment).
OC Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;

```

```

RN SEQUENCE.
RP MEDLINE=95332492; PubMed=7608337;
RA Denburg J.L., Caldwell R.T., Marner J.M.;
RA "Developmental changes in epitope accessibility as an indicator of
RT multiple states of an immunoglobulin-like neural cell adhesion
RT molecule.";
RL J. Comp. Neurol. 354:533-550(1995).
SQ SEQUENCE 19 AA; 2051 MW; 83B67BEE484EBD03 CRC64;

Query Match 30.0%; Score 3; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPT 6
Db 16 PPT 18

RESULT 72
Q9PRN4
ID Q9PRN4 PRELIMINARY; PRT; 19 AA.
AC Q9PRN4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Melanotropin MSH-A.
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
OX NCBI_TaxID=7757;
[1]
RN SEQUENCE.
RP MEDLINE=96122167; PubMed=8537171;
RA Takahashi A., Amemiya Y., Nozaki M., Sower S.A., Joss J., Gorbman A.,
RA Kawachi H.;
RA "Isolation and characterization of melanotropins from lamprey
RT pituitary glands.";
RL Int. J. Pept. Protein Res. 46:197-204(1995).
SQ SEQUENCE 19 AA; 2400 MW; 0F4CD35F7E0BC340 CRC64;

Query Match 30.0%; Score 3; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPT 6
Db 15 PPT 17

RESULT 73
Q9ORF8
ID Q9ORF8 PRELIMINARY; PRT; 19 AA.
AC Q9ORF8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=97CG276;
RC Taniguchi Y., Takehisa J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., Obengui, M'Pandi M., M'Pele P., Harada Y.,
RA Hayami M., Ichimura H., Farra J.H.;
RA "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RT Republic of Congo-Brazzaville.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF127550; AAK84913.1; -.
FT NON_TER 1
FT NON_TER 1

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FT NON TER 19 19  
SQ SEQUENCE 19 AA; 2304 MW; 2727D4B66AE69237 CRC64;

Query Match 30.0%; Score 3; DB 15; Length 19;  
Best Local Similarity 100.0%; Pred. No. 7.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4  
Db 16 PLP 18

RESULT 74  
Q905E8  
ID Q905E8 PRELIMINARY; PRT; 19 AA.  
AC Q905E8;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Tat protein (Fragment).  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=37CG314;  
RA Taniguchi Y., Takehsia J., Bikandou B., Mboudjeka I.,  
RA N'Doundou-N'Kodia M.-Y., M'Pandi M., M'Pele P., Harada Y., Hayami M.,  
RA Ichimura H., Parra H.-J.,  
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in  
RT Republic of Congo-Brazzaville.";  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF410452; AAL10274.1; -.  
FT NON\_TER 1 1  
FT NON\_TER 19 19  
SQ SEQUENCE 19 AA; 2200 MW; 367B64CAE5069886 CRC64;

Query Match 30.0%; Score 3; DB 15; Length 19;  
Best Local Similarity 100.0%; Pred. No. 7.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLP 4  
Db 16 PLP 18

RESULT 75  
Q9R4M9  
ID Q9R4M9 PRELIMINARY; PRT; 20 AA.  
AC Q9R4M9;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
DE Extracellular levansucrase (EC 2.4.1.10) (Fragment).  
OS Pseudomonas syringae.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Pseudomonas.  
OX NCBI\_TaxID=317;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=95270602; PubMed=7751294;  
RA Hettwer U., Gross M., Rudolph K.;  
RT "Purification and characterization of an extracellular levansucrase  
RT from Pseudomonas syringae pv. phaseolicola.";  
RL J. Bacteriol. 177:2834-2839(1995).  
SQ SEQUENCE 20 AA; 2218 MW; 9DCE15F23BEFF2B5 CRC64;

Query Match 30.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PTV 7  
|||

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:16:09 ; Search time 25.5233 Seconds  
(without alignments)  
62.189 Million cell updates/sec

Title: US-09-641-801-25  
Perfect score: 10  
Sequence: 1 QPLPPTVMFP 10

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3  
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : A\_Geneseq\_19Jun03.\*

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24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	100.0	10	22	Colostrinin derive
2	10	100.0	10	22	Colostrinin peptid
3	10	100.0	10	22	Colostrinin peptid
4	10	100.0	10	23	Colostrinin consti
5	10	100.0	10	23	Colostrinin consti
6	10	100.0	10	23	Neural cell regula
7	10	100.0	15	22	Colostrinin derive
8	10	100.0	15	22	Colostrinin peptid
9	10	100.0	15	22	Colostrinin peptid

10	100.0	15	22	AA59334	Ewe colostrinin pe
11	10	100.0	15	23	Colostrinin consti
12	10	100.0	15	23	Colostrinin consti
13	10	100.0	15	23	Neural cell regula
14	9	90.0	11	22	Colostrinin peptid
15	9	90.0	11	22	Colostrinin peptid
16	6	60.0	12	22	Modified colostrin
17	6	60.0	11	22	Ewe colostrinin pe
18	5	50.0	16	18	Grb2 N-terminal SH
19	5	50.0	7	20	Mammalian ion chan
20	5	50.0	7	23	SH3 antagonist pep
21	5	50.0	8	22	Src homology3 (SH3
22	5	50.0	8	22	Human protein frag
23	5	50.0	9	22	Human protein frag
24	5	50.0	12	22	Clone 1 scFv CDR L
25	5	50.0	13	16	P13K protein tyros
26	5	50.0	13	17	Src SH3 domain-bin
27	5	50.0	13	23	Escherichia coli 3
28	5	50.0	13	24	Human TPO peptide
29	5	50.0	13	24	Human TPO peptide
30	5	50.0	13	24	Human TPO peptide
31	5	50.0	13	24	Human TPO peptide
32	5	50.0	13	24	Human TPO peptide
33	5	50.0	14	20	Amino acid sequenc
34	5	50.0	14	22	Human protein frag
35	5	50.0	14	22	Bacille Calmette-G
36	5	50.0	14	22	BCG T-cell epitope
37	5	50.0	15	18	Peptide resembling
38	5	50.0	15	18	Peptide resembling
39	5	50.0	15	22	Growth hormone fam
40	5	50.0	15	23	Human K-ras 10.67
41	5	50.0	16	18	Yes SH3 domain bin
42	5	50.0	16	18	Src SH3 domain bin
43	5	50.0	16	18	Src SH3 domain bin
44	5	50.0	16	24	G protein-coupled
45	5	50.0	17	21	Gene 31 human secr
46	5	50.0	18	22	Human gene 10 enco
47	5	50.0	19	20	Ubiquitin fusion p
48	5	50.0	19	20	Ubiquitin fusion p
49	5	50.0	19	22	MT peptide. Unide
50	5	50.0	20	17	Src SH3 domain-bin
51	5	50.0	20	17	T-cell epitope use
52	5	50.0	20	18	Heatshock protein
53	5	50.0	20	18	Heatshock protein
54	5	50.0	20	19	Mycobacteria heat
55	5	50.0	20	23	Mycobacterium heat
56	4	40.0	4	16	Peptidase substrat
57	4	40.0	5	21	Rat amelogenin N-c
58	4	40.0	6	13	Casoxin D-like vas
59	4	40.0	6	19	Transcriptional ac
60	4	40.0	6	19	Transcriptional ac
61	4	40.0	7	15	Fragment of the 3B
62	4	40.0	7	17	Src SH3 domain-bin
63	4	40.0	7	17	Src SH3 domain-bin
64	4	40.0	7	17	Synthetic peptide
65	4	40.0	7	18	SH3 domain binding
66	4	40.0	7	18	Ferritin motif #17
67	4	40.0	7	19	Proline-rich pepti
68	4	40.0	7	20	Mammalian ion chan
69	4	40.0	7	20	Heat shock protein
70	4	40.0	7	21	SH3 antagonist pep
71	4	40.0	7	21	SH3 antagonist pep
72	4	40.0	7	21	SH3 antagonist pep
73	4	40.0	7	21	SH3 antagonist pep
74	4	40.0	7	21	SH3 antagonist pep
75	4	40.0	7	21	Src antagonist pep
76	4	40.0	7	21	Src SH3 region bin
77	4	40.0	7	22	Melanoma antigen,
78	4	40.0	7	22	H11 binding site c
79	4	40.0	7	22	H11 binding site c
80	4	40.0	7	22	H11 binding site c
81	4	40.0	7	22	H11 binding site c
82	4	40.0	7	22	H11 binding site c

83 4 40.0 7 22 AAB50762 Human CAMP-specifi  
 84 4 40.0 7 22 AAB50763 Human CAMP-specifi  
 85 4 40.0 7 23 ABB73219 Src homology3 (SH3  
 86 4 40.0 7 23 ABB73221 Src homology3 (SH3  
 87 4 40.0 7 23 ABB73222 Src homology3 (SH3  
 88 4 40.0 7 23 ABB73225 Src homology3 (SH3  
 89 4 40.0 7 23 ABB73226 Src homology3 (SH3  
 90 4 40.0 7 23 ABB73345 Exemplary pharmaco  
 91 4 40.0 7 23 AAU80708 Javelin peptide #1  
 92 4 40.0 8 16 AAR71945 Human 3BP1 peptide  
 93 4 40.0 8 19 AAW57875 C. felis esterase  
 94 4 40.0 8 20 AAV16845 Heat shock protein  
 95 4 40.0 8 22 AAE12921 Ctenocephalides fe  
 96 4 40.0 8 22 AAB31509 Amino acid sequenc  
 97 4 40.0 9 16 AAR7304 Plasmodium falcipa  
 98 4 40.0 9 16 AAR77565 HIV-B35-50(C-48),  
 99 4 40.0 9 16 AAR84612 HCV-1 derived pept  
 100 4 40.0 9 20 AAY10090 T cell epitope/MHC

## ALIGNMENTS

RESULT 1  
 AAB72270  
 ID AAB72270 standard; peptide; 10 AA.  
 XX  
 AC AAB72270;  
 XX  
 DT 14-MAY-2001 (first entry)  
 XX  
 DE Colostrinin derived cytokine inducing peptide SEQ ID 25.  
 XX  
 KW Colostrinin; immune response; cytokine; blood cell proliferation;  
 KW central nervous system disorder; neurological disorder; mental disorder;  
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;  
 KW neurosis; infection.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200111937-A2.  
 XX  
 XX  
 PD 22-FEB-2001.  
 XX  
 PF 17-AUG-2000; 2000WO-US222818.  
 XX  
 PR 17-AUG-1999; 99US-0149311.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 PA (REG-) REGEN THERAPEUTICS PLC.  
 XX  
 XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
 PI  
 XX WPI; 2001-202804/20.  
 DR  
 XX  
 XX Inducing a cytokine and modulating an immune response, useful for  
 PT treating central nervous system diseases and bacterial and viral  
 PT infections, comprises administering colostrinin as an immunological  
 PT regulator -  
 XX  
 PS Claim 1; Page 34; 50pp; English.  
 XX  
 CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,  
 CC a proline rich polypeptide aggregate contained in colostrum. The  
 CC peptides have immune response modulatory activity, and are capable of  
 CC inducing cytokines. Colostrinin and its derived peptides are useful for  
 CC inducing cytokine production, for modulating an immunological response  
 CC and for inducing blood cell proliferation. The peptides are useful in the  
 CC treatment of disorders of the central nervous system, neurological  
 CC disorders, mental disorders, dementia, neurodegenerative diseases,  
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic  
 CC disorders of the immune system, bacterial and viral infections and  
 CC acquired immunological deficiencies.

XX  
 SQ Sequence 10 AA;  
 Query Match 100.0%; Score 10; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.00023;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QPLPPTVMFP 10  
 DB 1 QPLPPTVMFP 10  
 RESULT 2  
 AAB72523  
 ID AAB72523 standard; Peptide; 10 AA.  
 XX  
 AC AAB72523;  
 XX  
 DT 09-MAY-2001 (first entry)  
 XX  
 DE Colostrinin peptide #24.  
 XX  
 KW Dermatalogical; oxidative stress regulator; colostrinin.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200112650-A2.  
 XX  
 PD 22-FEB-2001.  
 XX  
 PF 17-AUG-2000; 2000WO-US22665.  
 XX  
 PR 17-AUG-1999; 99US-0149310.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Stanton GJ, Hughes TK, Boldogh I;  
 XX  
 DR WPI; 2001-218342/22.  
 XX  
 PT Modulating oxidative stress level in a cell, involves contacting the  
 PT cell with an oxidative stress regulator selected from colostrinin, its  
 PT constituent peptide, analog or their combinations -  
 XX  
 PS Claim 6; Page 26; 48pp; English.  
 XX  
 CC The present invention relates to a method for modulating the oxidative  
 CC stress level in a cell or a patient, comprising contacting the cell with,  
 CC or administering to the patient, an oxidative stress regulator selected  
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),  
 CC to change the level of an oxidising species in the cell. The method can  
 CC be used to treat oxidative damage to skin, by decreasing or preventing an  
 CC increase in the level of damage to a biomolecule of the patient.  
 XX  
 SQ Sequence 10 AA;  
 Query Match 100.0%; Score 10; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.00023;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QPLPPTVMFP 10  
 DB 1 QPLPPTVMFP 10  
 RESULT 3  
 AAB72555  
 ID AAB72555 standard; Peptide; 10 AA.  
 XX  
 AC AAB72555;  
 XX  
 DT 09-MAY-2001 (first entry)  
 XX

DE Colostrinin peptide #24.  
 XX Neuroprotective; neural cell differentiation regulator; colostrinin;  
 KW colostrum.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200112651-A2.  
 XX  
 PD 22-FEB-2001.  
 XX  
 PF 17-AUG-2000; 2000WO-US22774.  
 XX  
 PR 17-AUG-1999; 99US-0149633.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Boldogh I;  
 XX  
 DR WPI; 2001-226545/23.  
 XX  
 PT Use of colostrinin, its constituent peptide or analog as a neural cell  
 PT regulator, for promoting neural cell differentiation and treating  
 PT damaged neural cells in a patient -  
 XX  
 PS Claim 6; Page 21; 35pp; English.  
 XX  
 CC The present invention relates to a method for promoting neural cell  
 CC differentiation and treating damaged neural cells, using colostrinin and  
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural  
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.  
 XX  
 SQ Sequence 10 AA;  
 Query Match 100.0%; Score 10; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.00023;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QPLPPTVMFP 10  
 DB |||||  
 1 QPLPPTVMFP 10  
 RESULT 4  
 AAE20252  
 ID AAE20252 standard; peptide; 10 AA.  
 AC  
 XX  
 AC AAE20252;  
 XX  
 DT 18-JUN-2002 (first entry)  
 XX  
 DE Colostrinin constituent peptide #24.  
 XX  
 KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;  
 KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;  
 KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;  
 KW transplantation; implantation; dermatological; vulnery.  
 XX  
 OS Unidentified.  
 XX  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 10 /note= "Optionally C-terminal amide"  
 XX  
 PN WO200213850-A1.  
 XX  
 PD 21-FEB-2002.  
 XX  
 PF 17-AUG-2000; 2000WO-US22776.  
 XX  
 PR 17-AUG-2000; 2000WO-US22776.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.

XX Stanton GJ, Hughes TK, Boldogh I;  
 PI  
 XX WPI; 2002-269151/31.  
 DR  
 XX  
 PT Composition useful for the modulation of blood cell proliferation in a  
 PT patient comprises a blood cell regulator selected from colostrinin, its  
 PT constituent peptide and/or analog -  
 XX  
 PS Claim 6; Page 26; 51pp; English.  
 XX  
 CC The invention relates to a composition which comprises a blood cell  
 CC regulator selected from colostrinin, its constituent peptide and/or  
 CC analogue. The invention is used for modulating the oxidative stress  
 CC level in a cell e.g. mammalian or human cell present in a cell culture,  
 CC tissue, organ, or organism; or for treating oxidative damage to the skin  
 CC of a patient e.g. animal or human; to modulate oxidative stress during/  
 CC after a premature birth or normal birth, preventing/delaying aging in a  
 CC patient, enhancing wound healing, and the reduction of side effects of  
 CC cosmetic procedures. The method changes the level of an oxidising species  
 CC in the cell, such as decreases or prevents increase in the level of  
 CC damage to a biomolecule of the patient selected from DNA, protein and/or  
 CC lipid, compared to the same conditions when the oxidative stress  
 CC regulator is not present. The modulation of oxidative stress results in  
 CC enhanced repair, regeneration, and replacement of cells, tissues and  
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
 CC external organs), as well as enhanced preservation of such organs for  
 CC transplantation, implantation, or scientific research. The present  
 CC sequence is a colostrinin constituent peptide.  
 XX  
 SQ Sequence 10 AA;  
 Query Match 100.0%; Score 10; DB 23; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.00023;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QPLPPTVMFP 10  
 DB |||||  
 1 QPLPPTVMFP 10  
 RESULT 5  
 AAM51059  
 ID AAM51059 standard; Peptide; 10 AA.  
 XX  
 AC AAM51059;  
 XX  
 DT 30-MAY-2002 (first entry)  
 XX  
 DE Colostrinin constituent peptide (casein amino acids 164-173).  
 XX  
 KW Colostrinin; colostrum; immunomodulator; cardiovascular;  
 KW blood cell regulator; cytokine inducer; beta-casein; human.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 10 /note= "optional C-terminal amidation"  
 XX  
 PN WO200213849-A1.  
 XX  
 PD 21-FEB-2002.  
 XX  
 PF 17-AUG-2000; 2000WO-US22775.  
 XX  
 PR 17-AUG-2000; 2000WO-US22775.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 PA (REGG-) REGEN THERAPEUTICS PLC.  
 XX  
 PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
 XX





CC inducing cytokine production, for modulating an immunological response  
 CC and for inducing blood cell proliferation. The peptides are useful in the  
 CC treatment of disorders of the central nervous system, neurological  
 CC disorders, mental disorders, dementia, neurodegenerative diseases,  
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic  
 CC disorders of the immune system, bacterial and viral infections and  
 CC acquired immunological deficiencies.  
 XX  
 XX  
 SQ Sequence 15 AA;

Query Match 100.0%; Score 10; DB 22; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 0.00032;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLPPTVMFP 10  
 Db 6 QLPPTVMFP 15

## RESULT 8

AAB72531  
 ID AAB72531 standard; Peptide; 15 AA.

XX AC AAB72531;

XX DT 09-MAY-2001 (first entry)

XX DE Colostrinin peptide #32.

XX KW Dermatological; oxidative stress regulator; colostrinin.

XX OS Unidentified.

XX PN WO200112650-A2.

XX PD 22-FEB-2001.

XX PF 17-AUG-2000; 2000WO-US22665.

XX PR 17-AUG-1999; 99US-0149310.

XX PA (TEXA ) UNIV TEXAS SYSTEM.

XX PI Stanton GJ, Hughes TK, Boldogh I;

XX DR WPI; 2001-218342/22.

XX PT Modulating oxidative stress level in a cell, involves contacting the  
 cell with an oxidative stress regulator selected from colostrinin, its  
 constituent peptide, analog or their combinations -

XX PS Claim 6; Page 26; 48pp; English.

XX CC The present invention relates to a method for modulating the oxidative  
 stress level in a cell or a patient, comprising contacting the cell with,  
 CC or administering to the patient, an oxidative stress regulator selected  
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),  
 CC to change the level of an oxidising species in the cell. The method can  
 CC be used to treat oxidative damage to skin, by decreasing or preventing an  
 CC increase in the level of damage to a biomolecule of the patient.  
 XX  
 XX

SQ Sequence 15 AA;

Query Match 100.0%; Score 10; DB 22; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 0.00032;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLPPTVMFP 10  
 Db 6 QLPPTVMFP 15

## RESULT 9

## AAB72563

ID AAB72563 standard; Peptide; 15 AA.

XX AC AAB72563;

XX DT 09-MAY-2001 (first entry)

XX DE Colostrinin peptide #32.

XX KW Neuroprotective; neural cell differentiation regulator; colostrinin;  
 colostrinum.

XX OS Unidentified.

XX PN WO200112651-A2.

XX PD 22-FEB-2001.

XX PF 17-AUG-2000; 2000WO-US22774.

XX PR 17-AUG-1999; 99US-0149633.

XX PA (TEXA ) UNIV TEXAS SYSTEM.

XX PI Boldogh I;

XX DR WPI; 2001-226545/23.

XX PT Use of colostrinin, its constituent peptide or analog as a neural cell  
 PT regulator, for promoting neural cell differentiation and treating  
 PT damaged neural cells in a patient -

XX PS Claim 6; Page 22; 35pp; English.

XX CC The present invention relates to a method for promoting neural cell  
 CC differentiation and treating damaged neural cells, using colostrinin and  
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural  
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 10; DB 22; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 0.00032;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLPPTVMFP 10  
 Db 6 QLPPTVMFP 15

## RESULT 10

## AAB59334

ID AAB59334 standard; Peptide; 15 AA.

XX AC AAB59334;

XX DT 21-MAR-2001 (first entry)

XX DE Ewe colostrinin peptide fragment C-9.

XX KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
 central nervous system disorder; dietary supplement; beta-amyloid plaque.

XX OS Ovis sp.

XX PN WO200075173-A2.

XX PD 14-DEC-2000.

XX PF 02-JUN-2000; 2000WO-GB02128.

XX PR 02-JUN-1999; 99GB-0012852.

PA (REG-) REGEN THERAPEUTICS PLC.  
XX Georgiades JA;  
XX WPI; 2001-071058/08.  
XX Peptides having an N-terminal amino acid sequence isolated from  
PT colostrinin for treating e.g. disorders of the central nervous system  
PT and immune system, viral and bacterial infections, and diseases  
PT characterized by amyloid plaques -  
XX  
XX Claim 7; Page 27; 63pp; English.  
XX  
XX The present invention provides the sequences of a number of peptides  
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
CC fragment of colostrum. These peptides can be used in the treatment of  
CC central nervous system disorders such as senile dementia, Parkinson's  
CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
CC disorders such as bacterial and viral infections, to improve the  
CC development of a child's immune system, as a dietary supplement, and to  
CC promote the dissolution of beta-amyloid plaques.  
XX  
XX  
SQ Sequence 15 AA;  
Query Match 100.0%; Score 10; DB 22; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.00032; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 QPLPPTVMFP 10  
| | | | |  
Db 6 QPLPPTVMFP 15  
RESULT 11  
AAE20261  
ID AAE20261 standard; peptide; 15 AA.  
XX  
AC AAE20261;  
XX  
XX 18-JUN-2002 (first entry)  
XX  
DE Colostrinin constituent peptide #32.  
XX  
KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;  
KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;  
KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;  
KW transplantation; implantation; dermatological; vulnery.  
XX  
OS Unidentified.  
XX  
XX Key Location/Qualifiers  
FH Modified-site 15  
FT /note= "Optionally C-terminal amide"  
FT  
XX  
XX WO200213850-A1.  
XX  
XX 21-FEB-2002.  
XX  
XX 17-AUG-2000; 2000WO-US22776.  
XX  
XX 17-AUG-2000; 2000WO-US22776.  
XX  
XX (TEXA ) UNIV TEXAS SYSTEM.  
XX  
XX Stanton GJ, Hughes TK, Boldogh I;  
XX  
XX WPI; 2002-269151/31.  
XX  
XX Composition useful for the modulation of blood cell proliferation in a  
PT patient comprises a blood cell regulator selected from colostrinin, its  
PT constituent peptide and/or analog -  
XX  
XX Claim 6; Page 26; 51pp; English.

XX The invention relates to a composition which comprises a blood cell  
CC regulator selected from colostrinin, its constituent peptide and/or  
CC analogue. The invention is used for modulating the oxidative stress  
CC level in a cell e.g. mammalian or human cell present in a cell culture,  
CC tissue, organ, or organism; or for treating oxidative damage to the skin  
CC of a patient e.g. animal or human; to modulate oxidative stress during/  
CC after a premature birth or normal birth, preventing/delaying aging in a  
CC patient, enhancing wound healing, and the reduction of side effects of  
CC cosmetic procedures. The method changes the level of an oxidizing species  
CC in the cell, such as decreases or prevents increase in the level of  
CC damage to a biomolecule of the patient selected from DNA, protein and/or  
CC lipid, compared to the same conditions when the oxidative stress  
CC regulator is not present. The modulation of oxidative stress results in  
CC enhanced repair, regeneration, and replacement of cells, tissues and  
CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
CC external organs), as well as enhanced preservation of such organs for  
CC transplantation, implantation, or scientific research. The present  
CC sequence is a colostrinin constituent peptide.  
XX  
SQ Sequence 15 AA;  
Query Match 100.0%; Score 10; DB 23; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.00032; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 QPLPPTVMFP 10  
| | | | |  
Db 6 QPLPPTVMFP 15  
RESULT 12  
AAM51066  
ID AAM51066 standard; Peptide; 15 AA.  
XX  
AC AAM51066;  
XX  
XX 30-MAY-2002 (first entry)  
XX  
DE Colostrinin constituent peptide (casein amino acids 159-173).  
XX  
KW Colostrinin; colostrum; immunomodulator; cardiovascular;  
KW blood cell regulator; cytokine inducer; beta-casein; human.  
XX  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH Modified-site 15  
FT /note= "optional C-terminal amidation"  
FT  
XX  
XX WO200213849-A1.  
XX  
XX 21-FEB-2002.  
XX  
XX 17-AUG-2000; 2000WO-US22775.  
XX  
XX 17-AUG-2000; 2000WO-US22775.  
XX  
XX (TEXA ) UNIV TEXAS SYSTEM  
XX (REG-) REGEN THERAPEUTICS PLC.  
XX  
XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
XX WPI; 2002-269150/31.  
XX  
XX Modulation of blood cell proliferation in a patient involves use of  
PT blood cell regulator selected from colostrinin, its constituent peptide  
PT and/or analogue -  
XX  
XX Claim 1; Page 34; 54pp; English.  
XX  
XX The present sequence is that of a colostrinin constituent peptide  
CC that is used as an immunological regulator and as a blood cell

CC regulator in claimed methods of the invention. It is classified  
 CC as having a beta-casein homologue precursor, and corresponds to  
 CC casein amino acids 159-173. Methods are claimed for: inducing a  
 CC cytokine in a cell by contact with an immunological regulator,  
 CC where the cell is present in a cell culture, a tissue, an organ  
 CC or an organism, and the cell is mammalian, including human;  
 CC modulating an immune response in a cell by contact with the  
 CC immunological regulator under conditions effective to induce a  
 CC cytokine; modulating an immune response in a patient by administering  
 CC an immunological regulator under conditions effective to induce a  
 CC cytokine, where the immunological regulator is administered topically  
 CC or as part of a dietary supplement, and where the immune response is  
 CC specific or non specific, an interferon response or an antibody  
 CC response; modulating blood cell proliferation by contacting blood  
 CC cells with a blood cell regulator, where the blood cells are present  
 CC in a cell culture or an organism, are mammalian or human, and where  
 CC the blood cells are increased in number or differentiated; and a  
 CC method for modulating blood cell proliferation in a patient. A  
 CC claimed cytokine-inducing composition comprises a pharmaceutical  
 CC carrier and an active agent such as the present peptide.  
 CC  
 SQ Sequence 15 AA;  
 Query Match 100.0%; Score 10; DB 23; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 0.00032;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QLPPTVMFP 10  
 DB 6 QLPPTVMFP 15  
 RESULT 13  
 ID AAO14610 standard; peptide; 15 AA.  
 AC AAO14610;  
 XX  
 XX 27-MAY-2002 (first entry)  
 DE Neural cell regulatory colostrinin peptide 32.  
 KW Neural cell differentiation; neural cell regulator; colostrinin peptide;  
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;  
 KW neural cell treatment.  
 XX  
 OS Unidentified.  
 FH Key Location/Qualifiers  
 FT Modified-site 15  
 FT /note= "Optional C-terminal amide"  
 XX  
 FN WO200213851-A1.  
 PD 21-FEB-2002.  
 XX  
 PF 17-AUG-2000; 2000WO-US22777.  
 XX  
 PR 17-AUG-2000; 2000WO-US22777.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Boldogh I, Stanton JG, Hughes TK;  
 XX  
 DR WPI; 2002-269152/31.  
 XX  
 PT Promoting cell differentiation in a patient involves use of blood cell  
 PT regulator selected from colostrinin, its constituent peptide and/or  
 PT analog -  
 XX  
 PS Claim 7; Page 22; 37pp; English.  
 XX  
 CC The invention comprises a method for promoting cell differentiation (e.g.

CC neural cell differentiation). The method involves contacting cells with a  
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the  
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich  
 CC polypeptide aggregate that is present in colostrum. The method of the  
 CC invention is useful for promoting the differentiation of cells and for  
 CC treating damaged neural cells in a patient. The present amino acid  
 CC sequence represents a specifically claimed colostrinin peptide used in  
 CC the method of the invention.  
 XX  
 SQ Sequence 15 AA;  
 Query Match 100.0%; Score 10; DB 23; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 0.00032;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QLPPTVMFP 10  
 DB 6 QLPPTVMFP 15  
 RESULT 14  
 ID AAE07192 standard; peptide; 11 AA.  
 AC AAE07192;  
 XX  
 XX 06-NOV-2001 (first entry)  
 DE Colostrinin peptide 8.  
 KW Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;  
 KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;  
 KW central nervous system disorder; neurodegenerative disorder; weight loss;  
 KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;  
 KW acquired immunological deficiency; neurological disorder; dementia;  
 KW antiviral.  
 XX  
 OS Unidentified.  
 XX  
 FN WO200155199-A1.  
 XX  
 PD 02-AUG-2001.  
 XX  
 PF 26-JAN-2001; 2001WO-GB00329.  
 XX  
 PR 26-JAN-2000; 2000GB-0001825.  
 XX  
 PA (REGE-) REGEN THERAPEUTICS PLC.  
 XX  
 PI Georgiades JA;  
 XX  
 DR WPI; 2001-488775/53.  
 XX  
 PT Peptide useful as an inter alia in the treatment of e.g. disorders of  
 PT the immune system and the central nervous system comprises ten  
 PT amino-terminal amino acid sequence derived from peptides present in  
 PT colostrinin -  
 XX  
 PS Claim 1; Page 15; 40pp; English.  
 XX  
 CC The invention relates to colostrinin peptide fragments which are useful,  
 CC inter alia, in the treatment of chronic disorders of the immune system  
 CC and the central nervous system. Colostrinin peptides are used as a  
 CC medicament in the treatment of neurological disorders e.g., dementia,  
 CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron  
 CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and  
 CC neurosis, in acquired immunological deficiencies, chronic bacterial and  
 CC viral infections and diseases characterised by the presence of beta-  
 CC amyloid plaques and as a dietary supplement for babies, small children,  
 CC adults and senile persons, who have been subjected to chemotherapy or  
 CC have suffered from cachexia or weight loss due to the chronic disease.  
 CC Colostrinin peptides are also used as food additives and as an auxiliary  
 CC withdrawal treatment for drug addicts, after a period of detoxification

CC and in persons dependent on stimulants. Colostrinin peptides are used to  
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional  
 CC disturbances of psychiatric patients in a state of depression. These  
 CC colostrinin peptides improves the development of immune system in a new  
 CC born child and to correct the immunological deficiencies in a child.  
 CC The present sequence is colostrinin peptide 8 related to the invention.  
 CC Colostrinin peptide 8 corresponds to position 165-175 of beta-caesin.  
 XX  
 SQ Sequence 11 AA;

Query Match 90.0%; Score 9; DB 22; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.0028;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPPTVMFP 10  
 |||||  
 Db 1 PLPPTVMFP 9

## RESULT 15

AAE07202  
 ID AAE07202 standard; peptide; 12 AA.

XX AC

XX AC AAE07202;

DT 06-NOV-2001 (first entry)

XX DE Modified colostrinin cyclic peptide #8.

XX KW Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;  
 KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;  
 KW central nervous system disorder; neurodegenerative disorder; weight loss;  
 KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;  
 KW acquired immunological deficiency; neurological disorder; dementia;  
 KW antiviral; cyclic.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-terminal acetyl; this residue forms a cyclic  
 FT linkage with Gln found at the C-terminal end"

XX PN WO200155199-A1.

XX PD 02-AUG-2001.

XX PF 26-JAN-2001; 2001WO-GB00329.

XX PR 26-JAN-2000; 2000GB-0001825.

XX PA (REG-) REGEN THERAPEUTICS PLC.

XX PI Georgiades JA;

XX XX WPI; 2001-488775/53.

XX PT Peptide useful as an inter alia in the treatment of e.g. disorders of  
 PT the immune system and the central nervous system comprises ten  
 PT amino-terminal amino acid sequence derived from peptides present in  
 PT colostrinin -

XX PS Example 2; Page 9; 40pp; English.

XX CC The invention relates to colostrinin peptide fragments which are useful,  
 CC inter alia, in the treatment of chronic disorders of the immune system  
 CC and the central nervous system. Colostrinin peptides are used as a  
 CC medicament in the treatment of neurological disorders e.g., dementia,  
 CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron  
 CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and  
 CC neurosis, in acquired immunological deficiencies, chronic bacterial and  
 CC viral infections and diseases characterised by the presence of beta-  
 CC amyloid plaques and as a dietary supplement for babies, small children,

CC adults and senile persons, who have been subjected to chemotherapy or  
 CC have suffered from cachexia or weight loss due to the chronic disease.  
 CC Colostrinin peptides are also used as food additives and as an auxiliary  
 CC withdrawal treatment for drug addicts, after a period of detoxification  
 CC and in persons dependent on stimulants. Colostrinin peptides are used to  
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional  
 CC disturbances of psychiatric patients in a state of depression. These  
 CC colostrinin peptides improves the development of immune system in a new  
 CC born child and to correct the immunological deficiencies in a child.  
 CC The present sequence is modified colostrinin cyclic peptide #8 related to  
 CC the invention.

XX SQ Sequence 12 AA;

Query Match 90.0%; Score 9; DB 22; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 0.003;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPPTVMFP 10

|||||

Db 2 PLPPTVMFP 10

## RESULT 16

AAE59333

ID AAE59333 standard; Peptide; 11 AA.

XX AC AAE59333;

XX XX 21-MAR-2001 (first entry)

DT Ewe colostrinin peptide fragment C-8.

XX DE Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
 XX central nervous system disorder; dietary supplement; beta-amyloid plaque.

XX OS Ovis sp.

XX PN WO200075173-A2.

XX PD 14-DEC-2000.

XX PF 02-JUN-2000; 2000WO-GB02128.

XX PR 02-JUN-1999; 99GB-0012852.

XX PA (REG-) REGEN THERAPEUTICS PLC.

XX PI Georgiades JA;

XX DR WPI; 2001-071058/08.

XX PT Peptides having an N-terminal amino acid sequence isolated from  
 PT colostrinin for treating e.g. disorders of the central nervous system  
 PT and immune system, viral and bacterial infections, and diseases  
 PT characterized by amyloid plaques -

XX PS Claim 7; Page 27; 63pp; English.

XX CC The present invention provides the sequences of a number of peptides  
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
 CC fragment of colostrum. These peptides can be used in the treatment of  
 CC central nervous system disorders such as senile dementia, Parkinson's  
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
 CC disorders such as bacterial and viral infections, to improve the  
 CC development of a child's immune system, as a dietary supplement, and to  
 CC promote the dissolution of beta-amyloid plaques.

XX SQ Sequence 11 AA;

Query Match 60.0%; Score 6; DB 22; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3.9;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPLPPT 6  
 Db 1 QPLPPT 6

RESULT 17  
 AAW25442  
 ID AAW25442 standard; peptide; 16 AA.

XX AAW25442;

XX 27-MAR-1998 (first entry)

XX Grb2 N-terminal SH3 domain binding peptide SEQ ID NO:227.

XX Cortactin; SH3 domain; binding peptide; Src homology region 3;  
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;  
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.

XX Synthetic.  
 OS Unidentified.

XX WO9730074-A1.

XX 21-AUG-1997.

XX 14-FEB-1997; 97WO-US02298.

XX 16-FEB-1996; 96US-0602999.

XX (CYTO-) CYTOGEN CORP.

XX (UYNC-) UNIV NORTH CAROLINA.

XX Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;  
 PI Sparks AB, Thorn JM;

XX WPI; 1997-424572/39.

XX Src homology region 3 binding peptide - used to activate Src  
 PT tyrosine kinase(s) and to stimulate immune response by increasing  
 PT production of certain lymphokine(s), e.g. interleukin-1

PS Claim 20; Page 101; 131pp; English.

XX The present sequence represents a Src homology region 3 (SH3) binding  
 CC peptide. SH3 binding peptides are selected from: (a) peptides which  
 CC bind the SH3 domain of Cortactin; (b) peptides which bind the middle  
 CC SH3 domain of Nck; (c) peptides which bind the SH3 domain of Abl; (d)  
 CC peptides which bind the SH3 domain of Src; (e) peptides which bind the  
 CC SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain of  
 CC p53bp2; (g) peptides which bind the amino-terminal SH3 domain of Crk;  
 CC (h) peptides which bind the SH3 domain of Yes; and (i) peptides which  
 CC bind the amino-terminal SH3 domain of Grb2. The purified binding  
 CC peptides can be used in the method to identify inhibitors of their  
 CC binding to their respective SH3 domains which could be used to  
 CC modulate the pharmacological activity of proteins or polypeptide  
 CC containing the SH3 domain. The peptides can also be used to activate  
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune  
 CC response by increasing the production of certain lymphokines, e.g.  
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a  
 CC conjugated molecule to certain cellular compartments containing Src or  
 CC Src related proteins.

XX Sequence 16 AA;

Query Match 60.0%; Score 6; DB 18; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 5.4; Indels 0; Gaps 0;  
 Matches 6; Conservative 0; Mismatches 0;

Qy 3 LPPTVM 8  
 Db 9 LPPTVM 14

RESULT 18  
 AAY41630

XX AAY41630 standard; peptide; 7 AA.

XX AAY41630;

XX 02-DEC-1999 (first entry)

XX Mammalian ion channel proline rich motif containing peptide #24.

XX SH3 domain; binding motif; potassium channel; protein tyrosine kinase;  
 KW proline rich.

XX Mus sp.

XX US5955259-A.

XX 21-SEP-1999.

XX 19-DEC-1996; 96US-0769745.

XX 19-DEC-1996; 96US-0769745.

XX (UYBR-) UNIV BRANDEIS.

XX Holmes TC, Levitan IB;

XX WPI; 1999-560490/47.

XX Identification of compounds that modulate potassium ion channel binding  
 PT with protein tyrosine kinase SH3 domains

XX Disclosure; Column 8; 18pp; English.

XX A method has been developed for determining if a compound modulates the  
 CC binding of a potassium ion channel to the SH3 domain of a protein  
 CC tyrosine kinase by contacting the channel with a polypeptide comprising  
 CC the SH3 domain and the compound to be assessed and measuring channel-SH3  
 CC binding. The method is useful for assessing the ability of a compound to  
 CC modulate the formation of channel-SH3 domain complexes to improve the  
 CC understanding of mechanisms of potassium channel blockage and assess the  
 CC ability of potential therapeutics to inhibit blockage. AAY41607 to  
 CC AAY41644 represent mammalian ion channel peptides with proline-rich  
 CC motifs.

XX Sequence 7 AA;

Query Match 50.0%; Score 5; DB 20; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPLPP 5

Db 1 QPLPP 5

RESULT 19  
 AAB17247

XX AAB17247 standard; Peptide; 7 AA.

XX AAB17247;

XX 31-OCT-2000 (first entry)

XX SH3 antagonist peptide sequence SEQ ID NO:303.

XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;  
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;  
 KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;  
 KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;  
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;

KW vascular endothelial growth factor; matrix metalloproteinase;  
 KW asthma; thrombosis; pharmaceutical.  
 XX  
 OS Synthetic.  
 XX WO200024782-A2.  
 XX  
 PN 04-MAY-2000.  
 XX  
 PD  
 XX  
 PF 25-OCT-1999; 99WO-US25044.  
 XX  
 XX 23-OCT-1998; 98US-0105371.  
 PR 22-OCT-1999; 99US-0428082.  
 XX  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 XX Feige U, Liu C, Cheetham J, Boone TC;  
 XX WPI; 2000-350702/30.  
 DR  
 XX  
 XX Novel composition of matter comprising an Fc domain and  
 PT pharmacologically active peptides, useful for treating cancer and  
 PT autoimmune diseases -  
 XX  
 XX Claim 39; Page 302; 608pp; English.  
 PS  
 XX The present invention describes composition of matter (I) comprising an  
 CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:  
 CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each  
 CC independently selected from - (L1)c-P1, - (L1)c-P1-(L2)d-P2,  
 CC - (L1)c-P1-(L2)d-P2-(L3)e-P3, or - (L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4  
 CC where P1, P2, P3, and P4 = are each independently sequences of  
 CC pharmacologically active peptides; L1, L2, L3, and L4 = are each  
 CC independently linkers; and a, b, c, d, e, and f = are each independently  
 CC 0 or 1, provided that at least 1 of a and b is 1. The composition can  
 CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive  
 CC activities. DNAs, vectors and host cells from the present invention can  
 CC be used for producing pharmaceutical compositions. The compositions are  
 CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.  
 CC The use of an Fc domain (rather than a Fab domain) can provide a longer  
 CC half-life or incorporate functions such as Fc receptor binding, protein  
 CC A binding, complement fixation, and possibly placental transfer. AAA69443  
 CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid  
 CC sequences used in the exemplification of the present invention.  
 XX  
 SQ Sequence 7 AA;  
 Query Match 50.0%; Score 5; DB 21; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 PLPPT 6  
 Db |||||  
 2 PLPPT 6  
 RESULT 20  
 ABB73240  
 ID ABB73240 standard; Peptide; 7 AA.  
 XX  
 AC ABB73240;  
 XX  
 DT 05-APR-2002 (first entry)  
 XX  
 XX Src homology3 (SH3) antagonist peptide SEQ ID NO:303.  
 DE  
 XX Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG;  
 KW EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor;  
 KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TNP;  
 KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;  
 KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;  
 KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;  
 KW antianaemic; anorectic; antiinfertility; haemostatic; dermatological;

KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;  
 KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;  
 KW sleep disorder; neurological degenerative disease; anaemia;  
 KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;  
 KW Fanconi's syndrome.  
 XX  
 XX Homo sapiens.  
 OS Synthetic.  
 XX WO200183525-A2.  
 XX  
 PN 08-NOV-2001.  
 XX  
 PD  
 XX  
 PF 02-MAY-2001; 2001WO-US14310.  
 XX  
 XX 03-MAY-2000; 2000US-0563286.  
 PR  
 XX (AMGE-) AMGEN INC.  
 XX  
 XX Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;  
 PI WPI; 2002-130313/17.  
 XX  
 DR Novel vehicle-peptide molecule or its multimers useful for treating  
 XX inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,  
 PT diabetic retinopathy, obesity, sleep disorders and infertility -  
 PT  
 XX Claim 39; Page 55; 176pp; English.  
 PS  
 XX The present invention describes a vehicle-peptide molecule (I) or its  
 CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,  
 CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,  
 CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and  
 CC neuroprotective activities. (I) can be used as a therapeutic or  
 CC prophylactic agent as well as for screening purposes. (I) is useful for  
 CC diagnosing diseases characterised by dysfunction of their associated  
 CC protein of interest, for identifying normal or abnormal proteins of  
 CC interest, as a part of diagnostic kit to detect the presence of their  
 CC proteins of interest in a biological sample. Additionally, (I) is useful  
 CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,  
 CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,  
 CC infertility, and neurological degenerative diseases. (I), comprising  
 CC EPO-mimetic compounds are useful for treating disorders characterised by  
 CC low red blood cell levels such as anaemia. The TPO-mimetic comprising  
 CC compounds are useful for treating conditions that involve an existing  
 CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet  
 CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic  
 CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,  
 CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777  
 CC represent amino acid and nucleic acid sequences used in the  
 CC exemplification of the present invention.  
 XX  
 SQ Sequence 7 AA;  
 Query Match 50.0%; Score 5; DB 23; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 PLPPT 6  
 Db |||||  
 2 PLPPT 6  
 RESULT 21  
 AAM00293  
 ID AAM00293 standard; Peptide; 8 AA.  
 XX  
 AC AAM00293;  
 XX  
 XX 01-OCT-2001 (first entry)  
 XX  
 XX Human protein fragment SEQ ID NO: 837.  
 DE  
 XX

KW Human; single nucleotide polymorphism; SNP; paternity test;  
KW forensic test; aberrant protein expression.  
XX Homo sapiens.

XX WO200151670-A2.  
XX 19-JUL-2001.  
XX 05-JAN-2001; 2001WO-US00322.  
XX 07-JAN-2000; 2000US-0174962.

XX (CURA-) CURAGEN CORP.  
XX Shimkets RA, Leach MD;  
XX WPI; 2001-451871/48.  
XX N-PSDB; AAH89406.

XX Isolated human polynucleotides containing single nucleotide  
XX polymorphisms, useful for the treatment and diagnosis of e.g. cancer,  
XX infection and diabetes -  
XX Disclosure; Page 344; 475pp; English.

XX The present invention relates to human nucleic acids containing single  
XX nucleotide polymorphisms (SNPs). These can be used in forensic and  
XX paternity tests, and to aid in the treatment of diseases associated with  
XX aberrant protein expression, including cancer, amyloidosis, diabetes,  
XX Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,  
XX glomerulonephritis, haemolytic anaemia, thrombocytopaenia, arthritis,  
XX meningitis, muscular disorders, dementia, neurological diseases, tubercu-  
XX sclerosis, male infertility, hypercalcaemia, blood pressure disorders,  
XX osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or  
XX autoimmunity. The present sequence is a peptide encoded by a  
XX polymorphism-containing oligonucleotide fragment of the invention.

XX Sequence 8 AA;  
XX Query Match 50.0%; Score 5; DB 22; Length 8;  
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPLPP 5  
DB 1 QPLPP 5

RESULT 22  
AAM00294  
ID AAM00294 standard; Peptide; 8 AA.  
XX AC AAM00294;  
XX 01-OCT-2001 (first entry)

XX Human protein fragment SEQ ID NO: 838.  
XX Human; single nucleotide polymorphism; SNP; paternity test;  
XX forensic test; aberrant protein expression.  
XX Homo sapiens.

XX WO200151670-A2.  
XX 19-JUL-2001.  
XX 05-JAN-2001; 2001WO-US00322.  
XX 07-JAN-2000; 2000US-0174962.  
XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach MD;  
XX WPI; 2001-451871/48.  
XX N-PSDB; AAH89407.

XX Isolated human polynucleotides containing single nucleotide  
XX polymorphisms, useful for the treatment and diagnosis of e.g. cancer,  
XX infection and diabetes -  
XX Disclosure; Page 345; 475pp; English.

XX The present invention relates to human nucleic acids containing single  
XX nucleotide polymorphisms (SNPs). These can be used in forensic and  
XX paternity tests, and to aid in the treatment of diseases associated with  
XX aberrant protein expression, including cancer, amyloidosis, diabetes,  
XX Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,  
XX glomerulonephritis, haemolytic anaemia, thrombocytopaenia, arthritis,  
XX meningitis, muscular disorders, dementia, neurological diseases, tubercu-  
XX sclerosis, male infertility, hypercalcaemia, blood pressure disorders,  
XX osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or  
XX autoimmunity. The present sequence is a peptide encoded by a  
XX polymorphism-containing oligonucleotide fragment of the invention.

XX Sequence 8 AA;  
XX Query Match 50.0%; Score 5; DB 22; Length 8;  
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPLPP 5  
DB 1 QPLPP 5

RESULT 23  
AAB84971  
ID AAB84971 standard; protein; 9 AA.  
XX AC AAB84971;  
XX 06-AUG-2001 (first entry)

XX Clone 1 scFv CDR L3 region binding to target antigen M.  
XX Antinflammatory; antiallergic; cytostatic; antibacterial; antiviral;  
XX immunosuppressive; antidiabetic; neuroprotective; antirheumatic;  
XX antiarthritic; dermatological; immune response; modulator; enzyme;  
XX antigen M; T-cell receptor; complementary determining region; CDR.

XX Homo sapiens.  
XX WO200140312-A2.  
XX 07-JUN-2001.  
XX 04-DEC-2000; 2000WO-GB04629.  
XX 03-DEC-1999; 99GB-0028789.  
XX (DIVE-) DIVERSYS LTD.

XX Hoit LJ, De Wildt RMT, Tomlinson I;  
XX WPI; 2001-374801/39.  
XX Isolating a polypeptide of interest from a naive polypeptide repertoire  
XX which has not been preselected with a specific target ligand involves  
XX direct screening of naive polypeptide repertoire with the target ligand

XX Example 2; Page 29; 41pp; English.



CC The invention relates to isolating, from a naive polypeptide (I)  
 CC repertoire (antibody or T-cell receptor polypeptides), which has not been  
 CC preselected with a specific target ligand, a polypeptide of interest (II)  
 CC capable of interacting with the specific target ligand. The method  
 CC involves direct screening of (I) with the target ligand in order to  
 CC identify (II). The polypeptides selected by the method may be used in any  
 CC process which involves ligand-polypeptide binding including in vivo  
 CC therapeutic and prophylactic applications, in vitro and in vivo  
 CC diagnostic applications, in vitro assay and reagent applications. Enzyme  
 CC variants generated and selected by the method may be assayed for  
 CC activity, either in vitro or in vivo using standard techniques. Antibody  
 CC polypeptides selected by the method are used diagnostically in Western  
 CC analysis and in situ protein detection. The selected antibodies are  
 CC useful for preventing, suppressing or treating inflammatory states,  
 CC allergic hypersensitivity, cancer, bacterial or viral infection and  
 CC autoimmune disorders e.g., type I diabetes, multiple sclerosis,  
 CC rheumatoid arthritis, systemic lupus erythematosus, Crohn's disease and  
 CC myasthenia gravis. The selected polypeptides may be used extracorporeally  
 CC or in vitro selectively to kill, deplete or effectively remove a target  
 CC cell population from a heterogeneous collection of cells. Sequences  
 CC AA884968-979 represent complementary determining regions (CDRs) of scFv  
 CC heavy and light chains binding to target antigens M and D.  
 CC  
 CC Sequence 9 AA;

Query Match 50.0%; Score 5; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPLPP 5  
 Db 3 QPLPP 7  
 |||||  
 |||||

RESULT 24  
 AAM00291  
 ID AAM00291 standard; Peptide; 12 AA.  
 AC AAM00291;  
 XX  
 XX 01-OCT-2001 (first entry)  
 DT  
 XX Human protein fragment SEQ ID NO: 835.  
 DE  
 XX Human; single nucleotide polymorphism; SNP; paternity test;  
 KW forensic test; aberrant protein expression.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WO200151670-A2.  
 FN  
 XX 19-JUL-2001.  
 PD  
 XX 05-JAN-2001; 2001WO-US00322.  
 PF  
 XX 07-JAN-2000; 2000US-0174962.  
 PR  
 XX (CURA-) CURAGEN CORP.  
 PA  
 XX Shimkets RA, Leach MD;  
 XX  
 XX WPI; 2001-451871/48.  
 DR  
 XX N-PSDB; AAH89404.  
 DR

PT Isolated human polynucleotides containing single nucleotide  
 PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,  
 PT infection and diabetes -  
 XX  
 XX Disclosure; Page 344; 475pp; English.  
 PS  
 XX

CC The present invention relates to human nucleic acids containing single  
 CC nucleotide polymorphisms (SNPs). These can be used in forensic and  
 CC paternity tests, and to aid in the treatment of diseases associated with

CC aberrant protein expression, including cancer, amyloidosis, diabetes,  
 CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,  
 CC glomerulonephritis, haemolytic anaemia, thrombocytopaenia, arthritis,  
 CC meningitis, muscular disorders, dementia, neurological diseases, tuberos  
 CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,  
 CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or  
 CC autoimmunity. The present sequence is a peptide encoded by a  
 CC polymorphism-containing oligonucleotide fragment of the invention.  
 CC  
 CC Sequence 12 AA;

Query Match 50.0%; Score 5; DB 22; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 48;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPLPP 5  
 Db 5 QPLPP 9  
 |||||  
 |||||

RESULT 25  
 AAR93368  
 ID AAR93368 standard; peptide; 13 AA.  
 XX  
 AC AAR93368;  
 XX

XX 24-APR-1996 (first entry)  
 DT  
 XX  
 XX PI3K protein tyrosine kinase derived peptide #3.  
 DE

XX SH3 ligand; SH3 binding agent; biased phage library;  
 KW recognition sequence; src SH3 domain; Paget's disease; restenosis;  
 KW rheumatoid arthritis; gout; neutrophil oxidase; tyrosine kinase; p47;  
 KW p67; complex; chronic myelogenous leukaemia; cancer.  
 XX  
 OS Synthetic.

XX WO9524419-A1.  
 FN

XX 14-SEP-1995.  
 PD

XX 13-MAR-1995; 95WO-US03208.  
 PF

XX 06-JAN-1995; 95US-0369832.  
 PR

XX 11-MAR-1994; 94US-0209835.  
 PR

XX (ARIA-) ARIAD PHARM INC.  
 PA

XX Botfield MC, Brugge JS, Rickles RJ, Zoller MJ;  
 FI

XX WPI; 1995-328231/42.  
 DR

XX Identification of peptide(s) binding specifically to SH3 domains -  
 PT for use in inhibiting interactions mediated by SH3 domains in  
 PT treatment of e.g. osteoporosis and cancer  
 XX

XX Disclosure; Fig 2; 74pp; English.

CC The sequences given in AAR93343-68 represent peptides which are SH3  
 CC ligands/SH3 binding agents. They represent a biased phage library  
 CC which comprises six random amino acids flanking the hexapeptide  
 CC RSLRPL- which was identified as a recognition sequence for the src  
 CC SH3 domain. These sequences were identified using the method of the  
 CC invention. The method comprises contacting the SH3 domain with a  
 CC mixture of peptides under conditions permitting a ligand to bind to  
 CC an SH3 domain to form a complex. Any unbound peptides are removed  
 CC and the complexed peptide ligands are dissociated from the complexes.  
 CC The selected peptides are enriched by re-contacting them with the  
 CC SH3 domain and then candidates which bind to the SH3 domain are  
 CC detected. The isolated SH3 binding peptides may be used in the  
 CC diagnosis, prevention and treatment of conditions or diseases resulting  
 CC from cellular processes mediated by an SH3-based interaction. Such  
 CC diseases include Paget's disease. Other conditions treatable with these

CC peptides include restenosis, rheumatoid arthritis, gout and other  
 CC problems in which an SH3 of neutrophil oxidase p47 and p67 complex is  
 CC implicated, etc.  
 XX  
 SQ Sequence 13 AA;

Query Match 50.0%; Score 5; DB 16; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 51;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPPT 6  
 |||||  
 Db 5 PLPPT 9

RESULT 26  
 AAW11112  
 ID AAW11112 standard; peptide; 13 AA.  
 XX  
 AC AAW11112;  
 XX  
 DT 25-JUN-1997 (first entry)  
 XX  
 DE Src SH3 domain-binding peptide used in signal transduction modulation.  
 XX  
 KW Src; SH3; Src homology region 3; binding affinity; oncogenic protein;  
 KW protein tyrosine kinase; signal transduction; RNA processing;  
 KW trafficking; translation.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9603649-A1.  
 XX  
 PD 08-FEB-1996.  
 XX  
 PF 24-JUL-1995; 95WO-US09382.  
 XX  
 PR 07-JUN-1995; 95US-0483555.  
 PR 22-JUL-1994; 94US-0278865.  
 XX  
 XX (UYNC-) UNIV NORTH CAROLINA.  
 PA  
 XX Der CJ, Kay BK, Quilliam LA, Sparks AB, Thorn JM;  
 XX WPI; 1996-117151/12.  
 DR  
 XX Peptide with binding affinity for Src homology region 3 (SH3)  
 PT domains of proteins - useful for e.g. modulating signal transduction  
 PT pathways at the cellular level, esp. protein tyrosine  
 PT kinase-mediated  
 XX  
 PS Claim 38; Page 87; 116pp; English.  
 XX

AAW11098-W1124 are peptides that bind to the Src SH3 domain. The SH3  
 binding peptides are useful in modulating signal transduction pathways  
 at the cellular level (especially protein tyrosine kinase-mediated),  
 modulating oncogenic protein activity, or providing compounds for the  
 development of drugs with the ability to modulate broad classes, as  
 well as specific classes, of proteins involved in signal transduction  
 and also for regulating the processing, trafficking or translation of  
 RNA. Conjugates of the peptides with detectable labels or imaging agents  
 are useful for imaging cells, tissues and organs in which Src or  
 Src-related proteins are expressed.

SQ Sequence 13 AA;  
 Query Match 50.0%; Score 5; DB 17; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 51;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPPT 6  
 |||||  
 Db 5 PLPPT 9

RESULT 27  
 AAE21396  
 ID AAE21396 standard; peptide; 13 AA.  
 XX  
 AC AAE21396;  
 XX  
 DT 01-JUL-2002 (first entry)  
 XX  
 DE Escherichia coli 3-isopropylmalate dehydrogenase (IPMDH) peptide #1.  
 XX  
 KW Protein thermostability; 3-isopropylmalate dehydrogenase; IPMDH;  
 KW isocitrate dehydrogenase; ICDH; enzyme.  
 XX  
 OS Escherichia coli.  
 XX  
 PN EP1182253-A2.  
 XX  
 PD 27-FEB-2002.  
 XX  
 PF 03-JUL-2001; 2001EP-0115642.  
 XX  
 PR 04-JUL-2000; 2000JP-0201920.  
 PR 31-MAY-2001; 2001JP-0164332.  
 XX  
 PA (AJIN ) AJINOMOTO CO INC.  
 XX  
 XX Yamagishi A;  
 PI  
 XX WPI; 2002-294076/34.  
 DR

Improving protein thermostability of protein by estimating amino acid  
 sequence of ancestral protein (AP), and replacing amino acids of  
 desired protein, which differ from those of AP with the same amino  
 acids of AP -  
 XX  
 XX Example 4; Fig 9; 73pp; English.  
 PS  
 XX The invention relates to a method for improving thermostability of  
 CC proteins. The method involves comparing amino acid sequences derived  
 CC from two or more species which evolutionarily correspond to each other  
 CC in phylogenetic tree; estimating amino acid sequence of ancestral  
 CC protein and replacing amino acids of desired protein, which differ  
 CC from those of ancestral protein with the same amino acids of ancestral  
 CC protein. The method is used for improving thermostability of proteins  
 CC preferably 3-isopropylmalate dehydrogenase (IPMDH) and isocitrate  
 CC dehydrogenase (ICDH). The invention also relates to a protein having  
 CC an improved thermostability and a nucleic acid encoding such protein.  
 CC The present sequence is Escherichia coli IPMDH peptide.  
 XX  
 SQ Sequence 13 AA;

Query Match 50.0%; Score 5; DB 23; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 51;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPLPP 5  
 |||||  
 Db 1 QPLPP 5

RESULT 28  
 ABP81159  
 ID ABP81159 standard; peptide; 13 AA.  
 XX  
 AC ABP81159;  
 XX  
 DT 27-FEB-2003 (first entry)  
 XX  
 DE Human TPO peptide with MCH class II binding activity #112.  
 XX  
 KW Human; thrombopoietin; TPO; non-immunogenic; T-cell epitope; allergy;

KW MHC class II; immunosuppressive; antiallergic; autoimmune disease.  
 XX Homo sapiens.  
 XX WO200268469-A2.  
 XX 06-SEP-2002.  
 XX 22-FEB-2002; 2002WO-EP01931.  
 XX 26-FEB-2001; 2001EP-0104702.  
 XX (MERE ) MERCK PATENT GMBH.  
 PA Carr FJ, Carter G;  
 PI WPI; 2003-103168/09.  
 DR Modified thrombopoietin molecule for use in pharmaceutical  
 XX compositions, has same activity of human thrombopoietin, but is  
 PT non-immunogenic or less immunogenic than other non-modified molecules  
 PT with same activity -  
 XX Disclosure; Page 12; 36pp; English.  
 XX The invention relates to a novel modified molecule having the biological  
 CC activity of human thrombopoietin (TPO) and being substantially  
 CC non-immunogenic or less immunogenic than any non-modified molecule having  
 CC the same biological activity when used in vivo. The invention also  
 CC discloses T-cell epitope peptides created from non-modified TPO, and  
 CC having potential MHC class II binding activity. The protein of the  
 CC invention has immunosuppressive and antiallergic activity. A peptide of  
 CC the invention is useful in the manufacture of TPO having substantially no  
 CC or less immunogenicity than any non-modified molecule with the same  
 CC biological activity when used in vivo. The protein is useful in  
 CC pharmaceutical compositions, and is suitable for therapeutic use, e.g.  
 CC allergies and autoimmune disease treatment. The sequences shown in  
 CC ABP81048 - ABP81172 represent the MHC class II binding peptides of the  
 CC invention.  
 XX Sequence 13 AA;  
 SQ Query Match 50.0%; Score 5; DB 24; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 51;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 PLPPT 6  
 Db |||||  
 7 PLPPT 11  
 RESULT 29  
 ABP81160  
 ID ABP81160 standard; peptide; 13 AA.  
 XX AC ABP81160;  
 XX 27-FEB-2003 (first entry)  
 DT Human TPO peptide with MCH class II binding activity #113.  
 DE Human; thrombopoietin; TPO; non-immunogenic; T-cell epitope; allergy;  
 KW MHC class II; immunosuppressive; antiallergic; autoimmune disease.  
 XX Homo sapiens.  
 XX WO200268469-A2.  
 XX 06-SEP-2002.  
 XX 22-FEB-2002; 2002WO-EP01931.  
 XX 26-FEB-2001; 2001EP-0104702.  
 XX (MERE ) MERCK PATENT GMBH.  
 PA Carr FJ, Carter G;  
 PI WPI; 2003-103168/09.  
 DR Modified thrombopoietin molecule for use in pharmaceutical  
 XX compositions, has same activity of human thrombopoietin, but is  
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 PT with same activity -  
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 XX The invention relates to a novel modified molecule having the biological  
 CC activity of human thrombopoietin (TPO) and being substantially  
 CC non-immunogenic or less immunogenic than any non-modified molecule having  
 CC the same biological activity when used in vivo. The invention also  
 CC discloses T-cell epitope peptides created from non-modified TPO, and  
 CC having potential MHC class II binding activity. The protein of the  
 CC invention has immunosuppressive and antiallergic activity. A peptide of  
 CC the invention is useful in the manufacture of TPO having substantially no  
 CC or less immunogenicity than any non-modified molecule with the same  
 CC biological activity when used in vivo. The protein is useful in  
 CC pharmaceutical compositions, and is suitable for therapeutic use, e.g.  
 CC allergies and autoimmune disease treatment. The sequences shown in  
 CC ABP81048 - ABP81172 represent the MHC class II binding peptides of the  
 CC invention.  
 XX Sequence 13 AA;  
 SQ Query Match 50.0%; Score 5; DB 24; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 51;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 PLPPT 6  
 Db |||||  
 7 PLPPT 11  
 RESULT 29  
 ABP81160  
 ID ABP81160 standard; peptide; 13 AA.  
 XX AC ABP81160;  
 XX 27-FEB-2003 (first entry)  
 DT Human TPO peptide with MCH class II binding activity #113.  
 DE Human; thrombopoietin; TPO; non-immunogenic; T-cell epitope; allergy;  
 KW MHC class II; immunosuppressive; antiallergic; autoimmune disease.  
 XX Homo sapiens.  
 XX WO200268469-A2.  
 XX 06-SEP-2002.  
 XX 22-FEB-2002; 2002WO-EP01931.  
 XX 26-FEB-2001; 2001EP-0104702.  
 XX (MERE ) MERCK PATENT GMBH.  
 PA Carr FJ, Carter G;  
 PI WPI; 2003-103168/09.  
 DR Modified thrombopoietin molecule for use in pharmaceutical  
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 CC non-immunogenic or less immunogenic than any non-modified molecule having  
 CC the same biological activity when used in vivo. The invention also  
 CC discloses T-cell epitope peptides created from non-modified TPO, and  
 CC having potential MHC class II binding activity. The protein of the  
 CC invention has immunosuppressive and antiallergic activity. A peptide of  
 CC the invention is useful in the manufacture of TPO having substantially no  
 CC or less immunogenicity than any non-modified molecule with the same  
 CC biological activity when used in vivo. The protein is useful in  
 CC pharmaceutical compositions, and is suitable for therapeutic use, e.g.  
 CC allergies and autoimmune disease treatment. The sequences shown in  
 CC ABP81048 - ABP81172 represent the MHC class II binding peptides of the  
 CC invention.  
 XX Sequence 13 AA;  
 SQ Query Match 50.0%; Score 5; DB 24; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 51;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 PLPPT 6  
 Db |||||  
 5 PLPPT 9  
 RESULT 30  
 ABP81161  
 ID ABP81161 standard; peptide; 13 AA.  
 XX AC ABP81161;  
 XX 27-FEB-2003 (first entry)  
 DT Human TPO peptide with MCH class II binding activity #114.  
 DE Human; thrombopoietin; TPO; non-immunogenic; T-cell epitope; allergy;  
 KW MHC class II; immunosuppressive; antiallergic; autoimmune disease.  
 XX Homo sapiens.  
 XX WO200268469-A2.  
 XX 06-SEP-2002.  
 XX 22-FEB-2002; 2002WO-EP01931.  
 XX 26-FEB-2001; 2001EP-0104702.  
 XX (MERE ) MERCK PATENT GMBH.  
 PA Carr FJ, Carter G;  
 PI WPI; 2003-103168/09.  
 DR Modified thrombopoietin molecule for use in pharmaceutical  
 XX compositions, has same activity of human thrombopoietin, but is  
 PT non-immunogenic or less immunogenic than other non-modified molecules  
 PT with same activity -

XX (MERE ) MERCK PATENT GMBH.  
 PA Carr FJ, Carter G;  
 XX WPI; 2003-103168/09.  
 DR Modified thrombopoietin molecule for use in pharmaceutical  
 XX compositions, has same activity of human thrombopoietin, but is  
 PT non-immunogenic or less immunogenic than other non-modified molecules  
 PT with same activity -  
 XX Disclosure; Page 12; 36pp; English.  
 XX The invention relates to a novel modified molecule having the biological  
 CC activity of human thrombopoietin (TPO) and being substantially  
 CC non-immunogenic or less immunogenic than any non-modified molecule having  
 CC the same biological activity when used in vivo. The invention also  
 CC discloses T-cell epitope peptides created from non-modified TPO, and  
 CC having potential MHC class II binding activity. The protein of the  
 CC invention has immunosuppressive and antiallergic activity. A peptide of  
 CC the invention is useful in the manufacture of TPO having substantially no  
 CC or less immunogenicity than any non-modified molecule with the same  
 CC biological activity when used in vivo. The protein is useful in  
 CC pharmaceutical compositions, and is suitable for therapeutic use, e.g.  
 CC allergies and autoimmune disease treatment. The sequences shown in  
 CC ABP81048 - ABP81172 represent the MHC class II binding peptides of the  
 CC invention.  
 XX Sequence 13 AA;  
 SQ Query Match 50.0%; Score 5; DB 24; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 51;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 PLPPT 6  
 Db |||||  
 5 PLPPT 9  
 RESULT 30  
 ABP81161  
 ID ABP81161 standard; peptide; 13 AA.  
 XX AC ABP81161;  
 XX 27-FEB-2003 (first entry)  
 DT Human TPO peptide with MCH class II binding activity #114.  
 DE Human; thrombopoietin; TPO; non-immunogenic; T-cell epitope; allergy;  
 KW MHC class II; immunosuppressive; antiallergic; autoimmune disease.  
 XX Homo sapiens.  
 XX WO200268469-A2.  
 XX 06-SEP-2002.  
 XX 22-FEB-2002; 2002WO-EP01931.  
 XX 26-FEB-2001; 2001EP-0104702.  
 XX (MERE ) MERCK PATENT GMBH.  
 PA Carr FJ, Carter G;  
 PI WPI; 2003-103168/09.  
 DR Modified thrombopoietin molecule for use in pharmaceutical  
 XX compositions, has same activity of human thrombopoietin, but is  
 PT non-immunogenic or less immunogenic than other non-modified molecules  
 PT with same activity -

XX PS Disclosure; Page 12; 36pp; English.

XX CC The invention relates to a novel modified molecule having the biological

XX CC activity of human thrombopoietin (TPO) and being substantially

XX CC non-immunogenic or less immunogenic than any non-modified molecule having

XX CC the same biological activity when used in vivo. The invention also

XX CC discloses T-cell epitope peptides created from non-modified TPO, and

XX CC having potential MHC class II binding activity. The protein of the

XX CC invention has immunosuppressive and antiallergic activity. A peptide of

XX CC the invention is useful in the manufacture of TPO having substantially no

XX CC or less immunogenicity than any non-modified molecule with the same

XX CC biological activity when used in vivo. The protein is useful in

XX CC pharmaceutical compositions, and is suitable for therapeutic use, e.g.

XX CC allergies and autoimmune disease treatment. The sequences shown in

XX CC ABP81048 - ABP81172 represent the MHC class II binding peptides of the

XX CC invention.

XX SQ Sequence 13 AA;

Query Match 50.0%; Score 5; DB 24; Length 13;

Best Local Similarity 100.0%; Pred. No. 51;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPPT 6

Db 4 PLPPT 8

RESULT 31

ABP81162

ID ABP81162 standard; peptide; 13 AA.

XX AC ABP81162;

XX XX

XX DT 27-FEB-2003 (first entry)

XX DE Human TPO peptide with MCH class II binding activity #115.

XX KW Human; thrombopoietin; TPO; non-immunogenic; T-cell epitope; allergy;

XX KW MHC class II; immunosuppressive; antiallergic; autoimmune disease.

XX OS Homo sapiens.

XX XX

XX PN WO200268469-A2.

XX PD 06-SEP-2002.

XX PF 22-FEB-2002; 2002WO-EP01931.

XX PR 26-FEB-2001; 2001EP-0104702.

XX PA (MERE ) MERCK PATENT GMBH.

XX PI Carr FU, Carter G;

XX DR WPI; 2003-103168/09.

XX PT Modified thrombopoietin molecule for use in pharmaceutical

XX PT compositions, has same activity of human thrombopoietin, but is

XX PT non-immunogenic or less immunogenic than other non-modified molecules

XX PT with same activity -

XX PS Disclosure; Page 12; 36pp; English.

XX PI Carr FU, Carter G;

XX DR WPI; 2003-103168/09.

XX PT Modified thrombopoietin molecule for use in pharmaceutical

XX PT compositions, has same activity of human thrombopoietin, but is

XX PT non-immunogenic or less immunogenic than other non-modified molecules

XX PT with same activity -

XX PS Disclosure; Page 12; 36pp; English.

XX CC The invention relates to a novel modified molecule having the biological

XX CC activity of human thrombopoietin (TPO) and being substantially

XX CC non-immunogenic or less immunogenic than any non-modified molecule having

XX CC the same biological activity when used in vivo. The invention also

XX CC discloses T-cell epitope peptides created from non-modified TPO, and

XX CC having potential MHC class II binding activity. The protein of the

XX CC invention has immunosuppressive and antiallergic activity. A peptide of

XX CC the invention is useful in the manufacture of TPO having substantially no

XX CC or less immunogenicity than any non-modified molecule with the same

XX CC biological activity when used in vivo. The protein is useful in

XX CC pharmaceutical compositions, and is suitable for therapeutic use, e.g.

XX CC allergies and autoimmune disease treatment. The sequences shown in

XX CC ABP81048 - ABP81172 represent the MHC class II binding peptides of the

XX CC invention.

CC or less immunogenicity than any non-modified molecule with the same

CC biological activity when used in vivo. The protein is useful in

CC pharmaceutical compositions, and is suitable for therapeutic use, e.g.

CC allergies and autoimmune disease treatment. The sequences shown in

CC ABP81048 - ABP81172 represent the MHC class II binding peptides of the

CC invention.

XX SQ Sequence 13 AA;

Query Match 50.0%; Score 5; DB 24; Length 13;

Best Local Similarity 100.0%; Pred. No. 51;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPPT 6

Db 2 PLPPT 6

RESULT 32

ABP81163

ID ABP81163 standard; peptide; 13 AA.

XX AC ABP81163;

XX XX

XX DT 27-FEB-2003 (first entry)

XX DE Human TPO peptide with MCH class II binding activity #116.

XX KW Human; thrombopoietin; TPO; non-immunogenic; T-cell epitope; allergy;

XX KW MHC class II; immunosuppressive; antiallergic; autoimmune disease.

XX OS Homo sapiens.

XX XX

XX PN WO200268469-A2.

XX PD 06-SEP-2002.

XX PF 22-FEB-2002; 2002WO-EP01931.

XX PR 26-FEB-2001; 2001EP-0104702.

XX PA (MERE ) MERCK PATENT GMBH.

XX PI Carr FU, Carter G;

XX DR WPI; 2003-103168/09.

XX PT Modified thrombopoietin molecule for use in pharmaceutical

XX PT compositions, has same activity of human thrombopoietin, but is

XX PT non-immunogenic or less immunogenic than other non-modified molecules

XX PT with same activity -

XX PS Disclosure; Page 12; 36pp; English.

XX CC The invention relates to a novel modified molecule having the biological

XX CC activity of human thrombopoietin (TPO) and being substantially

XX CC non-immunogenic or less immunogenic than any non-modified molecule having

XX CC the same biological activity when used in vivo. The invention also

XX CC discloses T-cell epitope peptides created from non-modified TPO, and

XX CC having potential MHC class II binding activity. The protein of the

XX CC invention has immunosuppressive and antiallergic activity. A peptide of

XX CC the invention is useful in the manufacture of TPO having substantially no

XX CC or less immunogenicity than any non-modified molecule with the same

XX CC biological activity when used in vivo. The protein is useful in

XX CC pharmaceutical compositions, and is suitable for therapeutic use, e.g.

XX CC allergies and autoimmune disease treatment. The sequences shown in

XX CC ABP81048 - ABP81172 represent the MHC class II binding peptides of the

XX CC invention.

XX SQ Sequence 13 AA;

Query Match 50.0%; Score 5; DB 24; Length 13;

Best Local Similarity 100.0%; Pred. No. 51;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPPT 6  
| | | | |  
Db 1 PLPPT 5

RESULT 33  
AAY03679  
ID AAY03679 standard; peptide; 14 AA.  
XX AC  
XX AAY03679;  
XX XX  
XX 07-JUN-1999 (first entry)  
XX DE  
XX Amino acid sequence of the malaria (M) string CTL epitope BCG.  
XX CD8+ T-cell; immune response; antigen; priming composition; CTL; epitope;  
KW cytotoxic T lymphocyte; boosting; poxvirus vector; PVV; pathogen; tumour;  
KW malaria; parasite; P. falciparum; viral; bacterial; parasitic; cancer;  
KW melanoma; HIV; breast; colon; vaccination.  
XX Mycobacterium tuberculosis.  
XX OS  
XX WO9856919-A2.  
XX PN  
XX 17-DEC-1998.  
XX PD  
XX 09-JUN-1998; 98WO-GB01681.  
XX PF  
XX 09-JUN-1997; 97GB-0011957.  
XX PR  
XX (ISIS-) ISIS INNOVATION LTD.  
XX PA  
XX Blanchard T, Gilbert SC, Hanke T, Hill AVS, McMichael AJ;  
PI Piebanski M, Schneider J, Smith GL;  
PI WPI; 1999-070325/06.  
XX DR  
XX N-PSDB; AAX29219.  
XX XX  
XX Generating CD8-positive T cell response to target antigen using  
PT recombinant poxvirus - for treating or preventing malaria and HIV  
PT infection, also epitope strings from Plasmodium and HIV  
PT XX  
PS Claim 38; Page 19; 85pp; English.  
XX CC  
CC The invention relates to methods and reagents for generating a  
CC protective CD8+ T-cell immune response against at least one target  
CC antigen. The kits of the invention comprises (i) as priming composition,  
CC a source of one or more CD8+ T-cell [cytotoxic T lymphocytes-(CTL)]  
CC epitopes of the target antigen, plus a carrier and (ii) as boosting  
CC composition a source of CTL epitopes, with at least one CTL epitope the  
CC same as used in (i), with this source being a non-replicating or  
CC replication-impaired recombinant poxvirus vector (PVV) plus a carrier. If  
CC the source of CTL epitopes in (i) is a viral vector, then the vector in  
CC (ii) is from a different virus. The kits are used to generate an immune  
CC response (prophylactic or therapeutic) against pathogens or tumours,  
CC specifically against malaria parasites such as P. falciparum, or HIV, and  
CC also many other bacterial, viral or parasitic pathogens. The kits are  
CC also used for protective response against melanoma and cancer of breast  
CC or colon, and generally wherever a strong CD8+ response is protective.  
CC The boosting composition may be used alone to boost a naturally primed  
CC response against malaria. The specified PVV provide an excellent booster  
CC effect, better than that from wild-type poxvirus, resulting in complete  
CC rather than partial protection against sporozoite challenge. Also PVV are  
CC safer to use than wild-type virus. Sequences AAY03661-680 represent CTL  
CC peptide epitopes of the malaria (M) string.  
XX XX  
SQ Sequence 14 AA;

Query Match 50.0%; Score 5; DB 20; Length 14;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPPT 6  
| | | | |  
Db 1 PLPPT 5

RESULT 34  
AAM00448  
ID AAM00448 standard; Peptide; 14 AA.  
XX XX  
XX AAM00448;  
XX AC  
XX 01-OCT-2001 (first entry)  
XX DT  
XX Human protein fragment SEQ ID NO: 996.  
XX DE  
XX Human; single nucleotide polymorphism; SNP; paternity test;  
KW forensic test; aberrant protein expression.  
XX KW  
XX Homo sapiens.  
XX OS  
XX WO200151670-A2.  
XX PN  
XX 19-JUL-2001.  
XX PD  
XX 05-JAN-2001; 2001WO-US00322.  
XX PF  
XX 07-JAN-2000; 2000US-0174962.  
XX PR  
XX (CURA-) CURAGEN CORP.  
XX PA  
XX Shimkets RA, Leach MD;  
XX FI  
XX WPI; 2001-451871/48.  
XX DR  
XX N-PSDB; AAH89565.  
XX DR  
XX Isolated human polynucleotides containing single nucleotide  
PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,  
PT infection and diabetes -  
PT XX  
XX Disclosure; Page 389; 475pp; English.  
XX PS  
XX The present invention relates to human nucleic acids containing single  
CC nucleotide polymorphisms (SNPs). These can be used in forensic and  
CC paternity tests, and to aid in the treatment of diseases associated with  
CC aberrant protein expression, including cancer, amyloidosis, diabetes,  
CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,  
CC glomerulonephritis, haemolytic anaemia, thrombocytopaenia, arthritis,  
CC meningitis, muscular disorders, dementia, neurological diseases, tuberculous  
CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,  
CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or  
CC autoimmunity. The present sequence is a peptide encoded by a  
CC polymorphism-containing oligonucleotide fragment of the invention.  
XX XX  
SQ Sequence 14 AA;

Query Match 50.0%; Score 5; DB 22; Length 14;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPLPP 5  
| | | | |  
Db 5 QPLPP 9

RESULT 35  
AAB46171  
ID AAB46171 standard; peptide; 14 AA.  
XX XX  
XX AAB46171;  
XX AC  
XX 04-APR-2001 (first entry)  
XX DT  
XX

DE XX Bacille Calmette-Guerin universal T epitope.  
 KW Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;  
 KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;  
 KW amyloid precursor protein; Alzheimer's disease.  
 OS Mycobacterium tuberculosis.  
 XX WO200072880-A2.  
 PN 07-DEC-2000.  
 XX 26-MAY-2000; 2000WO-US14810.  
 PF 28-MAY-1999; 99US-0322289.  
 PR (NEUR-) NEURALAB LTD.  
 PA Schenk DB, Bard F, Vasquez NJ, Yednock T;  
 PI WPI; 2001-032104/04.  
 XX Preventing or treating a disease associated with amyloid deposits,  
 PT especially Alzheimer's disease, comprises administering amyloid  
 PT specific antibody -  
 XX Disclosure; Page 28; 143pp; English.  
 PS This invention describes a novel method of preventing or treating a  
 CC disease associated with amyloid deposits of amyloid precursor protein  
 CC (APP) beta fragments in the brain of a patient, which comprises  
 CC administering to the patient: (a) an antibody that binds to Abeta, the  
 CC antibody binds to an amyloid deposit and induces a clearing response (Fc  
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing  
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent  
 CC that induces an immunogenic response against residues 1-3 to 7-11 of  
 CC Abeta. The products of the invention have nootropic and neuroprotective  
 CC activity. The method is also useful for monitoring a course of treatment  
 CC being administered to a patient e.g. active and passive immunization. The  
 CC methods are useful for prophylactic and therapeutic treatment of  
 CC Alzheimer's disease.  
 XX Sequence 14 AA;  
 SQ Query Match 50.0%; Score 5; DB 22; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QPLPP 5  
 Db |||||  
 5 QPLPP 9  
 RESULT 36  
 AAB49070 ID AAB49070 standard; peptide; 14 AA.  
 XX AC AAB49070;  
 XX 27-MAR-2001 (first entry)  
 XX BCG T-cell epitope, SEQ ID NO:6.  
 KW Amyloid disease; amyloid fibril deposition; amyloid plaque;  
 KW immunogenic; antibody; vaccine; Alzheimer's disease;  
 KW type 2 diabetes; reactive system amyloidosis;  
 KW systemic senile amyloidosis; familial amyloid cardiomyopathy;  
 KW transmissible spongiform encephalopathy; Creutzfeldt-Jakob disease; Kuru;  
 KW haemodialysis-associated beta-2-microglobulin deposition;  
 KW carrier protein; universal T-cell epitope.  
 XX Mycobacterium bovis.  
 OS  
 XX

PN WO200072876-A2.  
 XX 07-DEC-2000.  
 PF 01-JUN-2000; 2000WO-US15239.  
 XX 01-JUN-1999; 99US-0137010.  
 PR (NEUR-) NEURALAB LTD.  
 PA Schenk DB;  
 PI WPI; 2001-070921/08.  
 XX Pharmaceutical composition comprising immunogen against amyloid  
 PT component such as fibril peptide or protein, or antibody against  
 PT amyloid component useful for treating amyloid diseases or amyloidoses -  
 XX Disclosure; Page 43; 140pp; English.  
 PS The invention relates to a novel pharmaceutical composition for  
 CC preventing or treating a disease characterised by amyloid fibril  
 CC deposits (amyloid plaques) in a patient. The pharmaceutical composition  
 CC comprises an agent that will induce an immune response against an amyloid  
 CC component, or an antibody or antibody fragment that binds to an amyloid  
 CC component. The invention also relates to a method for determining  
 CC the prognosis of a patient undergoing treatment for an amyloid disorder  
 CC which involves measuring a patient serum amount of immunoreactivity  
 CC against a selected amyloid component. A patient serum immunoreactivity  
 CC of at least four times a base line serum immunoreactivity control level  
 CC indicates a prognosis of improved status with respect to the disorder.  
 CC The pharmaceutical compositions of the invention are useful for treating  
 CC a wide variety of disorders characterised by amyloid fibril deposition in  
 CC a patient. Such disorders include Alzheimer's disease characterised by  
 CC amyloid beta peptide fibril deposits; type 2 diabetes characterised by  
 CC islet amyloid protein peptide (IAPP, amylin) fibrils; reactive systemic  
 CC amyloidosis associated with systemic inflammatory diseases (e.g.,  
 CC rheumatoid arthritis, osteomyelitis, tuberculosis) characterised by AA  
 CC fibrils derived from serum amyloid A protein (ApoSAA); systemic senile  
 CC amyloidosis and familial amyloid cardiomyopathy characterised by ATTR  
 CC fibrils derived from transthyretin (TTR); transmissible spongiform  
 CC encephalopathies (e.g. Creutzfeldt-Jakob disease, Kuru) characterised by  
 CC prion protein deposits; and beta-2-microglobulin deposits which form as  
 CC a result of long term haemodialysis treatment. The present sequence  
 CC represents a universal T-cell epitope which may be used as a  
 CC carrier for an epitope derived from an amyloid plaque component in a  
 CC composition of the invention.  
 XX Sequence 14 AA;  
 SQ Query Match 50.0%; Score 5; DB 22; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QPLPP 5  
 Db |||||  
 5 QPLPP 9  
 RESULT 37  
 AAW38958 ID AAW38958 standard; peptide; 15 AA.  
 XX AC AAW38958;  
 XX 27-MAR-1998 (first entry)  
 DT Peptide resembling an SH3 domain binding peptide SEQ ID NO:355.  
 DE Cortactin; SH3 domain; binding peptide; Src homology region 3;  
 XX tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;  
 KW Ab1; PLCgamma; p53bp2; Crk; Yes; Grb2.  
 XX

OS Synthetic.  
 PN WO9730074-A1.  
 XX  
 PD 21-AUG-1997.  
 XX  
 PF 14-FEB-1997; 97WO-US02298.  
 XX  
 PR 16-FEB-1996; 96US-0602999.  
 XX  
 XX (CYTO-) CYTOGEN CORP.  
 PA (UYNC-) UNIV NORTH CAROLINA.  
 XX  
 PI Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;  
 PI Sparks AB, Thorn JM;  
 XX  
 DR WPI; 1997-424972/39.  
 XX  
 XX Src homology region 3 binding peptide - used to activate Src  
 PT tyrosine kinase(s) and to stimulate immune response by increasing  
 PT production of certain lymphokine(s), e.g. interleukin-1  
 XX  
 PS Claim 22; Page 91; 131pp; English.  
 XX  
 CC The present sequence represents a peptide which resembles a Src homology  
 CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:  
 CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which  
 CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3  
 CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)  
 CC peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind  
 CC the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3  
 CC domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)  
 CC binding peptides can be used in the method to identify inhibitors of  
 CC their binding to their respective SH3 domains, which could be used to  
 CC modulate the pharmacological activity of proteins or polypeptide  
 CC containing the SH3 domain. The peptides can also be used to activate  
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune  
 CC response by increasing the production of certain lymphokines, e.g.  
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a  
 CC conjugated molecule to certain cellular compartments containing Src or  
 CC Src related proteins.  
 XX  
 SQ Sequence 15 AA;  
 Query Match 50.0%; Score 5; DB 18; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 58;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2 PLPPT 6  
 Db 9 PLPPT 13  
 RESULT 38  
 AAW39036  
 ID AAW39036 standard; peptide, 15 AA.  
 XX  
 AC AAW39036;  
 XX  
 XX 27-MAR-1998 (first entry)  
 DT  
 DE Peptide resembling an SH3 domain binding peptide SEQ ID NO:437.  
 XX  
 KW Cortactin; SH3 domain; binding peptide; Src homology region 3;  
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;  
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.  
 XX  
 XX Synthetic.  
 OS  
 XX WO9730074-A1.  
 PN  
 XX 21-AUG-1997.  
 PD

XX 14-FEB-1997; 97WO-US02298.  
 XX  
 PR 16-FEB-1996; 96US-0602999.  
 XX  
 PA (CYTO-) CYTOGEN CORP.  
 PA (UYNC-) UNIV NORTH CAROLINA.  
 XX  
 PI Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;  
 PI Sparks AB, Thorn JM;  
 XX  
 DR WPI; 1997-424972/39.  
 XX  
 XX Src homology region 3 binding peptide - used to activate Src  
 PT tyrosine kinase(s) and to stimulate immune response by increasing  
 PT production of certain lymphokine(s), e.g. interleukin-1  
 XX  
 PS Claim 22; Page 94; 131pp; English.  
 XX  
 CC The present sequence represents a peptide which resembles a Src homology  
 CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:  
 CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which  
 CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3  
 CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)  
 CC peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind  
 CC the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3  
 CC domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)  
 CC binding peptides can be used in the method to identify inhibitors of  
 CC their binding to their respective SH3 domains, which could be used to  
 CC modulate the pharmacological activity of proteins or polypeptide  
 CC containing the SH3 domain. The peptides can also be used to activate  
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune  
 CC response by increasing the production of certain lymphokines, e.g.  
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a  
 CC conjugated molecule to certain cellular compartments containing Src or  
 CC Src related proteins.  
 XX  
 SQ Sequence 15 AA;  
 Query Match 50.0%; Score 5; DB 18; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 58;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 QPLPP 5  
 Db 2 QPLPP 6  
 RESULT 39  
 AAG78855  
 ID AAG78855 standard; Peptide; 15 AA.  
 XX  
 AC AAG78855;  
 XX  
 XX 12-DEC-2001 (first entry)  
 DT  
 DE Growth hormone family protein 11 peptide fragment.  
 XX  
 KW Growth hormone; cytostatic; virucidal; immunomodulator; antiinflammatory;  
 KW haemostatic; gene therapy; malignant tumour; haemopathy; HIV infection;  
 KW immunological disease; inflammation.  
 XX  
 OS Unidentified.  
 OS  
 XX WO200172832-A1.  
 PN  
 XX 04-OCT-2001.  
 PD  
 XX 26-MAR-2001; 2001WO-CN00489.  
 XX  
 PF 27-MAR-2000; 2000CN-0115180.  
 PR  
 XX

PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.  
 XX Mao Y, Xie Y;  
 XX WPI; 2001-602854/68.  
 XX New polypeptide for the diagnosis and treatment of malignant neoplasm,  
 PT hemopathy, HIV infection, immunological diseases and inflammations,  
 PT comprises protein 11 of the growth hormone family -  
 XX Example 5; Page 19; 35pp; Chinese.  
 XX The present invention relates to protein 11 of the growth hormone family  
 CC (see AAF165179 and AAG78854). The growth hormone protein and its coding  
 CC sequence are useful in the diagnosis and treatment of malignant tumours,  
 CC haemopathy, HIV infection, immunological diseases and various  
 CC inflammations. The present sequence is an N-terminal peptide fragment of  
 CC the growth hormone protein which was used in an example from the present  
 CC invention.  
 XX SQ Sequence 15 AA;  
 Query Match 50.0%; Score 5; DB 22; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 58;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 PLPPT 6  
 DB 8 PLPPT 12  
 RESULT 40  
 ABG72660  
 ID ABG72660 standard; Peptide; 15 AA.  
 XX AC ABG72660;  
 XX 26-FEB-2003 (first entry)  
 DT Human K-ras 10.67 proto-oncogene protein, N-terminus.  
 DE Human; K-ras 10.67; proto-oncogene; tumour; haemopathy;  
 XX development disorder; human immunodeficiency virus infection; HIV;  
 KW immunological disease; inflammation.  
 KW Homo sapiens.  
 OS CNI352063-A.  
 XX 05-JUN-2002.  
 PD 02-NOV-2000; 2000CN-0127155.  
 PF 02-NOV-2000; 2000CN-0127155.  
 PR (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
 XX Mao Y, Xie Y;  
 XX WPI; 2002-658691/71.  
 XX New human K-ras proto-oncogene protein 10.67 polypeptide for treating  
 PT malignant tumors, hemopathy, development disorder, human  
 PT immunodeficiency virus infection, immunological diseases and various  
 PT inflammations -  
 XX Example 5; Page 19 (disclosure); 33pp; Chinese.  
 XX The present invention discloses a new kind of polypeptide,  
 CC human K-ras proto-oncogene protein 10.67, polynucleotides encoding the  
 CC polypeptide and a DNA recombination process to produce the polypeptide.  
 CC The present invention also discloses applying the polypeptide in  
 CC treating various diseases, such as malignant tumors, haemopathy,  
 CC development disorder, human immunodeficiency virus (HIV) infection,  
 CC immunological diseases and various inflammations. The present invention  
 CC also discloses the antagonist resisting the polypeptide and its  
 CC treatment effect. The present invention also discloses application of  
 CC the polynucleotides encoding human K-ras proto-oncogene protein 10.67.  
 CC The present sequence represents human K-ras proto-oncogene protein  
 CC 10.67, N-terminus, used in an ELISA (enzyme-linked immunosorbent assay)  
 CC experiment.  
 XX SQ Sequence 15 AA;  
 Query Match 50.0%; Score 5; DB 23; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 58;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QPLPP 5  
 DB 11 QPLPP 15  
 RESULT 41  
 AAW25427  
 ID AAW25427 standard; peptide; 16 AA.  
 XX AC AAW25427;  
 XX 27-MAR-1998 (first entry)  
 DT Yes SH3 domain binding peptide SEQ ID NO:213.  
 DE Cortactin; SH3 domain; binding peptide; Src homology region 3;  
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;  
 KW Abi; PLCgamma; p53bp2; Crk; Yes; Grb2.  
 XX Synthetic.  
 OS Unidentified.  
 XX WO9730074-A1.  
 XX 21-AUG-1997.  
 PD 14-FEB-1997; 97WO-US02298.  
 PF 16-FEB-1996; 96US-0602999.  
 PR (CYTO-) CYTOGEN CORP.  
 XX (UYNC-) UNIV NORTH CAROLINA.  
 PA Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;  
 PI Sparks AB, Thorn JM;  
 XX WPI; 1997-424972/39.  
 XX Src homology region 3 binding peptide - used to activate Src  
 PT tyrosine kinase(s) and to stimulate immune response by increasing  
 PT production of certain lymphokine(s), e.g. interleukin-1  
 XX Claim 19; Page 100; 131pp; English.  
 XX The present sequence represents a Src homology region 3 (SH3) binding  
 CC peptide. SH3 binding peptides are selected from: (a) peptides which  
 CC bind the SH3 domain of Cortactin; (b) peptides which bind the middle  
 CC SH3 domain of Nck; (c) peptides which bind the SH3 domain of Abi; (d)  
 CC peptides which bind the SH3 domain of Src; (e) peptides which bind the  
 CC SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain of  
 CC p53bp2; (g) peptides which bind the amino-terminal SH3 domain of Crk;  
 CC (h) peptides which bind the SH3 domain of Yes; and (i) peptides which  
 CC bind the amino-terminal SH3 domain of Grb2. The purified binding  
 CC peptides can be used in the method to identify inhibitors of their  
 CC binding to their respective SH3 domains, which could be used to  
 CC modulate the pharmacological activity of proteins or polypeptide  
 CC containing the SH3 domain. The peptides can also be used to activate  
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune



CC response by increasing the production of certain lymphokines, e.g.  
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a  
 CC conjugated molecule to certain cellular compartments containing Src or  
 CC Src related proteins.

XX Sequence 16 AA;

Query Match 50.0%; Score 5; DB 18; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 61;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPPT 6  
 Db 5 PLPPT 9  
 |||||

RESULT 42  
 AAW25376  
 ID AAW25376 standard; peptide; 16 AA.

XX AAW25376;

XX 27-MAR-1998 (first entry)

DE Src SH3 domain binding peptide SEQ ID NO:158.

XX Cortactin; SH3 domain; binding peptide; Src homology region 3;  
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;  
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.

XX Synthetic.  
 OS Unidentified.

XX WO9730074-A1.

XX 21-AUG-1997.

XX 14-FEB-1997; 97WO-US02298.

XX 16-FEB-1996; 96US-0602999.

XX (CYTO-) CYTOGEN CORP.

XX (UYNC-) UNIV NORTH CAROLINA.

XX Der CU, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;

XX Sparks AB, Thorn JM;

XX WPI; 1997-424972/39.

XX Src homology region 3 binding peptide - used to activate Src  
 PT tyrosine kinase(s) and to stimulate immune response by increasing  
 PT production of certain lymphokine(s), e.g. interleukin-1

XX Claim 16; Page 99; 131pp; English.

XX The present sequence represents a Src homology region 3 (SH3) binding  
 CC peptide. SH3 binding peptides are selected from: (a) peptides which  
 CC bind the SH3 domain of Cortactin; (b) peptides which bind the middle  
 CC SH3 domain of Nck; (c) peptides which bind the SH3 domain of Abl; (d)  
 CC peptides which bind the SH3 domain of Src; (e) peptides which bind the  
 CC SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain of  
 CC p53bp2; (g) peptides which bind the amino-terminal SH3 domain of Crk;  
 CC (h) peptides which bind the SH3 domain of Yes; and (i) peptides which  
 CC bind the amino-terminal SH3 domain of Grb2. The purified binding  
 CC peptides can be used in the method to identify inhibitors of their  
 CC binding to their respective SH3 domains, which could be used to  
 CC modulate the pharmacological activity of proteins or polypeptide  
 CC containing the SH3 domain. The peptides can also be used to activate  
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune  
 CC response by increasing the production of certain lymphokines, e.g.  
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a  
 CC conjugated molecule to certain cellular compartments containing Src or  
 CC Src related proteins.

XX SQ Sequence 16 AA;

Query Match 50.0%; Score 5; DB 18; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 61;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPPT 6  
 Db 5 PLPPT 9  
 |||||

RESULT 43  
 AAW25380  
 ID AAW25380 standard; peptide; 16 AA.

XX AAW25380;

XX 27-MAR-1998 (first entry)

XX Src SH3 domain binding peptide SEQ ID NO:147.

XX Cortactin; SH3 domain; binding peptide; Src homology region 3;  
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;  
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.

XX Synthetic.  
 OS Unidentified.

XX WO9730074-A1.

XX 21-AUG-1997.

XX 14-FEB-1997; 97WO-US02298.

XX 16-FEB-1996; 96US-0602999.

XX (CYTO-) CYTOGEN CORP.

XX (UYNC-) UNIV NORTH CAROLINA.

XX Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;

XX Sparks AB, Thorn JM;

XX WPI; 1997-424972/39.

XX Src homology region 3 binding peptide - used to activate Src  
 PT tyrosine kinase(s) and to stimulate immune response by increasing  
 PT production of certain lymphokine(s), e.g. interleukin-1

XX Claim 16; Page 99; 131pp; English.

XX The present sequence represents a Src homology region 3 (SH3) binding  
 CC peptide. SH3 binding peptides are selected from: (a) peptides which  
 CC bind the SH3 domain of Cortactin; (b) peptides which bind the middle  
 CC SH3 domain of Nck; (c) peptides which bind the SH3 domain of Abl; (d)  
 CC peptides which bind the SH3 domain of Src; (e) peptides which bind the  
 CC SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain of  
 CC p53bp2; (g) peptides which bind the amino-terminal SH3 domain of Crk;  
 CC (h) peptides which bind the SH3 domain of Yes; and (i) peptides which  
 CC bind the amino-terminal SH3 domain of Grb2. The purified binding  
 CC peptides can be used in the method to identify inhibitors of their  
 CC binding to their respective SH3 domains, which could be used to  
 CC modulate the pharmacological activity of proteins or polypeptide  
 CC containing the SH3 domain. The peptides can also be used to activate  
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune  
 CC response by increasing the production of certain lymphokines, e.g.  
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a  
 CC conjugated molecule to certain cellular compartments containing Src or  
 CC Src related proteins.

XX SQ Sequence 16 AA;

Query Match 50.0%; Score 5; DB 18; Length 16;

Best Local Similarity 100.0%; Pred. No. 61;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPPT 6  
Db 5 PLPPT 9

RESULT 44  
ABP82678  
ID ABP82678 standard; Peptide; 16 AA.  
XX  
AC ABP82678;  
XX  
DT 04-MAR-2003 (first entry)  
XX  
DE G protein-coupled receptor (GPCR) antigenic peptide SEQ ID NO:1351.  
XX  
KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;  
KW G protein-coupled receptor modulator; antibody; immune-related disease;  
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;  
KW immunological-related cell proliferative disease; autoimmune disease;  
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;  
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;  
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;  
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;  
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;  
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;  
KW ulcer.  
XX  
OS Homo sapiens.  
XX  
PN WO200261087-A2.  
XX  
PD 08-AUG-2002.  
XX  
PF 19-DEC-2001; 2001WO-US50107.  
XX  
PR 19-DEC-2000; 2000US-257144P.  
XX  
PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
XX  
PI Burmer GC, Roush CL, Brown JP;  
XX  
DR WPI; 2003-046718/04.  
XX  
PT New isolated antigenic peptides e.g., for G protein-coupled receptors  
PT (GPCR), useful for diagnosing and designing drugs for treating  
PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,  
PT cancer or autoimmune diseases -  
XX  
PS Claim 1; Fig 2; 523pp; English.

The present invention describes antigenic peptides (I) comprising:  
(a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino acids. Also described: (1) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR, and in the production of specific antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, growth-related diseases, cell regeneration-related disease, immunological-related cell proliferative diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease, atherosclerosis, bacterial, fungal, protozoan or viral infections, osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, diabetes, graft versus host disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, anxiety, depression, schizophrenia, dementia, mental retardation, memory loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,

CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or  
CC any other disorder in which GPCRs are involved. The antibodies may be  
CC used in immunoassays and immunodiagnosis. ABP82678 to ABP82869 encode  
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the  
CC exemplification of the present invention.

XX  
SQ Sequence 16 AA;  
Query Match 50.0%; Score 5; DB 24; Length 16;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPPT 6  
Db 10 PLPPT 14

RESULT 45  
AAB39277  
ID AAB39277 standard; Protein; 17 AA.  
XX  
AC AAB39277;  
XX  
DT 02-FEB-2001 (first entry)  
XX  
DE Gene 31 human secreted protein homologous amino acid sequence #157.  
XX  
KW Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic;  
KW antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;  
KW neurotropic; neuroprotective; antibacterial; virucide; fungicide; neoplasm;  
KW ophthalmological; autoimmune disease; rheumatoid arthritis; angioedema;  
KW hyperproliferative disorder; cardiovascular disorder; infection;  
KW cerebrovascular disorder; nervous system disorder; ocular disorder;  
KW wound healing; chemotaxis.  
XX  
OS Homo sapiens.  
XX  
PN WO2000056754-A1.  
XX  
PD 28-SEP-2000.  
XX  
PF 16-MAR-2000; 2000WO-US06792.  
XX  
PR 19-MAR-1999; 99US-0125362.  
PR 10-DEC-1999; 99US-0169980.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen GA, Ruben SM, Komatsoulis G;  
XX  
DR WPI; 2000-579483/54.  
XX  
PT Isolated nucleic acid molecule encoding a human secreted protein is  
PT used in preventing, treating or ameliorating a medical condition -  
XX  
PS Disclosure; Page 52; 434pp; English.

The polynucleotide sequences given in AAC74223-C74279 encode the human secreted proteins represented in AAB39179-B39226. Sequences AAB39227-B39308 are alternative proteins encoded by the genes, and also protein sequences with which they share homology. The proteins have activities based on the tissues and cells in which they are expressed. Examples of activities include: immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; neurotropic; neuroprotective; antibacterial; virucide; fungicide; and ophthalmological. The human secreted proteins, polynucleotides, antagonists and agonists of the invention may be useful in the treatment, prevention, and/or diagnosis of various disease, disorders and conditions such as autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angioedema, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and

CC fungi and ocular disorders e.g. corneal infection. The polypeptides can  
 CC also be used to aid wound healing and epithelial cell proliferation, to  
 CC regenerate tissues, maintain organs before transplantation, in  
 CC chemotaxis and as a food additive or preservative e.g. to increase  
 CC storage capabilities. Sequences AAC74214-C74222 and AAB39178 are used  
 CC during the isolation and characterisation of the genes of the invention.  
 XX  
 SQ Sequence 17 AA;

Query Match 50.0%; Score 5; DB 21; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 64;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPLPP 5  
 |||||  
 Db 1 QPLPP 5

## RESULT 46

AAE03955  
 ID AAE03955 standard; peptide; 18 AA.

AC AAE03955;

DT 09-AUG-2001 (first entry)

DE Human gene 10 encoded secreted protein fragment, SEQ ID NO:126.

XX Human; secreted protein; proliferative disorder; cancer; tumour;  
 KW foetal abnormality; developmental abnormality; haematopoietic disorder;  
 KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;  
 KW inflammation; allergy; neurological disorder; Alzheimer's disease;  
 KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;  
 KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;  
 KW cardiovascular disorder; angiogenic disorder; kidney disorder;  
 KW gastrointestinal disorder; pregnancy-related disorder;  
 KW endocrine disorder; infection; wound healing; vulnerability;  
 KW cell culture; chemotaxis; food additive; gene therapy;  
 KW binding partner identification.

XX Homo sapiens.

XX W0200077022-A1.

XX 21-DEC-2000.

XX 01-JUN-2000; 2000WO-US15136.

XX 11-JUN-1999; 99US-0138629.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM, Komatsoulis GA;

XX WPI; 2001-367020/38.

XX Nucleic acids encoding 50 human secreted polypeptides, useful for  
 PT preventing, diagnosing and/or treating diseases, e.g. Parkinson's  
 PT disease, botulism, cancers and Scimitar syndrome -  
 XX

PS Disclosure; Page 566-567; 61pp; English.

XX AAD08345-AAD08394 represent cDNAs corresponding to 50 human secreted  
 CC protein genes and AAE03898-AAE03947 represent the proteins they encode.  
 CC AAE03948-AAE03996 represent human secreted protein fragments or variants.  
 CC The genes and their secreted proteins are useful for preventing,  
 CC treating or ameliorating medical conditions, e.g., by protein or gene  
 CC therapy. Pathological conditions can be diagnosed by determining the  
 CC amount of the new protein in a sample or by determining the presence of  
 CC mutations in the new genes. Specific uses are described for each of the  
 CC 50 genes, based on the tissues in which they are most highly expressed,  
 CC and include developing products for the diagnosis or treatment of  
 CC proliferative disorders, cancer, tumours, foetal and developmental

CC abnormalities, haematopoietic disorders, diseases of the immune system,  
 CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,  
 CC allergies, neurological disorders (e.g., Alzheimer's disease,  
 CC Parkinson's disease), cognitive disorders, schizophrenia, asthma,  
 CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,  
 CC cardiovascular disorders, angiogenic disorders, kidney disorders,  
 CC gastrointestinal disorders, pregnancy-related disorders, endocrine  
 CC disorders, and infections. The proteins can also be used to aid wound  
 CC healing and epithelial cell proliferation, to prevent skin aging due to  
 CC sunburn, to maintain organs before transplantation, for supporting cell  
 CC culture of primary tissues, to regenerate tissues, to identify their  
 CC cognate ligands or binding partners, and in chemotaxis, and can be used  
 CC as a food additive or preservative to modify storage properties.  
 CC Antibodies specific for a protein of the invention can be used in  
 CC alleviating symptoms associated with the disorders mentioned above, and  
 CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked  
 CC immunosorbent assay (ELISA). The present sequence represents a human  
 CC secreted protein fragment referred to in the disclosure of the invention.  
 XX

SQ Sequence 18 AA;

Query Match 50.0%; Score 5; DB 22; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 67;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPLPP 5  
 |||||  
 Db 11 QPLPP 15

## RESULT 47

AAAY31181

ID AAY31181 standard; peptide; 19 AA.

AC AAY31181;

XX 28-OCT-1999 (first entry)

XX Ubiquitin fusion protein T cell epitope.

XX Ubiquitin; immunocastration; fusion protein; heat shock protein; epitope;  
 KW immune response stimulation; vaccine; T cell; viral; infection; cancer;  
 KW bacterial; parasitic; treatment; gastrointestinal disease; HIV infection;  
 KW pulmonary infection; respiratory infection; scaffold; anti-self; pig;  
 KW steridogenesis; Gamete maturation; prostate; breast; castration; TNF;  
 KW tumour necrosis factor; septic shock; arthritis; Crohn's disease;  
 KW inflammatory bowel disease; ulcerative colitis; chorionic gonadotropin;  
 KW fertility; sperm protein; growth rate; antibody; detection.

XX Synthetic.

XX W09942472-A1.

XX 26-AUG-1999.

XX 26-JAN-1999; 99WO-US01588.

XX 19-FEB-1998; 98US-0026276.

XX (IGEN-) IGEN INT INC.

XX Kenten JH, Lohnas GL, Pilon AL, Roberts SF, Tramontano A;

XX WPI; 1999-518582/43.

XX Epitope-containing fusion proteins used to generate a highly  
 PT specific immune responses

XX Example 4; Page 42; 67pp; English.

XX This invention describes a novel fusion protein, comprising a heat shock  
 CC protein (e.g. ubiquitin), fused to an epitope(s) in a defined manner  
 CC which is useful for the stimulation of a highly specific immune response

CC when administered to an animal. The protein of the invention may be  
 CC post-translationally modified (e.g. by the addition of fatty acids to  
 CC enhance immunogenicity). The fusion proteins of the invention can be  
 CC used as vaccines to induce an immune response. When a T cell epitope is  
 CC attached, they can be used for control of viral infections, bacterial  
 CC infections, parasitic infection and cancer. The fusion proteins can be  
 CC used in pharmaceutical compositions for the treatment of gastrointestinal  
 CC diseases, pulmonary infections, respiratory infections, and HIV  
 CC infections. The use of ubiquitin as a scaffold is also useful for the  
 CC presentation and stimulation of anti-self immune responses, e.g.  
 CC generation of anti-gonadotropin releasing hormone antibodies which result  
 CC in the suppression of luteinizing hormone and follicle stimulating  
 CC hormone. This indirectly suppresses steroidogenesis and gamete maturation  
 CC in males and females. This type of anti-self response in humans is useful  
 CC in the treatment of prostate cancer and breast cancer. In livestock, the  
 CC ability to stimulate an anti-self response provides a simple alternative  
 CC to physical castration. Immunocastration of pigs is a better alternative  
 CC side effects associated with physical castration. Other examples of  
 CC diseases and conditions treated with self proteins fused with ubiquitin  
 CC are TNF and its epitopes to modulate septic shock, arthritis,  
 CC inflammatory bowel disease, Crohn's disease, and ulcerative colitis; Ig  
 CC epsilon heavy chain for the control of allergic reactions; chorionic  
 CC gonadotropin for fertility control; and sperm proteins for fertility  
 CC control. A further use of the fusion proteins is as part of a vaccine to  
 CC enhance growth rate and thereby the final weight of the livestock prior  
 CC to shipment to market. In addition, the fusion proteins of the invention  
 CC can be used to detect and identify antibodies from experimental samples.  
 CC This sequence represents a T cell epitope used in the construction of  
 CC a ubiquitin fusion protein described in the method of the invention.

XX Sequence 19 AA;

Query Match 50.0%; Score 5; DB 20; Length 19;

Best Local Similarity 100.0%; Pred. No. 71;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLPP 5

Db 6 QLPP 10

RESULT 48

AAY31165

ID AAY31165 standard; peptide; 19 AA.

XX AC AAY31165;

XX DT 28-OCT-1999 (first entry)

XX DE Ubiquitin fusion protein MT peptide.

XX Ubiquitin; immunocastration; fusion protein; heat shock protein; epitope;  
 KW immune response stimulation; vaccine; T cell; viral; infection; cancer;  
 KW bacterial; parasitic; treatment; gastrointestinal disease; HIV infection;  
 KW pulmonary infection; respiratory infection; scaffold; anti-self; pig;  
 KW steroidogenesis; gamete maturation; prostate; breast; castration; TNF;  
 KW tumour necrosis factor; septic shock; arthritis; Crohn's disease;  
 KW inflammatory bowel disease; ulcerative colitis; chorionic gonadotropin;  
 KW fertility; sperm protein; growth rate; antibody; detection.

XX OS Synthetic.

XX FN WO9942472-A1.

XX PD 26-AUG-1999.

XX PF 26-JAN-1999; 99WO-US01588.

XX PR 19-FEB-1998; 98US-0026276.

XX PA (IGEN-) IGEN INT INC.

XX

PI Kenten JH, Lohnas GL, Pilon AL, Roberts SF, Tramontano A;  
 XX WPI; 1999-518582/43.

XX PT Epitope-containing fusion proteins used to generate a highly  
 XX specific immune responses

XX PS Example 1; Page 27; 67pp; English.

XX This invention describes a novel fusion protein, comprising a heat shock  
 CC protein (e.g. ubiquitin), fused to an epitope(s) in a defined manner  
 CC which is useful for the stimulation of a highly specific immune response  
 CC when administered to an animal. The protein of the invention may be  
 CC post-translationally modified (e.g. by the addition of fatty acids to  
 CC enhance immunogenicity). The fusion proteins of the invention can be  
 CC used as vaccines to induce an immune response. When a T cell epitope is  
 CC attached, they can be used for control of viral infections, bacterial  
 CC infections, parasitic infection and cancer. The fusion proteins can be  
 CC used in pharmaceutical compositions for the treatment of gastrointestinal  
 CC diseases, pulmonary infections, respiratory infections, and HIV  
 CC infections. The use of ubiquitin as a scaffold is also useful for the  
 CC presentation and stimulation of anti-self immune responses, e.g.  
 CC generation of anti-gonadotropin releasing hormone antibodies which result  
 CC in the suppression of luteinizing hormone and follicle stimulating  
 CC hormone. This indirectly suppresses steroidogenesis and gamete maturation  
 CC in males and females. This type of anti-self response in humans is useful  
 CC in the treatment of prostate cancer and breast cancer. In livestock, the  
 CC ability to stimulate an anti-self response provides a simple alternative  
 CC to physical castration. Immunocastration of pigs is a better alternative  
 CC side effects associated with physical castration. Other examples of  
 CC diseases and conditions treated with self proteins fused with ubiquitin  
 CC are TNF and its epitopes to modulate septic shock, arthritis,  
 CC inflammatory bowel disease, Crohn's disease, and ulcerative colitis; Ig  
 CC epsilon heavy chain for the control of allergic reactions; chorionic  
 CC gonadotropin for fertility control; and sperm proteins for fertility  
 CC control. A further use of the fusion proteins is as part of a vaccine to  
 CC enhance growth rate and thereby the final weight of the livestock prior  
 CC to shipment to market. In addition, the fusion proteins of the invention  
 CC can be used to detect and identify antibodies from experimental samples.  
 CC This sequence represents a MT peptide used in the method of the  
 CC invention.

XX SQ Sequence 19 AA;

Query Match 50.0%; Score 5; DB 20; Length 19;

Best Local Similarity 100.0%; Pred. No. 71;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLPP 5

Db 6 QLPP 10

RESULT 49

AAB71936

ID AAB71936 standard; Peptide; 19 AA.

XX AC AAB71936;

XX DT 10-MAY-2001 (first entry)

XX DE MT peptide.

XX Immunostimulant; antiallergic; growth promoting; vaccine;  
 KW heat shock fusion protein; ubiquitin; self-epitope; immunogen;  
 KW male-specific peptide hormone; female-specific peptide hormone; MT.

XX OS Unidentified.

XX PN WO200112216-A1.

XX PD 22-FEB-2001.

XX PF 14-AUG-2000; 2000WO-US22121.  
 XX PR 13-AUG-1999; 99US-0374721.  
 XX PA (PROT-) PROTEINIX CO.  
 XX PR 13-AUG-1999; 99US-0374721.  
 XX PA (PROT-) PROTEINIX CO.  
 XX KI Kanten JH, Roberts S, Lohnas G;  
 XX WPI; 2001-202829/20.  
 XX Novel fusion proteins for stimulating immune response in animals  
 PT against self-antigen, has heat shock protein fused to single or a group  
 PT of epitope-containing segments having identical or non-identical self  
 PT epitopes -  
 XX Example 1; Page 27; 94pp; English.  
 XX The present sequence is given in an example illustrating an invention  
 CC disclosing self-epitope-containing heat shock fusion proteins. The  
 CC proteins comprise a heat shock protein, preferably ubiquitin, fused to a  
 CC single epitope-containing segment or two or more non-contiguous epitope  
 CC containing segments, each epitope-containing segment comprising one or  
 CC more identical or non-identical self-epitopes. The heat shock fusion  
 CC proteins are useful for stimulating an immune response in an animal,  
 CC especially a pig, directed towards a self-antigen, in particular a male  
 CC or female-specific peptide hormone. The physiological consequence is  
 CC substantially similar to the consequences of surgical castration. The  
 CC proteins are useful for identifying antibodies in experimental or  
 CC diagnostic samples and for reducing levels of a predetermined endogenous  
 CC protein, such as gonadotropin releasing hormone, tumour necrosis factor  
 CC or growth hormone protein. They are also useful for reducing allergic  
 CC response and for increasing the growth rate of an animal. The proteins  
 CC have a high specific immune response and do not result in detrimental  
 CC side-effects. The present sequence encodes a peptide sequence which is  
 CC inserted into a ubiquitin scaffold to test the peptide as an immunogen  
 CC for eliciting a targeted immune response.  
 XX SQ Sequence 19 AA;  
 Query Match 50.0%; Score 5; DB 22; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 71;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 QPLPP 5  
 Db 6 QPLPP 10  
 RESULT 50  
 AAW16997  
 ID AAW16997 standard; peptide; 20 AA.  
 AC AAW16997;  
 XX DT 27-JUN-1997 (first entry)  
 XX DE SRC SH3 domain-binding peptide.  
 XX KW Src; SH3; Src homology region 3; binding affinity; oncogenic protein;  
 KW protein tyrosine kinase; signal transduction; RNA processing;  
 KW trafficking; translation.  
 XX OS Synthetic.  
 XX WO9603649-A1.  
 XX PD 08-FEB-1996.  
 XX

PF 24-JUL-1995; 95WO-US09382.  
 XX PR 07-JUN-1995; 95US-0483555.  
 XX PR 22-JUL-1994; 94US-0278865.  
 XX PA (TYNC-) UNIV NORTH CAROLINA.  
 XX Der CJ, Kay BK, Quilliam LA, Sparks AB, Thorn JM;  
 XX WPI; 1996-117151/12.  
 XX Peptide with binding affinity for Src homology region 3 (SH3)  
 PT domains of proteins - useful for e.g. modulating signal transduction  
 PT pathways at the cellular level, esp. protein tyrosine  
 PT kinase-mediated  
 XX Example 14; Page 58; 116pp; English.  
 XX AAW16996-W17009 are SRC SH3-binding peptides derived from a biased  
 CC peptide library, exhibiting selective SH3 binding. The SH3 binding  
 CC peptides are useful in modulating signal transduction pathways at the  
 CC cellular level (especially protein tyrosine kinase-mediated), modulating  
 CC oncogenic protein activity, or providing compounds for the development  
 CC of drugs with the ability to modulate broad classes, as well as specific  
 CC classes, of proteins involved in signal transduction and also for  
 CC regulating the processing, trafficking or translation of RNA. Conjugates  
 CC of the peptides with detectable labels or imaging agents are useful for  
 CC imaging cells, tissues and organs in which Src or Src-related proteins  
 CC are expressed.  
 XX SQ Sequence 20 AA;  
 Query Match 50.0%; Score 5; DB 17; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 74;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2 PLPPT 6  
 Db 7 PLPPT 11  
 RESULT 51  
 AAR99513  
 ID AAR99513 standard; peptide; 20 AA.  
 XX AC AAR99513;  
 XX DT 09-JAN-1997 (first entry)  
 XX DE T-cell epitope used in construction of chimeric immunoglobulin.  
 XX KW Chimera; chimeric; immunoglobulin; Ig; B-cell; T-cell; lymphocyte;  
 KW epitope; immune response; vaccine; pathogen; antibody; influenza;  
 KW measles; hepatitis; foot and mouth disease; tetanus toxoid;  
 KW human immunodeficiency virus; HIV; heat shock protein; M protein;  
 KW hen egg white lysozyme; nuclease.  
 XX OS Mycobacteria sp.  
 XX WO9619584-A1.  
 XX PD 27-JUN-1996.  
 XX 21-DEC-1995; 95WO-US16718.  
 XX 22-DEC-1994; 94US-0363276.  
 XX (MOUN ) MOUNT SINAI SCHOOL MEDICINE.  
 XX Bona C, Zaghouani H;  
 XX WPI; 1996-309598/31.  
 XX

PT Chimeric immunoglobulin with CDR loop substtd. for T and or B cell  
PT epitope - useful in vaccine composition to enhance immune response  
PT to pathogens  
XX  
PS Disclosure; Page 19; 131pp; English.  
XX  
CC Chimeric immunoglobulins (Ig) having a CDR loop of the parent Ig  
CC replaced with a foreign peptide sequence corresponding to a T- or B-  
CC cell epitope, may be used in vaccine compositions to enhance an  
CC immune response to a pathogen. Chimeric Ig comprising a B-cell  
CC epitope can also be used to label B-cells, to test the ability of a  
CC subject to mount a humoral response to a particular B-cell epitope  
CC or to collect B-cells which recognise the epitope.. An antibody  
CC comprising a chimeric Ig molecule which comprises an antigen binding  
CC site may be used in diagnostic assays to detect the presence of a  
CC particular target antigen, which binds to the antibody binding site.  
CC Sequences of B-cell epitopes are given in AAR9503-08. Sequences of  
CC T-cell epitopes are given in AAR9509-17. The term T-cell epitope  
CC refers to a peptide which is associated with MHC self antigens and  
CC is recognised by a T-cell and which functionally activates the T  
CC cell. This peptide is an epitope of Mycobacteria heat shock  
CC protein.  
XX  
SQ Sequence 20 AA;  
XX  
Query Match 50.0%; Score 5; DB 17; Length 20;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QPLPP 5  
Db |||||  
6 QPLPP 10  
XX  
RESULT 52  
AAW35439  
ID AAW35439 standard; peptide; 20 AA.  
XX  
AC AAW35439;  
XX  
DT 25-MAR-2003 (updated)  
DT 22-APR-1998 (first entry)  
XX  
DE T-cell stimulatory peptide from Mycobacterium tuberculosis 38kd antigen.  
XX  
XX T-cell stimulatory peptide; immunogen; non-dendritic; carrier; tumour;  
KW scaffold; inhibition; metastasis; wound healing; solid phase.  
XX  
OS Mycobacterium tuberculosis.  
XX  
XX WO9738011-A1.  
XX  
PD 16-OCT-1997.  
XX  
PF 03-APR-1997; 97WO-DK00146.  
XX  
PR 03-APR-1996; 96DK-0000398.  
XX  
XX (PEPR-) PEPRESEARCH AS.  
XX  
XX Heegaard PMH, Jakobsen PH;  
XX  
XX WPI; 1997-512645/47.  
XX  
XX Non-dendritic peptide carrier linked to a solid phase - useful as a  
PT diagnostic agent and as a scaffold for production of chemical  
PT derivatives  
XX  
XX Claim 30; Page 199; 262pp; English.  
PS  
XX A non-dendritic peptide carrier (A) has been developed which is coupled  
CC through a linker to a solid phase, forming a complex of (A)-solid phase.  
CC Where (A) comprises 10-50 amino acids capable of forming a secondary  
CC

CC structure in a benign buffer after liberation from the solid phase, and  
CC further the (A)-solid phase complex comprises an immunogenic substance  
CC and/or an immune mediator coupled on (A). The present sequence  
CC represents a specifically claimed T-cell stimulatory peptide from the  
CC present invention. An (A)-solid phase complex can be used as a scaffold  
CC for the production of chemical derivatives, characterised by covalently  
CC attaching molecules at attachment points. Alternatively (A) is used as  
CC a scaffold-peptide for the incorporation into an Immunostimulating  
CC Complex (Iscm) resulting in an (A)-Iscm complex which is used for the  
CC chemical coupling of antigenic substances in an aqueous solution by  
CC conjugation. (A) derivatised with one or more peptides having  
CC fibronectin-, laminin- or vitronectin-like binding activities can be  
CC used for the promotion of cell-attachment to plastic surfaces, in  
CC particular to inhibit tumour growth and metastasis, and for promotion  
CC of wound healing. Also a derivatised (A) can be used for the selection  
CC of specifically-binding aptamers or as a diagnostic agent. Such  
CC diagnostic-(A) molecules could be used to detect molecules derived from  
CC or indicative of pregnancy or of a disease, such as an infectious,  
CC autoimmune or cancerous disease.  
CC (Updated on 25-MAR-2003 to correct PF field.)  
XX  
SQ Sequence 20 AA;  
XX  
Query Match 50.0%; Score 5; DB 18; Length 20;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QPLPP 5  
Db |||||  
6 QPLPP 10  
XX  
RESULT 53  
AAW12237  
ID AAW12237 standard; peptide; 20 AA.  
XX  
AC AAW12237;  
XX  
DT 06-AUG-1997 (first entry)  
DT  
XX  
DE Heatshock protein T-cell epitope.  
XX  
KW B-cell epitope; gp120; hypervariable region 3 loop; envelope protein;  
XX immunoglobulin; vaccine; cancer; viral infection; leukaemia; V3 loop;  
KW influenza virus; target antigen; helper T-cell epitope; immune response;  
XX cell-surface receptor; HIV-1; immune system; therapy.  
XX  
OS Mycobacterium bovis.  
XX  
XX WO9636357-A1.  
XX  
XX 21-NOV-1996.  
XX  
XX 13-MAY-1996; 96WO-US06756.  
XX  
XX 07-JUN-1995; 95US-0477424.  
XX 15-MAY-1995; 95US-0441328.  
XX  
XX (BONA/) BONA C A.  
XX (BRUM/) BRUMEANU T.  
XX (DEHA/) DEHAZYA P.  
XX (LEEY/) LEE Y C.  
XX  
XX Bona CA, Brumeanu T, Dehazy P, Lee YC;  
XX WPI; 1997-011851/01.  
XX  
XX New methods of coupling peptide(s) to immuno-globulin(s) via  
PT carbohydrate - and related conjugates, useful for treating cancer  
PT and viral infections and in vaccines  
XX  
XX Disclosure; Page 12; 69pp; English.  
XX

CC AAW12233-W12241 represent T-cell epitopes that can be used in the method  
 CC of the invention. The method of the invention is for conjugating a  
 CC peptide (such as this sequence) to an immunoglobulin (Ig) molecule, via  
 CC a carbohydrate (CB) residue of the Ig. The method comprises  
 CC enzymatically oxidising the CB residue of the Ig, then reacting this  
 CC residue with an amino group of the peptide. The product of this reaction  
 CC is then stabilised by reacting it with a reducing agent. The conjugate  
 CC may be used as a vaccine and in diagnostic and therapeutic methods. The  
 CC conjugates are used to treat cancer and viral infections, such as  
 CC leukaemia and influenza viruses. The conjugates are used to obtain a  
 CC ligand of the peptide using affinity purification, and to detect and  
 CC quantitate the amount of a target antigen of the Ig. When the peptide is  
 CC a B-cell epitope, the conjugates are used to label B-cells, and when the  
 CC peptide is a helper T-cell epitope, the conjugates are used to test the  
 CC ability of a subject to mount an immune response to that epitope. The  
 CC conjugates are more effective in eliciting an immune response than  
 CC unconjugated peptides. The conjugates increase the half-life of the  
 CC peptide and also, via binding of the Fc region of the Ig to cell-surface  
 CC receptor, recruit elements of the immune system to improve the overall  
 CC efficiency of the immune response.  
 XX Sequence 20 AA;

Query Match 50.0%; Score 5; DB 18; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 74;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPLPP 5  
 |||||  
 Db 6 QPLPP 10

RESULT 54  
 AAW60693  
 ID AAW60693 standard; peptide; 20 AA.  
 AC AAW60693;  
 XX  
 XX 22-SEP-1998 (first entry)  
 DT  
 DE Mycobacteria heat shock protein T cell epitope (residues 350-369).  
 XX  
 XX Immunisation; target antigen; epitope; inoculation; infant mammal;  
 KW viral antigen; depressed humoral response; respiratory syncytial virus;  
 KW rotavirus; measles virus; human immunodeficiency virus; hepatitis virus;  
 KW herpes simplex virus; influenza virus; Streptococcus pneumoniae;  
 KW Hemophilus influenzae; Neisseria meningitidis; Staphylococcus aureus;  
 KW protozoan antigen; malaria; heat shock protein.  
 XX  
 OS Mycobacterium sp.  
 XX  
 XX WO9822145-A1.  
 PN  
 XX  
 XX 28-MAY-1998.  
 PD  
 XX  
 XX 21-NOV-1997; 97WO-US21687.  
 PF  
 XX  
 XX 22-NOV-1996; 96US-0755034.  
 PR  
 XX  
 XX (MOUN ) MOUNT SINAI SCHOOL MEDICINE.  
 PA  
 XX  
 XX Bona C, Bot A;  
 PI  
 XX  
 XX WPI; 1998-312182/27.  
 DR  
 XX  
 XX Immunisation of infant mammals - by inoculating the mammal with a  
 PT nucleic acid encoding a relevant epitope of a target antigen  
 PT  
 XX  
 XX Disclosure; Page 10; 83pp; English.  
 PS  
 XX  
 XX Sequence shown in AAW60683 to AAW60700 are epitope sequences of various  
 CC viral antigens used to exemplify the method of invention of immunising  
 CC an infant mammal against a target antigen. The method comprises

CC inoculating the mammal with a nucleic acid encoding a relevant epitope  
 CC of a target antigen in a carrier, such that the relevant epitope is  
 CC expressed in the infant mammal. The genetic immunisation of infant  
 CC mammals can give rise to effective cellular (including the induction of  
 CC cytotoxic T lymphocytes) and humoral immune responses against the target  
 CC antigen. The methods are particularly used for treating infants with the  
 CC depressed humoral responses, that have high-zone tolerances against the  
 CC target antigens or have a Th2 biased immune response. The target antigen  
 CC may be a viral antigen, e.g. a respiratory syncytial virus antigen, a  
 CC rotavirus antigen, a measles virus antigen, a human immunodeficiency  
 CC virus antigen, a hepatitis virus antigen, a hepatitis B virus antigen, a  
 CC herpes simplex virus antigen or an influenza virus antigen, a bacterial  
 CC antigen e.g. Streptococcus pneumoniae antigen, Hemophilus influenzae  
 CC antigen, Neisseria meningitidis antigen, Staphylococcus aureus antigen  
 CC or a protozoan antigen such as a malaria antigen.  
 XX

Sequence 20 AA;  
 Query Match 50.0%; Score 5; DB 19; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 74;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPLPP 5  
 |||||  
 Db 6 QPLPP 10

RESULT 55  
 ABB79926  
 ID ABB79926 standard; Peptide; 20 AA.  
 XX  
 AC ABB79926;  
 XX  
 XX 12-DEC-2002 (first entry)  
 DT  
 DE Mycobacterium heat shock protein T-cell epitope.  
 XX  
 XX Vaccine; genetic immunisation; gene therapy; antigen; epitope;  
 KW heat shock protein; T-cell; T-lymphocyte.  
 XX  
 OS Mycobacterium sp.  
 XX  
 XX US2002115625-A1.  
 PN  
 XX 22-AUG-2002.  
 PD  
 XX 08-MAR-2001; 2001US-0801540.  
 PF  
 XX 19-MAY-1999; 99US-0308511.  
 PR  
 XX (BOTA/) BOT A.  
 PA (BONA/) BONA C.  
 XX  
 XX Bot A, Bona C;  
 XX  
 XX WPI; 2002-712482/77.  
 DR

Immunizing an infant mammal against a target antigen or inducing a  
 PT cytotoxic T cell response against a pathogen in the mammal, comprises  
 PT administering nucleic acid encoding relevant epitopes of pathogen  
 PT associated target antigens -  
 XX  
 PS Disclosure; Page 4; 45pp; English.  
 XX  
 XX The present sequence is that of a T-cell epitope from Mycobacteria  
 CC heat shock protein (residues 350-369). This is a Th epitope which,  
 CC in the context of MHC Class II self antigens, may be recognised by a  
 CC helper T-cell and thereby promote B-cell antibody production via the  
 CC Th cell. It is an example of T-cell epitopes which may be used  
 CC according to the invention. The invention relates to immunising an  
 CC infant mammal against a target antigen or inducing a cytotoxic T-cell  
 CC response against a pathogen. The method involves inoculating the  
 CC infant with a nucleic acid encoding one or more relevant epitopes of

CC one or more target antigens associated with the pathogen in a carrier,  
 CC so that the relevant epitope(s) is expressed in the infant mammal.  
 CC B- or T-cell epitopes may be used, and the pathogen may be a virus,  
 CC bacterium, protozoan, fungus, yeast, or parasite. The method may  
 CC reduce the need for subsequent boost administrations and may  
 CC prevent the side-effects associated with live attenuated vaccines.  
 CC Administration of multiple epitopes directed to antigens  
 CC associated with more than one pathogen may provide an infant with a  
 CC broader spectrum of protection, and may be a means for inducing an  
 CC immune response to a variety of childhood pathogens.  
 XX  
 XX

SQ Sequence 20 AA;

Query Match 50.0%; Score 5; DB 23; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 74;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPLPP 5  
 |||||  
 Db 6 QPLPP 10

RESULT 56

AAR80055  
 ID AAR80055 standard; peptide; 4 AA.

XX  
 AC AAR80055;

XX DT 25-APR-1996 (first entry)

XX XX Peptidase substrate #9.

XX KW Peptidase; o-phenanthroline; 2-mercaptoethanol; oligoproline;  
 KW cerebral function.

XX OS Synthetic.

XX FN JP07227281-A.

XX PD 29-AUG-1995.

XX PF 15-FEB-1994; 94JP-0042027.

XX PR 15-FEB-1994; 94JP-0042027.

XX PA (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.

XX PA (NIHA-) NIPPON HAM KK.

XX DR WPI; 1995-331519/43.

XX PT 140 kDa peptidase hydrolyses proline rich proteins - useful for  
 PT prevention and treatment of diseases related to proline rich  
 PT proteins and studies of cerebral functions

XX PS Example 4; Page 6; 7pp; Japanese.

XX CC The sequences represented by AAR80046 and AAR80048-R80059 are substrates  
 CC for the novel peptidase of the invention. The peptidase hydrolyses  
 CC P-P-P, P-P-P, and P-P and recognises the proline at the second residue  
 CC from the N-terminal of a peptide to release the N-terminal amino acid.  
 CC The enzyme's activity is stimulated with MnCl2 and inhibited with  
 CC o-phenanthroline and 2-mercaptoethanol. The peptidase is useful for the  
 CC hydrolysis of proline containing physiologically active peptides.  
 CC oligoproline and proline rich proteins in the living body, particularly  
 CC in the brain of mammals. The peptidase is useful for the prevention and  
 CC treatment of proline rich protein related diseases and study of cerebral  
 CC functions.  
 XX

SQ Sequence 4 AA;

Query Match 40.0%; Score 4; DB 16; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5  
 |||||  
 Db 1 PLPP 4

RESULT 57

AA45075  
 ID AA45075 standard; peptide; 5 AA.

XX AC AA45075;

XX DT 31-MAY-2000 (first entry)

XX DE Rat amelogenin N-terminal peptide.

XX KW Amelogenin; splice variant; rat; chondrogenesis; osteogenesis;  
 KW chondrogenic inducing molecule; CIM; cartilage growth; osteopathic;  
 KW extracellular matrix protein; tooth enamel; enamel mineralisation;  
 KW ameloblast; bone regeneration; composite cell construct.  
 XX

OS Rattus sp.

XX FN WO200006734-A1.

XX PD 10-FEB-2000.

XX PF 29-JUL-1999; 99WO-US17342.

XX PR 29-JUL-1998; 98US-0094489.

XX XX (NOUN ) UNIV NORTHWESTERN.

XX PI Veis A, Nebgen DR;

XX DR WPI; 2000-205464/18.

XX PT Novel amelogenin polypeptides and polynucleotides, useful for enhancing  
 PT bone generation in mammals and synthesizing bone matrix or articular  
 PT surfaces at implant sites -  
 XX

XX PS Example 1; Page 70; 79pp; English.

XX CC The present sequence is the amino terminal peptide of the secreted form  
 CC of rat amelogenin protein, that corresponds to amino acids 1-5. This  
 CC peptide is used to design forward PCR primer P1, to clone and sequence  
 CC amelogenin protein. This peptide is highly conserved in bovine, pig  
 CC and human species. The amelogenin splice variants functions as an  
 CC osteogenic or chondrogenic inducing molecule (CIM), which is useful for  
 CC enhancing bone or cartilage growth. It has osteopathic activity.  
 CC Amelogenin belongs to the family of extracellular matrix proteins, in  
 CC developing tooth enamel, that are produced by the ameloblasts and plays  
 CC a role in enamel mineralisation. Chondrogenic or osteogenic inducing  
 CC amelogenin molecules are useful to induce differentiation of cells to  
 CC the osteogenic and chondrogenic phenotypes and can be used in a  
 CC composite cell construct for bone and cartilage regeneration. The  
 CC polynucleotides can be employed to produce the polypeptides by  
 CC recombinant techniques.  
 XX

SQ Sequence 5 AA;

Query Match 40.0%; Score 4; DB 21; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5  
 |||||  
 Db 2 PLPP 5

RESULT 58

AAR28486  
 ID AAR28486 standard; peptide; 6 AA.